

# SEARCH REQUEST FORM

Requestor's Name: GAMBEL Serial Number: 023/427551  
Date: 12/17/1967 Phone: 302-3977 Art Unit: 1215

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

SEQUENCE INTERFERENCE SEARCH

SEQUENCE / INTERFERENCE

SEQ ID NOS. 1-12

11 (1-12) (1-12) (1-12)

APR 1962 (SIF 71 154 397 351)

(1) INTERFERENCE

(2) B7(W) 104 107(W) 2

(3) (1) + (2) PRINT FOR OFFICIAL USE ONLY

(4) (2) (4) (16 C10 OR 7 C10 OR)

20 C3 OR 7 C6

PRINT

REQUEST INFO

REMARKS

1-12

## STAFF USE ONLY

Date completed: 12/17/67  
Searcher: \_\_\_\_\_  
Terminal time: \_\_\_\_\_  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: \_\_\_\_\_  
Number of Searches: 2  
Number of Databases: 2

### Search Site

\_\_\_\_ STIC  
\_\_\_\_ CM-1  
\_\_\_\_ Pre-S

### Type of Search

☒ N.A. Sequence  
☒ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_ IG Suite  
\_\_\_\_ STN  
\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
\_\_\_\_ Other

\*\*\*\*\*

US-08-487-550-Lrge

\*\*\*\*\*

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 20:52:14 1996; MasPar time 430.89 Seconds  
1243.553 Million cell updates/sec.

Tabular output not generated.

Title: >US-08-487-550-1  
Description: (1-705) from US08487550.seq  
Perfect Score: 705  
N.A. Sequence: 1 ATGAGGTCGCCGCTCAGCT.....CCCTACAGAACTTCATGA 705  
Comp: TACTCCAGGGCCAGTCGA.....GGGATCTTACAGTACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 270440 seqs, 380027776 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb1-new3

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PIN  
9:PRI1 10:PRI2 11:PRO 12:ROD 13:SYN 14:UNC 15:VRT  
16:VIR1 17:VIR2

Database: genbank92

18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7  
25:BCT8 26:BCT9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5  
32:INV6 33:MAM1 34:MAM2 35:PAT1 36:PAT2 37:PAT3 38:PHG  
39:PLN1 40:PLN2 41:PLN3 42:PLN4 43:PLN5 44:PLN6 45:PLN7  
46:PLN8 47:PRI1 48:PRI2 49:PRI3 50:PRI4 51:PRI5 52:PRI6  
53:PRI7 54:PRI8 55:PRI9 56:PRI10 57:PRI11 58:PRI12  
59:PRI13 60:ROD1 61:ROD2 62:ROD3 63:ROD4 64:ROD5 65:ROD6  
66:ROD7 67:STR 68:SYN 69:UNA 70:VRL1 71:VRL2 72:VRL3  
73:VRL4 74:VRL5 75:VRL6 76:VRL7 77:VRT1 78:VRT2 79:VRT3

Database: genbank-new1

80:BCT 81:INV1 82:INV2 83:MAM 84:PHG 85:PIN 86:PRI  
87:ROD 88:STR 89:SYN 90:UNA 91:VRL 92:VRT  
93:part1

Database: u-emb145\_92

93:part1

Statistics: Mean 10.856; Variance 4.427; scale 2.452

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	ID	Description	Pred. No.
1	550	78.0	803 51	HSIGVL022	Human rearranged immu	0.00e+00
2	541	76.7	747 51	HSIGVL031	Human rearranged immu	0.00e+00
3	486	68.9	725 51	HSIGVL002	Human rearranged immu	0.00e+00
4	478	67.8	839 51	HSIGVL026	Human rearranged immu	0.00e+00
5	478	67.8	872 56	HUMIGLAM2	Human Ig rearranged 1	0.00e+00
6	474	67.2	791 51	HSIGVL028	Human rearranged immu	0.00e+00
7	472	67.0	737 51	HSIGVL023	Human rearranged immu	0.00e+00
8	472	67.0	780 51	HSIGVL011	Human rearranged immu	0.00e+00
9	468	66.4	806 51	HSIGVL005	Human rearranged immu	0.00e+00
10	449	63.7	664 51	HSIGVL004	Human rearranged immu	0.00e+00
11	427	60.6	750 51	HSIGVL027	Human rearranged immu	0.00e+00
12	421	59.7	810 51	HSIGVL025	Human rearranged immu	0.00e+00
13	421	59.7	870 51	HSIGVL	Human mRNA for Ig lam	0.00e+00
14	419	59.4	802 51	HSIGVL032	Human rearranged immu	0.00e+00
15	417	59.1	747 51	HSIGVL006	Human rearranged immu	0.00e+00
16	408	57.9	827 51	HSIGVL021	Human rearranged immu	0.00e+00
17	407	57.7	642 59	S42404	Ig lambda chain=anti-	0.00e+00
18	406	57.6	600 86	HUMIGTAT7F	Homo sapiens (clone t	0.00e+00
19	406	57.6	600 56	HUMIGTAT7F	Homo sapiens (clone t	0.00e+00
20	406	57.6	600 10	HSIGTAT7F	Homo sapiens (clone t	0.00e+00
21	404	57.3	877 56	HUMIGHEPAL	Human (hybridoma H210	0.00e+00
22	403	57.2	915 51	HSIGVL009	Human rearranged immu	0.00e+00
23	402	57.0	663 9	HS07991	Human lymphoma immuno	0.00e+00
24	402	57.0	663 52	HSU07991	Human lymphoma immuno	0.00e+00
25	400	56.7	783 51	HSIGVL001	Human rearranged immu	0.00e+00
26	397	56.3	756 51	HSIGVL034	Human rearranged immu	0.00e+00
27	394	55.9	666 52	HSU07992	Human myeloma immunog	0.00e+00
28	394	55.9	666 9	HS07992	Human myeloma immunog	0.00e+00
29	391	55.5	819 51	HSIGVL029	Human rearranged immu	0.00e+00
30	381	54.0	652 56	HUMIGLVX	Human immunoglobulin	0.00e+00
31	374	53.0	585 10	HSIGTATAB	Homo sapiens (clone t	0.00e+00
32	374	53.0	585 56	HUMIGTATAB	Homo sapiens (clone t	0.00e+00
33	374	53.0	585 86	HUMIGTATAB	Homo sapiens (clone t	0.00e+00
34	374	53.0	820 51	HSIGVL024	Human rearranged immu	0.00e+00
35	367	52.1	755 51	HSIGVL033	Human rearranged immu	0.00e+00
36	360	51.1	805 34	S66247	Ig lambda =immunoglob	0.00e+00
37	360	51.1	805 33	MVIGLAM	M.vison immunoglobuli	0.00e+00
38	350	49.6	838 51	HSIGLEV	Human mRNA for Ig lam	0.00e+00
39	339	48.1	780 51	HSIGVL030	Human rearranged immu	0.00e+00
40	339	48.1	881 56	HUMIGLYM1	Human immunoglobulin	0.00e+00
41	334	47.4	623 59	S77011	[pseudogene] Ig V lam	3.95e-302
42	331	47.0	577 59	S77601	anti-carcinoma surfac	4.91e-299
43	329	46.7	868 34	MVIGLVJCA	Mink immunoglobulin 1	5.67e-297
44	318	45.1	441 51	HSIGLCZA	H.sapiens gene for Ig	1.23e-285
45	318	45.1	8381 51	HSIGU266	Human U266 rearranged	1.23e-285

## ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM
1	HSIGVL022	Human rearranged immunoglobulin	X57812	g33723	Ig lambda light chain; immunoglobulin.	human.	Homo sapiens
	803 bp	RNA					Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
	04-NOV-1994	PRI					



Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrápoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo

REFERENCE	1 (bases 1 to 803)
AUTHORS	Klobeck, H.G.
TITLE	Direct Submission
JOURNAL	Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
REFERENCE	2 (bases 347 to 393)
AUTHORS	Combratio, G. and Klobeck, H.G.
TITLE	V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism
JOURNAL	Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE	91257162
COMMENT	for overlapping sequences see: X51754-55; J00252-54; M15641-42.

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NCBI gi: 33723
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                        /tissue_type="spleen"
                        /cell_type="B-cell"
                        /clone_lib="phage library cML"
                        /clone="cML2"
                        /isolate="individual ML"
                        /chromosome="22"
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                        /evidence="experimental"

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/gene="immunoglobulin lambda light chain"
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/translation="MAWTVLLGLLHCTGSVTSVLTPTSPSVAPKAAIRTCGGI
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/notes="variable region; V(lambda)III"
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/genes="immunoglobulin lambda light chain"
/notes="J-segment"
392..711
/genes="immunoglobulin lambda light chain"
/notes="constant region"
177 a 254 c 226 g 146 t
BASE COUNT
ORIGIN

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Query Match 78.0%; Score 550; DB 51; Length 803;  
Best Local Similarity 92.8%; Pred. No. 0.00e+00;  
Matches 596; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Db 68 cctatgtgtgactcagccacctcggctcagtcggtgccccaggaagcgccaggatta 127  
|||||

Qy	62	CTATGAACTGACTCAGCCACCTCGGTGTCTCACTGTCCCGAGCAGACAGAGCCGACGATCA	121
Db	128	ctgtgggggaatcaacattgcaagtcaaaagtgtgcactggtaccagcagagaagccagggc	187
Qy	122	CTGTGGGGGAGACAACAGTAGTAATAATGATGTCCATGTGTACAGCAGAGCCGACGGC	181
Db	188	aggccctgtgctgctcgtctatgtagtagcagcggccctcagggaatccctgaacat	247
Qy	182	GGGCCCCATATATGCTATGATATGATAGTACCGGCCCTCAGSGATCCCTGACGAT	241
Db	248	tctctggtcccaactctgggaacacagccaccctgaaacatcagtagggtcgaacccgggg	307
Qy	242	TCTCTGGCTCAAATCATAGGGAACACCGCCACCTGCACCATCAACGGGGTGCAGCGCGGGG	301
Db	308	atgagcgcgcctattactgctcaggtgtgggtagtagtagatgatcatgtggtattcggcg	367
Qy	302	ATCAGGCTGACTATTACTGTCTAGGTGTGGACAGGGCTAGTGTGATCATCCGGTCTTCGGAG	361
Db	368	gagggaaccaagctgaccgtcctaggtcagcccaaggtgccctcggctcaactctgttcc	427
Qy	362	GAGGACCCGGGTGACCGTCTAGGTGAGCCAAAGCTGCGCCCTGGGTCACTCTGTGTCC	421
Db	428	cgccctctctgaggaagcttcaagccaagaagccacactggtgtgtctcataagtact	487
Qy	422	CGCCCTCTCTTGAGAGCTTCAAGGCCAACGAAGGCCACACTGTGTGTCTATTAAGTGACT	481
Db	488	tctaccggggagccgtacagctggcctggaaggcagatagcagcccgctcaagcgggag	547
Qy	482	TCTACCCGGGAGCCGTGACAGTGGCTTGGAAAGGCAGATAGCAGCCCCGTCAAGCGGGAG	541
Db	548	tggagacaccacacccctccaaacaagaacacaacagtcacggcgccacagctatctga	607
Qy	542	TGGAGACACACACCCCTCCAAACAAGCAACAACAGTACGCGGCCAGCAGCTACCTGA	601
Db	608	gcctgacgctgagcagtggaagtcaccacagaagtcacagctgccaggtcacgcatgaag	667
Qy	602	GCCTGACGCCCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTCAACGCATGAG	661
Db	668	ggagcaccgtggagaagcagctggccctaccagaatgtcat	709
Qy	662	GGAGACCGTGGAGAGACAGGTGGCCCCCTCAGAGATGTTGAT	703
RESULT	2		
LOCUS	HS1GV031	747 bp	RNA
DEFINITION	Human rearranged immunoglobulin lambda light chain mRNA.	PRI	04-NOV-1994

2	HSIGVL031	747 bp	RNA	PRI	04-NOV-1994
RESULT	Human rearranged immunoglobulin lambda light chain mRNA.				
LOCUS	X57821				
DEFINITION	g33741				
ACCESSION	ig lambda light chain; immunoglobulin.				
NID	human.				
KEYWORDS	human.				
SOURCE	homo sapiens				
ORGANISM	Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 747)				
AUTHORS	Klobeck, H.G.				
TITLE	Direct Submission				
JOURNAL	Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G. Klobeck, Inst fuer Physiologische Chemie, Physiokalishe Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany				
REFERENCE	2 (bases 340 to 386)				

**AUTHORS** Combiato, G. and Klobeck, H. G.  
**TITLE** V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism  
**JOURNAL** Eur. J. Immunol. 21 (6), 1513-1522 (1991)  
**MEDLINE** 91257162  
**COMMENT** for overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33741

Location/Qualifiers

1..747

/organism="Homo sapiens"

/tissue type="spleen"

/cell type="B-cell"

/clone\_lib="phage library cML"

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/note="variable region; V(lambda)III"

347..384

/gene="immunoglobulin lambda light chain"

/note="J-segment"

385..704

/gene="immunoglobulin lambda light chain"

/note="constant region"

BASE COUNT 171 a 230 c 211 g 135 t

ORIGIN

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Best Local Similarity 93.3%; Pred. No. 0.00e+00;

Matches 599; Conservative 0; Mismatches 40; Indels 3; Gaps 2;

Db 64 cctatgtgtgactcagccaccctcgtgtcagtggtcccccaggaagcagccagtatta 123

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Qy 62 CCTATGAACCTGACTCAGCCACCCTCGTGTCTCAGTGTCCCGGACAGAGCGCCAGGATCA 121

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 124 cctgtggggaaataaacattggaagtataaagtgtcactggtaccagcagcagcagccg 183

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 122 CTTGTGGGGAGACACAGTAGAATAATGAAATATGTCACCTGTTACAGCAGAGAGCGCC 181

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 184 agggccctgtgctgtgtctatgatagcagccgacctcagggatccctgagcgat 243

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Qy 182 GGGCCCTTACTGTGTCATCTATGATGATAGTGACCGCCCTCAGGGATCCTGAGCGAT 241

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Db 244 tctctgctccaactctgggaacacggccacctgacctcagcaggtctgaagccggg 303

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Qy 242 TCTGTGCTCCAAATCAGGAACACACCCGCCCTGACCATCAACGGGTCGAGCGCGGG 301

Db 304 atgagcgcagctattactgtcaggtgtggatagtagtagtgatg-t--ggtattcgcg 360

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Qy 302 ATGAGGCTGACTATTACTCTCAGGTGTGGGACAGGGCTAGTCATATCGGGTCTTCGGAG 361

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Db 361 gagggaccaagctgaccgtcctaggtcagcccaaggctgccccctcggtcactctgttcc 420

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Qy 362 GAGGACCGGGTGACCGTCTAGGTACGCCCAAGGCTGCCCTCGGTCACTCTGTTC 421

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Db 421 cgcctcctctgaggagcttcaagccaacaggccacactggtgtgtctcataagtgact 480

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Qy 422 CGCCCTCTCTCAGGAGCTTCAAGCCCAAGCCACACTGCTGTCTCATAGTGACT 481

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Db 481 tctaccggggagcctgacagtggtcctggaaggcagatagcagcccgctcaaggcgaggag 540

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Qy 482 TCTACCGGGAGCGGTGACAGTGGCTTGAAGGCAGTAGCAGCCCGCTCAAGGCGGGAG 541

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Db 541 tggagaccaccacccctccaaacaaagcaacaaagtaacgagcgccgagcagctatctga 600

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Qy 542 TGGAGACCAACACACCTCTCAACCAAGCAACAGCTACCGCGCCAGCAGCTACCTGA 601

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Db 601 gcctgacgctgagcagtggaagtcccacagaagctacagctgccaggtcacgcatgaag 660

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Qy 602 CCCTGACGCTGAGCAGTGGAAAGTCCACAGAGCTACAGTGCAGGTCACGATGAG 661

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 661 ggagcaccgtgagaagacagctggccctacagaatgttcat 702

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Qy 662 GGAGCCCTGGAAGACAGCTGGCCCTTACAGATGTTTCA 703

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 3

LOCUS

HSIGVL002 725 bp RNA PRI 04-NOV-1994

DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.

ACCESSION X57802

NID g33701

KEYWORDS Ig lambda light chain; immunoglobulin.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; Mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;

Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 725)

AUTHORS Klobeck, H.G.

Direct Submission

Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.

Klobeck, Inst fuer Physiologische Chemie, Physikalische Chemie

und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000

Muenchen 2, Germany

REFERENCE 2 (bases 355 to 401)

AUTHORS Combiato, G. and Klobeck, H.G.

V lambda and J lambda-C lambda gene segments of the human

immunoglobulin lambda light chain locus are separated by 14 kb and

rearrange by a deletion mechanism

Eur. J. Immunol. 21 (6), 1513-1522 (1991)

91257162

COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33701

Location/Qualifiers

1..725

/organism="Homo sapiens"

FEATURES

source

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/notes="constant region"
BASE COUNT 164 a 226 c 199 g 136 t
ORIGIN
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Query Match 68.9%; Score 486; DB 51; Length 725;
Best Local Similarity 90.2%; Pred. No. 0.00e+00;
Matches 579; Conservative 0; Mismatches 57; Indels 6; Gaps 5;

Db 82 cctatgagctgactcagcaccctcagtgccgtgtccccaggacagaccagcatca 141
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QY 62 CCTATGAATGACTCAGCACCCCTCGGTGTGTCAGTGTCCCGGAGACAGCGCCAGGATCA 121

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Db 202 actccctctgctgtgctatttcaagataagcagcgccctcaggagatccctcagagat 261
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Db 322 atgagctgactattactgtcaggcgtggagacag--c-agg-a-c-tgcggtattcgccg 375
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QY 302 ATCAGGCTGACTATTTACTGTGTCAGGTGTGGGACAGGGCTAGTGATCATFCGGGTCTCGGAG 361

Db 376 gagggaccaagctgacctctcctaggtcagcccaagctgccctcctcgtcactctgttcc 435
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Db 556 tggagaccacacaccctccaaacaagcaacaagtacgcgcgagcagctatctga 615
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Db 616 ccctgagccctgagcagtggaagctccacagaagctacagctgcccaggtcacgcataag 675
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QY 602 CCCTGACGCTGACGAGTGGAGTCCACAGAGCTACAGCTGCCAGGTCCACCCATGAAG 661

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QY 662 GGAGCAGCTGCGAAGACAGCTGGCCCTTACAGAAATGTTTCAAT 703

RESULT 4
LOCUS HSIQVL026 839 bp RNA PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57816
NID g33731
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 839)
AUTHORS Klobeck, H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
REFERENCE 2 (bases 354 to 400)
AUTHORS Combriato, G. and Klobeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33731 Location/Qualifiers
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Db 555 tggagaccaccacccctcccaacaagcaacaagtacgcggccagcagctatctga 614
Qy 542 TGGAGACCACCAACCTCCAAACAAGCAACAAGTACGCGGCCGACGACGACTACCTGA 601
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Qy 662 GGACGACCTGGAGAGACAGTGGCCCTACAGATGTTTCAT 703
RESULT 5 HUMIGLAM2 872 bp mRNA PRI 05-JAN-1995
LOCUS Human Ig rearranged lambda-chain mRNA VJC-region subgroup lambda-IV
DEFINITION from heterohybridoma H6-3C4.
ACCESSION M18645
NID gi86103
KEYWORDS C-region; V-region; immunoglobulin lambda;
immunoglobulin light chain; variable region subgroup lambda-IV.
SOURCE human hybridoma H6-3C4 (cell fusion of mouse myeloma NS1 cells and
human peripheral blood lymphocytes), cDNA to mRNA, clone
p3C4-lambda-4.
ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
REFERENCE 1 (bases 1 to 872)
AUTHORS Yamasaki,N., Komori,S. and Watanabe,T.
TITLE Complementary DNA for a human subgroup IV immunoglobulin
lambda-chain
JOURNAL Mol. Immunol. 24 (9), 981-985 (1987)
MEDLINE 88013904
COMMENT NCBI gi: 186103
FEATURES Location/Qualifiers
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BASE COUNT 211 a 269 c 220 g 172 t
ORIGIN 254 bp upstream of BamHI site.
Query Match 67.8%; Score 478; DB 56; Length 872;
Best Local Similarity 87.5%; Pred. No. 0.00e+00;
Matches 558; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
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	Db	153	ccaaggtagacagocctcagaacctatcatcaagctggtaccagcagaagccaagcaggc	212
	Qy	126	TGGGGGAGACAACGTAGAATAAATGTAATGTCCACTGCTACAGACAGACCAGCGCGGC	185
	Db	213	cccgtacctgtctcatctatgatgaacaacccgcctcaggatccccacgccattctc	272
	Qy	186	CCCTAACTTGTCATTGATGATGACTACGCGGCCCTCAGGGATCCTCAGCGAATTC	245
	Db	273	tggctccacctcaggaaacacagacttccttgaccatacctgggctcaggcggaagatga	332
	Qy	246	TGCTCCAATACAGGACACCGCCACCTTGACCATCAACGGGGTGACGGGGGATGA	305
	Db	333	ggctgaacttactgtaaactccgggacagcagtggttaacctctggtattcggcgagg	392
	Qy	306	GCGTGACTTAITGTCAGGTCTGGACAGAGGGCTAGTGATCATCCGGTCTTCGGAGAGG	365
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	Db	453	ctectctgaggagctccaagccaacaggccacactggtgtctcataagtgactctcta	512
	Qy	426	CTCTCTCAGGAGCTTCAGGCCAACAGGCCACACTGGTGTGTCATAAGTGACTTCTA	485
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	Qy	486	CCGGGAGCCGTGACAGTGGCTTGGNAGCCATAGACAGCCCCGTCAAGCGGGAGTGA	545
	Db	573	gaccaccacacctccaacaaaacacaacagtacggcgccagcagctatctgagcct	632
	Qy	546	GACACACACACCTTCANACNAAGCANACACATACCGGGCCAGCAGCTACTGAGCCT	605
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	Qy	606	GACGCTCAGCAGTGGAAGTCCCACAGNAGCTACAGTGCACAGSTCACGCATGAAGGAG	665
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	Qy	666	CACCTTGAGAAACAGATGGCCCCCTACAGATGTTCAT	703

RESULT	6
LOCUS	HSIGVL028      791 bp      RNA      PRI
DEFINITION	Human rearranged immunoglobulin lambda light chain mRNA.
	04-NOV-1994

**KEYWORDS** Ig lambda light chain; immunoglobulin.

## ORGANISM

Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
 Eukaryotae; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
 Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
 Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 791)

**AUTHORS**  
Klobeck, H.G.  
**TITLE**  
Direct Submission  
**JOURNAL**  
Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G. Klobeck, Inst fuer Physiologische Chemie, Physiokalishe Biochemie

REFERENCE	und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
AUTHORS	2 (bases 341 to 387)
TITLE	Combiato, G. and Klobeck, H. G. V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism
JOURNAL	Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE	91257162
COMMENT	For overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33735  
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## misc feature

67.385

## misc feature

348.385

## misc feature

386.705

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Best Local Similarity 89.3%; Pred.No. 0.00e+00;  
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62  
121

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Qy	486	CCCGGAGGCCCTGACAGTGGCTTGGAGGCAGATAGACGCCCTGACGCCGGAGTGA	545
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Qy	546	GACCACACACCTTCCAAACAAAGCAACAAAGTAGCGCGCCAGCAGCTACTCTGAGCCT	605
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Qy	606	GACGCTCAGCAGTGGAGTCCCAAGAGTACAGCTCCAGTCCAGCTACGCATGAAGGAG	665
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LOCUS		HSIGVL011	780 bp RNA PRI 20-JUL-1995
DEFINITION		Human rearranged immunoglobulin lambda light chain mRNA.	
ACCESSION		X57810	
NID		g3717	
KEYWORDS		Ig lambda light chain; immunoglobulin.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		1 (bases 1 to 780)	
AUTHORS		Klobeck, H.G.	
TITLE		Direct Submission	
JOURNAL		Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany	
REFERENCE		2 (bases 317 to 363)	
AUTHORS		Combiato, G. and Klobeck, H.G.	
TITLE		V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism	
JOURNAL		Eur. J. Immunol. 21 (6), 1513-1522 (1991)	
MEDLINE		91257162	
COMMENT		for overlapping sequences see: X51754-55; J00252-54; M15641-42.	

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Qy	62 CCTATGACTACTAGCCACCTCGGTGTCACTGCCAGACAGACGCCGACGATCA 121	
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Qy	122 CCTGTGGGGAGAACAGTAGTAAATGAAATATGTCCTGGTACAGCAGACGACGGC 181	
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Qy 602 GCCTGACCGCTGACGAGTGGAGTCCACAGAGCTACAGCTGCCAGCTACCGCATGAG 661
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Qy 662 GGAGCACCGTGGAGAGACAGTGGCCCTACAGAAATGTTTCAT 703
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RESULT 9 HSI6VL005 806 bp RNA PRI 04-NOV-1994
LOCUS Human rearranged immunoglobulin lambda light chain mRNA.
DEFINITION X57805
ACCESSION
NID g33707
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chosnata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 806)
AUTHORS Klobeck, H.G.
TITLES Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
REFERENCE 2 (bases 354 to 400)
AUTHORS Combratio, G. and Klobeck, H.G.
TITLES V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

FEATURES
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363..398
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399..718
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BASE COUNT 191 a 255 c 208 g 152 t
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Best Local Similarity 86.7%; Pred. No. 0.00e+00;
Matches 553; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
Db 79 tgaagtgaactcaggaccctactgtgtgtggccttgggacagacgtcaggatcaaatg 138
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Qy 66 TGAAGTACTCAGCCACCTCGGTGTCAGTGTCCCGACAGACAGCGGCAGGATCACCTG 125
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Db 139 ccaaggagacaccatcagaagtattatgcaagtgtaccagcagaagccaggacaggc 198
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Qy 126 TGGGGGAGACAGAGTAGAATATGATGATGATGATGATGATGATGATGATGATGAT 185
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Db 199 ccctacactctcatcaatggttaaagacacccgcctcagggtatccacagccgattctc 258
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Qy 186 CCCTATATCTGGTCTATCATGATGATGATGATGATGATGATGATGATGATGATGAT 245
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Db 259 tggctccacctcaggaacacagcttccttgaccatcaactgggactcaggcggaagatga 318
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Qy 246 TGGCTCAAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCCAGCGCGGGATGA 305
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Qy 306 GGCTGATATTACTGTCAGGTCTGGGACAGGGCTAGTATCATTCGGGTCTTCGGAGGAGG 365
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Db 379 gaccagctgaccgtccttaagtgcagcccaaggtgcgccctcggtcactctgttccccgc 438
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Db 439 ctctctgagagcttcaagccaacaagccacacactggtgtgtctcataagtgaactcta 498
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Qy 426 CTCCTCTGAGGAGCTTCAAGCCCAACAAAGGCCACACCTGCTGTCTCTAAGTCACTTCTA 485
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Db 499 cccggagccgtgacagtggcgtggaagcagatagcagcccgctcaagcgcgaggatgga 558
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Qy 486 CCCGGGAGCGGTGCAGTGGCTGGAAGGCAGATAGCAGCCCGTCAAGCGCGGAGTGA 545
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Qy 546 GACCAACACACCTCCAAACAAACACACACACACACACACACACACACACACACACAC 605
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Db 619 gacgctgagcagtggagtcccacagaagctacagctgccaggtcacgcatgaaggag 678
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Qy 606 GACCGCTGAGCAGTGGAGACTCCACAGAAAGCTACAGCTGCCAGGTACCGCATGAAGGAG 665
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Db 679 caccgtgagagaagacagtggccctcacagaatgttcat 716
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Qy 666 CACCGTGGAGAAGACAGTGGCCCTACAGAAATGTTTCAT 703
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RESULT 10 HSI6VL004 664 bp RNA PRI 04-NOV-1994
LOCUS Human rearranged immunoglobulin lambda light chain mRNA.
DEFINITION X57804
ACCESSION
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NID g33705  
KEYWORDS Ig lambda light chain; immunoglobulin.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 664)  
AUTHORS Klobeck, H.G.  
TITLE Direct Submission  
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.  
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie  
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000  
Muenchen 2, Germany  
REFERENCE 2 (bases 211 to 257)  
AUTHORS Combriato, G. and Klobeck, H.G.  
TITLE V lambda and J lambda-C lambda gene segments of the human  
immunoglobulin lambda light chain locus are separated by 14 kb and  
rearrange by a deletion mechanism  
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)  
MEDLINE 91257162  
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33705 Location/Qualifiers  
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/isolate="individual ML"  
/chromosome="22"  
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/db\_xref="PID:g33706"  
/translation="DSLRYFANWHRKQ GPAPILVYQNNRPSGIPGRSSSSGN  
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220..255  
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/note="J-segment"  
256..575  
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/note="constant region"  
BASE COUNT 165 a 212 c 178 g 109 t  
ORIGIN

Query Match 63.7%; Score 449; DB 51; Length 664;  
Best Local Similarity 89.2%; Pred. No. 0.00e+00;  
Matches 511; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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Qy 131 GAGACAACAGTAGAATATGTCCACTGGTACAGCAAGAACCCAGCGCGGCCCTA 190  
Db 61 tacttgtatctatggtcaaaaacacggccctcaggatcccaggccgattcttggct 120  
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Qy 191 TACTGGTCTATGATGATGACCGCGCCCTCAGGGATCCCTCAGCGATTCTCTGGCT 250  
Db 121 ccagctcaggaaaacacagcttcttgaccatactggggcccccaggcgaagatgagctg 180  
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Qy 251 CCAAAACAGGGAACACGCGCACCTGACCACTCAAGGGGTGAGCGCGGGGATGAGGCTG 310  
Db 181 acttattactgtacctccgggacagcagtggttaaccatctggtgtcggcggaggacca 240  
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Qy 311 ACTATTACTGTCTGCTGGACAGGCTAGTGATCATCCGGCTTCGGAGGAGGACCC 370  
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Db 301 ctgaggagctcaagcaaacaggccacactggtgtgtctcataagtgaacttctaccgg 360  
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Qy 431 CTGAGGAGGCTTCAAGGCAACAGGCCACACTGGTGTCTCTATAAGTCACCTTCTACCCGG 490  
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Qy 491 GAGCGCTGACAGTGGCTGGAAGGACAGATAGCAGCCGCTCAAGCGGGAGTGGAGACCA 550  
Db 421 ccacacctccaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac 480  
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Qy 551 CCACACCTCCAAAC 610  
Db 481 ctgagcagtggaagtcacacaaagctacagctccaggtcacgcatgaaggagcaccg 540  
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Qy 611 CTGAGCAGTGGAACTCCACAAAGCTACAGCTGCCAGGTACCGCATGAAGGGGACCCG 670  
Db 541 tggagaagcagtggtccctacagaatgttcat 573  
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Qy 671 TGGAGAAGACAGTGGCGCCCTACAGAGATGTTCA 703

RESULT 11  
LOCUS H5IGVL027 750 bp RNA PRI 20-JUL-1995  
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.  
ACCESSION X57817  
NID g33733  
KEYWORDS Ig lambda light chain; immunoglobulin.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;  
Homo.  
REFERENCE 1 (bases 1 to 750)  
AUTHORS Klobeck, H.G.  
TITLE Direct Submission  
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.  
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie  
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000  
Muenchen 2, Germany  
REFERENCE 2 (bases 338 to 384)  
AUTHORS Combriato, G. and Klobeck, H.G.  
TITLE V lambda and J lambda-C lambda gene segments of the human  
immunoglobulin lambda light chain locus are separated by 14 kb and  
rearrange by a deletion mechanism

JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)  
MEDLINE 91257162  
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33733 Location/Qualifiers  
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/clone\_lib="phage library cML"  
/clone="cML39"  
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/chromosome="22"  
CDS  
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/codon\_start=1  
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52..382  
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/note="variable region; V(Lambda)I"  
J\_segment  
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/gene="immunoglobulin lambda light chain"  
/note="J-J-segment"  
C\_region  
383..702  
/gene="immunoglobulin lambda light chain"  
/note="constant region"

BASE COUNT 168 a 246 c 196 g 140 t  
ORIGIN

Query Match 60.6%; Score 427; DB 51; Length 750;  
Best Local Similarity 87.5%; Pred. No. 0.00e+00;  
Matches 498; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Db 132 caacatcggaagttaactgtaaactggtaccagcagctcccaagaagcggccccaact 191  
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Qy 135 CAACAGTAGAATCAATATGTCCATGTGTACGACGAAGCCGCGGCGCCCTATACT 194  
Db 192 cctcatctatgtaataatcagcggccctcaggggtccctgaccgattctctggctcaa 251  
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Qy 195 GGTCACTATGATGATGATGACCGGCGCTCAGGATCCCTGAGCGATTCTCTGGCTCAA 254  
Db 252 gtctggcactcagctccctggcactcagtggggtccagctgaggtgaggtgatta 311  
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Qy 255 ATCAGGGAAACCGCCACCCCTGACCATCAACGGGGTGCAGGCGGGGATGAGGCTGACTA 314  
Db 312 ttactgtgcagcatggatgacagcctgaatggtgtggtattcggcggaggaccagact 371  
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Qy 315 TTACTGTGAGGTGTGGGACAGGGCTAGTCATCCGCTTCGGAGGAGGACCGGGT 374  
Db 372 gaccgtctcagtcacccaaggtgcccctcggtcactctgttcccgccctcctcga 431  
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Qy 375 GACCGTCTAGTGCAGCGCAAGGCTGCCCTCGCTCACTCTGTTCGCCGCTCTCTGA 434  
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Qy 435 CGAGCTTCAAGCCCAACAAGCCGACACTGGTGTCTCATAAGTGACTTCTACCGGGAGC 494  
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Db 552 accctccaaacaaacaaacagtcacgcggccagcagctatctgagcctgacgcctga 611  
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Qy 555 ACCCTCCAAACAAAGACAAACAGTAGTACGCGGCCAGACGCTACCTGAGCCTGACCCCTGA 614  
Db 612 gcagtggaagtccacagaagctacagctgcccagctcacgcataaaggagcagccgtgga 671  
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Qy 615 CCAGTGGAAAGTCCACAGAGCTACAGCTGCCAGCTCACCCATGAAGGAGGACCGCTGGA 674  
Db 672 gaagacagtggtccctacagaatgttcat 700  
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Qy 675 GAAGACAGTGGCCCTACAGAAATGTTTCAAT 703

RESULT 12  
LOCUS H5IGVL025 810 bp RNA PRI 04-NOV-1994  
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.  
ACCESSION X57815  
NID g33729

KEYWORDS Ig lambda light chain; immunoglobulin.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 810)  
AUTHORS Klobeck, H.G.  
TITLE Direct Submission  
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.  
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie  
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000  
Muenchen 2, Germany

REFERENCE 2 (bases 349 to 395)  
AUTHORS Combriato, G. and Klobeck, H.G.  
TITLE V lambda and J lambda-C lambda gene segments of the human  
immunoglobulin lambda light chain locus are separated by 14 kb and  
rearrange by a deletion mechanism  
Eur. J. Immunol. 21 (6), 1513-1522 (1991)

COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

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/clone="cML39"  
/isolate="individual ML"  
/chromosome="22"  
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/gene="immunoglobulin lambda light chain"  
/note="cDNA"  
/evidence=experimental  
sig\_peptide 6..62  
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DFYPGAVTVAKRADSPVKAGVETTPFSKSNKRYAASSYLSLTPQMKSHRSYSQV
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/note="variable region; V(lambda)I"
359..393
/misc_feature 359..393
/gene="immunoglobulin lambda light chain"
/note="J-segment"
394..713
/misc_feature 394..713
/gene="immunoglobulin lambda light chain"
/note="constant region"
BASE COUNT 176 a 275 c 211 g 148 t
ORIGIN
Query Match 59.7%; Score 421; DB 51; Length 810;
Best Local Similarity 87.0%; Pred. No. 0.00e+00;
Matches 495; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
Db 143 caacatcgccactaatgatgtatcgtaccagcaactcagagaagcgccccaact 202
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Qy 135 CAACAGTAGAATGAATATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
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Db 203 cctcatctataggataatcagcggccctcaggggtccctgacggattctctggctcaa 262
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Qy 195 GGTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 254
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Db 263 gtctggctcctcagcctcctggccatcagtggtccctcagtcagagatgagtgatga 322
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Qy 255 ATCAGGGACACGCCACCCCTGACCATCAGCGGGTCTGAGGGCGGGATGACGCTGACTA 314
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Db 323 ttactgtgcagcatggatgacagcctcagtggtccggtgttcggcgaggaggaacaaagt 382
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Qy 315 TTACTGTGAGGTGGGACAGGGCTAGTATCATCATCGGGTCTTTCGGAGAGGACCCGGGT 374
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Db 383 gaccgtcctaggtcagcccaaggtgcccctcggtcactctgttccgcccctcctctga 442
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Qy 375 GACCGTCTAGGTGAGCCCAAGGCGTCCCGCTCGGTGCTACTGTGTCCGCGCTCTCTGA 434
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Db 443 ggaggttcaagcaacaagcccaactggtgtgtcctaagtgaacttctaccggagc 502
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Qy 435 GGAGCTTACGCCCAACAGGCCACACTGGTGTGCTCATAAGTCACTTCTACCGGGAGC 494
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Db 503 cgtgacagtggtcgtggaagcagatagcagcccgctcaaggcggagtgagaccaccac 562
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Qy 495 CTGACAGTGGCCTGAAGCAGATAGAGCGCCGCTCAGCGGGGATGAGACACCCAC 554
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Db 563 accctccaacaagcaacaagtcacggtccgagcagcagctatctgagctgagcctga 622
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Qy 555 ACCCTCCAAACAAACAAAGTACGCGGCGCAGCACTACTGAGCTGAGCGCTGA 614
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Db 623 gcagtggaagtcaccacagactcagctgacagtcacgcatgaaggagcagcgtgga 682
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Qy 615 GCAGTGGAAAGTCCCAACAGACTACAGCTGCCAGGTCAAGCATGAGGGACGCGTGA 674
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Db 683 gaagcagtggtccctcaacagaatgtcat 711
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Qy 675 GAACAGAGTGGCCCTACAGAAATGTTTCAT 703

RESULT 13
LOCUS HSLGLV 870 bp RNA PRI 27-NOV-1995
DEFINITION Human mRNA for Ig lambda-chain.
ACCESSION X14583
NID g33394
KEYWORDS Ig light chain; immunoglobulin; lambda-immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS Kishimoto,T.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-1989) Kishimoto T., Yoshitomi Pharmaceutical
Industries Ltd, Research Labs, 7-25 Koyata 3-chome, Iruma Shi,
Saitama, 358 Japan
REFERENCE 2 (bases 1 to 414)
AUTHORS Kishimoto,T., Okajima,H., Okumoto,T. and Taniguchi,M.
TITLE Nucleotide sequences of the cDNAs encoding the V-regions of H- and
L-chains of a human monoclonal antibody with broad reactivity to
malignant tumor cells
Nucleic Acids Res. 17 (11), 4385 (1989)
JOURNAL 89296497
MEDLINE
COMMENT hybridoma; clones=4G12 L6
Data kindly reviewed (03-JUL-1989) by Kishimoto T.
NCBI gi: 33394 Location/Qualifiers
source 1..870
/organism="Homo sapiens"
/tissue_type="lymph node"
/cell_type="lymphocyte"
/cell_line="4G12"
sig_peptide 25..84
/note="signal peptide (AA -20 to -1)"
CDS 25..732
/note="pid:g33395; NCBI gi: 33395"
/codon_start=1
/product="lambda-chain precursor (AA -20 to 215)"
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/translation="MTCSPLLTLHLHCTGSAQSVLTQPPSVSAAPGQKVTISCSGS
SSNIGNYVSWYQQLPGTAPKLIIYNNKRP SGIPDRFSGKSGTSATLIGTIGTQCD
EADYTCGTWDSLSLACGVTGGTKLTVLQPKAAPSVTLFPPSSEELQANKATLVCLIS
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THEGSTVEKTVAPTECS"
misc_feature 85..375
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misc_feature 376..414
/note="J region"
misc_feature 415..729
/note="C region"
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ORIGIN
Query Match 59.7%; Score 421; DB 51; Length 870;
Best Local Similarity 87.0%; Pred. No. 0.00e+00;
Matches 495; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
Db 162 caacattgggaataattatctcctggtaccagcagctcccaaggaacagccccaact 221
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Qy 135 CAACAGTAGAATGAATATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
```

[illegible]



Dec 17 20:45

US-08-487-550-1.rge

29

DB . 669 gaagacagtggccctacagaatgttcat 697  
|||||  
QY 675 GAAGACAGTGGCCCCCTACAGAATGTTTCAT 703

Search completed: Tue Dec 17 20:59:32 1996  
Job time : 438 secs.

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Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	478	67.8	872	1	N81655	VDJC regions of human	0.00e+00
2	419	59.4	884	1	Q03609	Sequence encoding 4G1	1.13e-262
3	413	58.6	654	8	Q49835	Anti-HIV-1 recombinan	1.55e-258
4	404	57.3	902	6	Q35100	Antibody D lambda lig	2.46e-252
5	318	45.1	8387	3	Q22489	Human U266 lambda gen	3.05e-193
6	318	45.1	9071	3	Q23370	U266-Lambda gene and	3.05e-193
7	318	45.1	9071	3	Q22491	Human U266 lambda gen	3.05e-193
8	250	35.5	387	6	Q35904	Anti-CD4 V-lambda cod	8.24e-147

## ATTACHMENTS

RESULT	1
ID	N81655 standard; DNA; 872 BP.
AC	N81655;
DT	09-NOV-1990 (first entry)
DE	VBJC regions of human sperm-immobilising monoclonal antibody..
KW	Anti-human sperm-immobilising monoclonal antibody; leader region;
KW	variable region; joining region; constant region; sterility;
KW	vaccine; contraceptive; ss.
OS	Homo sapiens.
Key	Location/Qualifiers
FFH	40..729
CDS	
FT	/tag= a
FT	/product=VJC region
FT	misc_feature 91..375
FT	/tag= b
FT	/label=v_region
FT	misc_feature 376..412
FT	/tag= c
FT	/label=j_region
FT	misc_feature 413..729
FT	/tag= d
FT	/label=C_region
PN	J63126482-A.

PD 30-MAY-1988.  
PR 15-NOV-1986; 272412.  
PA (TOFU) TOA NENRYO KOGYO KK.  
DR WPI; 88-187839/27.  
DR P-PSDB; P81260.  
PT Cell strain producing human sperm-immobilising monoclonal antibody -  
PT has at least V-gene in H chain coding genetic family and V gene in L  
PT chain of DNA originating from antibody of sterile woman.  
PS Disclosure; ; 14pp; Japanese.  
CC A VDJC segment is inserted into pSC41ambda5 together with a  
CC leader region. A cell strain, pref. a myeloma cell, can  
CC produce the Ab with immobilising value (SI50) of at least 5000,  
CC sperm agglutination value at least 1:1600 dilution, specifically  
CC reacting against human ejaculated sperm. The product can be used  
CC as a vaccine and contraceptive.  
CC See also N81654-N81656.  
SQ Sequence 872 BP; 211 A; 269 C; 220 G; 172 T;  
  
Query Match 67.8%; Score 478; DB 1; Length 872;  
Best Local Similarity 87.5%; Pred. No. 0.00e+00; Indels 0; Gaps 0;  
Matches 558; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
  
Db 93 tgaactgaactcaggaacctgtgtgtctgtgacctgtggagacagacagtcaggatcacatg 152  
QY 66 TGAATGACTGACCCACCCCTGGTGTGCTGATCTGCCAGGACAGAGCGCCGATCACCTG 125  
  
Db 153 ccaaggagagcagcctcagaacctatcatgcaagtgtgtaccagcagaagcaagcagc 212  
QY 126 TGGGGGAGACAGACAGTACGAATGATATCTCCACTGTTACCGAGAGAGCGGCGGGC 185  
  
Db 213 cctgtactgtcatctatgatgaaacaacccgacctcagggtatccagaccattctc 272  
QY 186 CCTATATCTGTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 245  
  
Db 273 tggctccacctcaggaacacagcttctgtgacctcactgaggtcagcggaagtga 332  
QY 246 TGCGTCCAAATACAGGACACACCCACCTGACCATCAACGGGGTCCAGGCGGGGATCA 305  
  
Db 333 ggcctgaattactgaactccgggagcagcagtggttaacgtctggtatctcgcggaag 392  
QY 306 GGCTGACTATTACTGTGTCAGGTGTGGCAGAGGGCTAGTATCATCCGCTTCGGAGGAG 365  
  
Db 393 gaccaagctgacctgactaggtcagcccaaggtgccccctcggtcactctgtcccgcc 452  
QY 366 GACCCGGGTGACCGTCTTAGTTCAGCGCCAGGCTGCGCTGCTGCTGCTGCTGCTGCT 425  
  
Db 453 ctctctgaggagcttcaagcacaagccacactggtgtgtctcataagtgaattcta 512  
QY 426 CTCTCTGAGGAGCTTCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCC 485  
  
Db 513 cccgggagccgtgacagtgccctggaaggagatagcagcccgctcaagcgaggagtgga 572  
QY 486 CCGGGAGCGCGTGACAGTGGCGCTGGGAAGGCAGATAGCAGCCCGCTCAAGGGCGGAGTGA 545  
  
Db 573 gaccacacacccctccaaacaagaagaacaacagatagcgggcgacagctatctgagcct 632  
QY 546 GACCACACACCCCTCCAAACAAGAACAAACAAGTACGCGGGCCAGCAGCTACCTGACGCT 605  
  
Db 633 gacgacctgagcagtggaagtccacagaagctacagctgccaggtcacgcattgaaggag 692  
QY 606 GACGCTGAGCAGCTGGAGTCCACAGAGCTACAGCTGCCAGGTACCCGATGAGAGGAG 665  
  
Db 693 caccgtggaagaagcagtgcccccctacagaatgttcat 730

QY 666 CACCGTGGAGAGACAGACAGTGGCCCTACAGATGTTTAT 703  
  
RESULT 2  
ID Q03609 standard; cDNA; 884 BP.  
AC Q03609;  
DT 06-AUG-1989 (first entry)  
DE Sequence encoding 4G12 monoclonal antibody (MAB) L chain .  
KW 4G12 MAb; human lung cancer; oesophageal carcinoma; ss.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT CDS 25..729  
FT /\*tag= a  
FT /product=4G12 L  
FT misc feature 25..375  
FT /\*tag= b  
FT /label=V region 376..414  
FT misc feature 376..414  
FT /\*tag= c  
FT /label=J region 415..729  
FT misc feature 415..729  
FT /\*tag= d  
FT /label=C region 835..840  
FT polyA\_signal 835..840  
FT /\*tag= e  
FT /number=1  
FT polyA\_signal 856..861  
FT /\*tag= f  
FT /number=2  
PN J02046289-A.  
PD 15-FEB-1990.  
PF 05-AUG-1988; 196647.  
PR 05-AUG-1988; JP-196647.  
PA (YOSH) Yoshitomi Pharm. Ind. KK.  
DR WPI; 90-094983/13.  
DR P-PSDB; R05555.  
PT DNA base sequence coding for 4G12 monoclonal antibody - which reacts  
PT specifically with human lung cancer and oesophageal carcinoma.  
PS Disclosure; Page 549; 9pp; Japanese.  
CC Sequence is cloned and synthetic DNA/RNA of human Ab L chain C regions  
CC is used as probe to obtain sequences coding for 4G12 MAB.  
CC See also Q03607-Q03610.  
SQ Sequence 884 BP; 219 A; 286 C; 212 G; 166 T; 1 Others;  
  
Query Match 59.4%; Score 419; DB 1; Length 884;  
Best Local Similarity 86.8%; Pred. No. 1.13e-262;  
Matches 494; Conservative 0; Mismatches 75; Indels 0; Gaps 0;  
  
Db 162 caacattgggaataaattatgtatctgttaccagagctcccaagaaacagcccccaact 221  
QY 135 CAACAGTAGAATAATGATATGTCCACTGGTACCAGACAGCCAGCGGGGCCCTATACT 194  
  
Db 222 cctcatttatgacaataataagcgacctcagggtattcctgaccgattctctggctccaa 281  
QY 195 GGTCACTATCATATAGTAGTACCGGCCCTCAGGGATCCCTGAGCGGATTTCTTGGCTCAA 254  
  
Db 282 gttcgcacgtcagccaccctgggcatcaccgggacctccagctgggagcagcgccgatta 341  
QY 255 ATACGGAACACCCGCCACCCCTGACCATCAACGGGGTCCAGGCCGGGCGATGAGGCTGACTA 314  
  
Db 342 ttactcgggaacatggatagcagcctcgtggtggtggtattcgcggagggagccaagct 401  
QY 315 TTACTCTCAGGTGTGGCAGAGGGCTAGTATCATCCGGTCTTCGGAGGAGGAGCCCGGT 374



Dbb 402 gaccgtctcaagtcagcccaaggctgcccctcagtcacactctgttccgcctcctctga 461  
|||||  
Qy 375 CACCCTCTAGGTGAGCCCAAGGCTGCCCTCGCTCACTGTGTCCGCGCTCCTCTGA 434  
|||||  
Dbb 462 ggagcttcaagcccaagcccaagcactggtgtgtctcctaagtgacttctaccggagc 521  
|||||  
Qy 435 GGAGCTTCAAGCCCAAGAGGCGACACTGCTGTGTCTCAATAAGTCACTTCTACCGGGAGC 494  
|||||  
Dbb 522 cgtgacagtggcctggaaggcagatagcagcccgctcaaggcggagtgagacaccac 581  
|||||  
Qy 495 CGTGACAGTGGCTCGAGGCGAGTAGAGCGCCGCTGAGGCGGCGAGTGGAGCACAC 554  
|||||  
Dbb 582 accctccaaacaagcaacaagtcacgcgcccagcagctatctgagcctgacgcctga 641  
|||||  
Qy 555 ACCCTCCAAACAAGCAACAAGTAGCGGGCGACGACTACCTGAGCCTCAGCGCTGA 614  
|||||  
Dbb 642 gcaagtggagtcctccacagaagctacagctgccagctcagcagatgaaggagacacgtgga 701  
|||||  
Qy 615 CGAGTGAAGTCCCGCAGAGCTACAGCTGCGCAGGTACCGCATGAGGAGCACCGTGA 674  
|||||  
Dbb 702 gaagacagtggcccctacagaatttcat 730  
|||||  
Qy 675 GAAGACAGTGGCGCCCTACAGAATGTTTAT 703  
|||||

## RESULT 3

ID Q49835 standard; cDNA; 654 BP.  
AC Q49835;  
DT 27-APR-1994 (first entry)  
DE Anti-HIV-1 recombinant antibody 447-52D light chain coding sequence.  
KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;  
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;  
KW acquired immune deficiency syndrome; chimeric antibody;  
KW surface glycoprotein gp120; V3 loop; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1..654  
FT /\*tag= a  
FT /note= "encodes recombinantly modified 447-52D  
FT light chain"  
PN W09319785-A.  
PD 14-OCT-1993.  
PF 23-MAR-1993; U02629.  
PR 01-APR-1992; US-861701.  
PA (MERI ) MERCK & CO INC.  
PA (JOHN/) JOHNSON L S.  
PA (PFAR/) PFARR D S.  
PI Conley AJ, Emami EA, Johnson LS, Mark GE, Pfarr DS;  
DR WPI; 93-336600/42.  
DR P-PSDB; R42163.  
PT New recombinant human antibody - with HIV neutralising activity  
PT against at least two isolates, useful for preventing or treating  
PT infection in diagnosis, etc.  
PS Example 9; Fig 2B; 154pp; English.  
CC EBV-transformed cell lines and mouse-human heterohybridomas  
CC producing human MAbs specific for the gp120 V3 loop of HIV-1 MN  
CC isolate were obtained. MAB 447-52D was found to recognise the  
CC tetrapeptide motif GPGR, i.e. the Principal Neutralising  
CC Determinant common to the V3 loop of different HIV isolates.  
CC A recombinant Ab was produced in which the L chain V region was  
CC derived from 447-52D and to which a signal sequence and a L chain  
CC intronic sequence are appended, fused to a fragment contg. a short  
CC intronic segment of the human lambda 2 C region and the human

CC lambda 2 constant encoding domain.  
SQ Sequence 654 BP; 156 A; 199 G; 178 C; 121 T;  
Query Match 58.6%; Score 413; DB 8; Length 654;  
Best Local Similarity 87.4%; Pred. No. 1.55e-258;  
Matches 500; Conservative 0; Mismatches 69; Indels 3; Gaps 3;  
Dbb 81 cacattgggaataaattatgattggtaccagcagttcccaaggaacacgccccaaact 140  
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Qy 135 CAACAGTAGAATAATATGCTCACTGCTACCAAGCAAGCCGCGGGCCCTATACT 194  
|||||  
Dbb 141 cctcaattatggcaataataagcagccctcagggaattcctgaccgattctctggctcaa 200  
|||||  
Qy 195 GGTCACTATGATGATAGTAGACGGGCGCTCAGGATCCCTGAGCGATTCTCTGGCTCCA 254  
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Dbb 201 gtctggcagctcagccacccctgggcatcaccggactccagactgggagcagggccgatta 260  
|||||  
Qy 255 ATCAGGGACACACCCGCCCTGACCAATCAACGGGTGAGGCGGGGNTGAGGCTGACTA 314  
|||||  
Dbb 261 ttctcgcacaatgggatagcgccctgagtgctgattggtgttcggcgagggagaccaa 320  
|||||  
Qy 315 TTACTGTGAGGTGTGGACAG-GGC-T-AGTGATCATCCGGTCTTCGGAGAGGGACCG 371  
|||||  
Dbb 321 gctgaccgtcctaagtcaagcccaagctgcccctcgggtcactctgttccgcctcctc 380  
|||||  
Qy 372 GGTGACCGTCTAGTACAGCCCAAGGCTGCCCTCGGTCACTCTGTCCCGCCCTCCTC 431  
|||||  
Dbb 381 tgaggagttccaagcccaagcccaagcactggtgtgtctcataagtgacttctaccggg 440  
|||||  
Qy 432 TGAGGAGCTTCAAGCCCAAGGCCACACTGCTGTCTCTATAAGTCACTTCTACCGGG 491  
|||||  
Dbb 441 agcgtgacagtggtcctggaaggcagatagcagcccgctcaaggcggagtgagagacc 500  
|||||  
Qy 492 AGCGGTGACAGTGGCTGGAAGGCGCATAGACAGCCCGCTCAAGCGGGGAGTGGAGACCAC 551  
|||||  
Dbb 501 cacacctccaaagcaacaagtcacggcgccagcagctatctgagcctgacgc 560  
|||||  
Qy 552 CACACCTCCAAACAAGCAACAAGTACGCGGCGCCAGCAGCTACCTGAGCCTGACGCG 611  
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Dbb 561 tgagcagtggaagtcacacagaagctcaagctgccaggtcacgcatgaaggagaccgt 620  
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Qy 612 TGAGCAGTGGAAAGTCCACAGAGCTACAGCTGCCAGGTCCAGGTCAAGCATGAAGGGACACCGT 671  
|||||  
Dbb 621 ggagaagacagtggcccctacagaatttcat 652  
|||||  
Qy 672 GGAGAAGACAGTGGCGCCCTACAGAATGTTTAT 703  
|||||

## RESULT 4

ID Q35100 standard; DNA; 902 BP.  
AC Q35100;  
DT 19-MAY-1993 (first entry)  
DE Antibody D lambda light chain.  
KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;  
KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;  
KW murine; B5B3; polyadenylated; cDNA library; human; kappa; lambda; H; ss.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT CDS 32..739  
FT /\*tag= a  
FT sig peptide 32..88  
FT /\*tag= b  
FT misc\_RNA 89..154  
FT /\*tag= c



Best Local Similarity 99.7%; Pred. No. 3,05e-193;  
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7062 aggtcagcccaaggtgccccctcggtcactctgttcccgccctcctctgagagcttca 7121  
|||||  
Qy 384 AGTCAAGCCAGGCTGCCCTCGGTCACTCTGTTCGCCGCCCTCTCTGAGGAGCTTCA 443  
Db 7122 agccaacaagccacactggtgtctcataagtgaacttctaccggagacgtgacagt 7181  
|||||  
Qy 444 AGCCACAAAGGCCACACTGGTGTCTCTATAAGTCACTTCTACCCGGGAGCGGTGACAGT 503  
Db 7182 ggcctggaagccagatagcagccccctcaaggcggagtgagagaccacaccctccaa 7241  
|||||  
Qy 504 GGCCTGGAGGACATAGCAGCCCGCTCAAGGGGAGTGGAGACACACACACCTCCAA 563  
Db 7242 aaaaagcaacaagaatcacgcccgcagcagctatctgacctgacgctgagcagtgaa 7301  
|||||  
Qy 564 ACAGACCAACAAGTACGGCGGCAGAGCTACTGTGACGCTGACGCTGAGAGTGGAA 623  
Db 7302 gtccacagaagctacagtgccaggtcacgcgtgaaggagaccctggagaagacagt 7361  
|||||  
Qy 624 GTCCACAGAAGCTACAGTCCAGGTCCAGGTCAAGGGAGCACCGTGGAGAAGACAGT 683  
Db 7362 ggcctcacagaatgttcat 7381  
|||||  
Qy 684 GGCCTTACAGAATGTTTAT 703

## RESULT 6

ID Q23370 standard; DNA; 9071 BP.  
AC Q23370;  
DT 14-AUG-1992 (first entry)  
DE U266-Lambda gene and downstream murine Ig heavy chain enhancer.  
KW Lambda-E-mu; rearranged; immunoglobulin; light chain; transgene;  
KW B cell deficiency; common variable immunodeficiency; CVID;  
KW ATCC # 72003; ds.  
OS Chimeric Mus.  
PN W09204443-A.  
PD 19-MAR-1992.  
PF 27-AUG-1991; U06106.  
PR 29-AUG-1990; US-575006.  
PA (HARD ) HARVARD COLLEGE.  
PI Vasicek TJ, Leder P;  
DR WPI; 92-114351/14.  
PT B cell deficient transgenic FVB/N mice - comprise DNA encoding  
PT the lambda light chain of a non-human animal for modelling of B  
PT cell deficiency  
PS Disclosure; Fig 7; 41pp; English.  
CC DNA from the IgE-lambda human myeloma U266 cell line was digested  
CC with EcoRI and used to prepare a phage library. The clone  
CC containing the active lambda gene was identified by probing the  
CC library with a radiolabelled BamHI fragment of the human lambda 2  
CC gene. (The complete sequence of U266-lambda gene has EMBL Acc.#  
CC X51754). The lambda-E-mu construct was prepared by cutting the  
CC lambda construct at the HindIII site 0.9kb downstream of  
CC C(lamba)2. The fragment was blunt-ended and ligated to a 995bp  
CC XbaI fragment of pTAR-7 containing the mouse Ig heavy chain  
CC enhancer. The transgene construct was used to transfect mouse  
CC cells for the production of B cell deficient transgenic mice. The  
CC mice can be used to study e.g. X-linked agammaglobulinemia.  
SQ Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T;

Query Match 45.1%; Score 318; DB 3; Length 9071;

Best Local Similarity 99.7%; Pred. No. 3,05e-193;  
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7061 aggtcagcccaaggtgccccctcggtcactctgttcccgccctcctctgagagcttca 7120  
|||||  
Qy 384 AGTCAAGCCAGGCTGCCCTCGGTCACTCTGTTCGCCGCCCTCTCTGAGGAGCTTCA 443  
Db 7121 agccaacaagccacactggtgtctcataagtgaacttctaccggagacgtgacagt 7180  
|||||  
Qy 444 AGCCACAAAGGCCACACTGGTGTCTCTATAAGTCACTTCTACCCGGGAGCGGTGACAGT 503  
Db 7181 ggcctggaagccagatagcagccccctcaaggcggagtgagagaccacaccctccaa 7240  
|||||  
Qy 504 GGCCTGGAGGACATAGCAGCCCGCTCAAGGGGAGTGGAGACACACACACCTCCAA 563  
Db 7241 aaaaagcaacaagaatcacgcccgcagcagctatctgacctgacgctgagcagtgaa 7300  
|||||  
Qy 564 ACAGACCAACAAGTACGGCGGCAGAGCTACTGTGACGCTGACGCTGAGAGTGGAA 623  
Db 7301 gtccacagaagctacagtgccaggtcacgcgtgaaggagaccctggagaagacagt 7360  
|||||  
Qy 624 GTCCACAGAAGCTACAGTCCAGGTCCAGGTCAAGGGAGCACCGTGGAGAAGACAGT 683  
Db 7361 ggcctcacagaatgttcat 7380  
|||||  
Qy 684 GGCCTTACAGAATGTTTAT 703

## RESULT 7

ID Q22491 standard; DNA; 9071 BP.  
AC Q22491;  
DT 31-JUL-1992 (first entry)  
DE Human U266 lambda gene.  
KW Human myeloma U266 cell line; rearranged lambda gene; Ig;  
KW immunoglobulin light chain; pTAR-7; heavy chain enhancer;  
KW humoral immunity; transgenic mouse; ATCC No. 72003; ds.  
OS Chimeric Homo sapiens.  
PN W09204440-A.  
PD 19-MAR-1992.  
PF 27-AUG-1991; 106124.  
PR 29-AUG-1990; US-575005.  
PA (HARD ) HARVARD COLLEGE.  
PI Vasicek TJ, Leder P;  
DR WPI; 92-114348/14.  
PT B cell deficient transgenic non-human animals - comprise DNA  
PT encoding the U266 immunoglobulin light chain and an enhancer  
PT region used as models of B cell deficiency  
PS Disclosure; Fig 7; 41pp; English.  
CC This sequence is the EcoRI/HindIII fragment of the rearranged lambda  
CC gene isolated from human myeloma U266 cell line ligated to the mouse  
CC heavy chain enhancer. The resulting transgene was used in the  
CC production of transgenic mice in which the proportion of spleen cells  
CC which are mature B cells is not more than a quarter of that in  
CC wild-type animals. The animals are more susceptible to infectious  
CC diseases than the wild-type and are models for severe B cell

CC region and an antigen (Ag) binding portion of an old world monkey Ig

CC region :

CC as typical (mouse x human) x human hybridomas and produce their  
 CC respective Abs in concs. ranging up to 25 mg/1 in standard  
 CC suspension culture. The heavy variable (VH) and light variable (LH)  
 CC chains of Abs P21-1, ZM1-1, ZM1-2 and MD3-4 were isolated and  
 CC sequenced. Total RNA was extracted from 10(7) hybridoma cells  
 CC of each cell line. ss DNA was synthesized using AMV-reverse  
 CC transcriptase and oligo-dT as primer. PCRa were performed and  
 CC amplified DNA was size selected. ss DNA for sequencing was isolated  
 CC from each positive clone after superinfection with M13K07.  
 CC Sequencing was by the dideoxy chain termination method (Sanger  
 CC et al.). The codon 'AAR' in Q64053 was printed in the spec. as  
 CC 'AA', but since the encoded AA was Lys, 'R' was inserted as the  
 CC final nucleotide.  
 SQ Sequence 324 BP; 71 A; 86 C; 103 G; 64 T;

Query Match 31.9%; Score 225; DB 10; Length 324;  
 Best Local Similarity 85.7%; Pred. No. 7.77e-130;  
 Matches 270; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 10 ctgacgcagccgcctcggtgtcagtggtgcccagggcagcagccaggtatctctgtggc 69  
 QY 70 CTCACTCAGCCACCCTCGGTGTCTAGTGTCTCCAGGACAGAGCCAGGATCACTGTGGG 129  
 Db 70 ggagcaacattggagtaaaagtgtgaactggttcacagcaagaagccagggccct 129  
 QY 130 GGAGACACAGTAGAATAATATATGTCCACTGTGTACACAGAGCCAGCGCGGCCCT 189  
 Db 130 gtccgtggtgtatgatgataacgaagccctcaggcatttctgagcgattctgtggc 189  
 QY 190 ATACTGGTCATCTATGATCATAGTAGACGGCCCTCAGGATCCCTGAGCGATCTCTGGC 249  
 Db 190 tccaactctgggaacacggccaccctgaccatcagcaggtgtgaagccgggtgagggc 249  
 QY 250 TCCAAATCAGGAAACACGCCACCTTGACCATCAACGGGGTCGAGGCGCGGGATGAGGCT 309  
 Db 250 gactattactgtagtggatagtagtagtattggtattcggcgagggacc 309  
 QY 310 GACTATTACTGTGAGGTGGGACGGGCTAGTCATCATCGGCTTCGGGAGGAGGACC 369  
 Db 310 aagtgaccgtccta 324  
 QY 370 CGGGTGACCGTCTCTA 384

RESULT 10  
 ID Q11187 standard; cDNA to mRNA; 318 BP.  
 AC Q11187;  
 DT 31-MAY-1991 (first entry)  
 DE Immunoglobulin lambda chain constant region.  
 KW Antibody; canine distemper virus; parvovirus; hepatitis; ss.  
 OS Canis familiaris.  
 PN EP-419858-A.  
 PD 03-APR-1991.  
 PF 24-AUG-1990; 116258.  
 PR 25-AUG-1989; JP-219889.  
 PR 30-SEP-1989; JP-255425.  
 PR 07-JUN-1990; JP-150673.  
 PA (KAGA ) CHEMO-SERO-THERAP.  
 PI Maeda H, Eda Y, Kimachi K, Ono Y, Tokiyoshi S;  
 DR WPI; 91-095353/14.  
 DR P-PSDB; R11366.  
 PT Gene fragments coding for constant region of canine  
 PT immunoglobulin(s) - used to produce mouse-dog antibodies for  
 PT diagnosis, treatment and prevention of canine.

PS Claim 6; Page 15; 49pp; English.  
 CC The DNA encodes the constant region of canine Ig lambda chain. It can  
 CC be used to produce mouse-dog chimeric antibodies for the diagnosis,  
 CC treatment and prevention of canine diseases caused by e.g. canine  
 CC distemper virus, canine parvovirus and canine hepatitis virus.  
 CC See also Q11188-91.  
 SQ Sequence 318 BP; 69 A; 115 C; 91 G; 43 T;

Query Match 31.8%; Score 224; DB 2; Length 318;  
 Best Local Similarity 85.7%; Pred. No. 3.70e-129;  
 Matches 269; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 1 cagcccaaggtcccccctcggtcacactcttcccgcctctctcgtgaggtctcggtgcc 60  
 QY 388 CAGCCCAAGGCTGCCCTCGGTCACTCTGTTCGCCCTCTCTGAGGAGCTTCAAGCC 447  
 Db 61 aacaagccacccctggtgtcctcatcagcagacttctaccacagcggtgaggtggcc 120  
 QY 448 AACAAAGGCCACACTGGTGTCTCTAATAGTGACTTCTACCCGGGAGCCGTGACAGTGGCC 507  
 Db 121 tgaaggaagaagcagcccggtcacccagggcgtggagaccacacagccctccaagcag 180  
 QY 508 TGAAGGCCAGATAGCAGCCCTCAAGGGGGAGTGGAGACCAACACACCTCCAAACAA 567  
 Db 181 agcaacaacaagtacgcggcagcagctactcagcgtgagcctgacaagtggaaatct 240  
 QY 568 AGCAACAACAGTAGTACGGCCAGCAGCTACTGAGCTGACCCCTGAGCAGTGGAGTCC 627  
 Db 241 cacagcagcttcagctgctcagcagcagggagcagccgtggagaagaaggtggcc 300  
 QY 628 CACAGAAGCTACAGCTGCCAGGTCAACCATGAAGGAGCACCCTGGAGAAGACAGTGGCC 687  
 Db 301 ccgcagagtgctc 314  
 QY 688 CCTACAGAAATGCTTC 701

RESULT 11  
 ID Q11946 standard; DNA; 333 BP.  
 AC Q11946;  
 DT 15-AUG-1991 (first entry)  
 DE Anti-human Rhd PAG-1 MAb (VL chain).  
 KW Monoclonal antibody; rhesus D; blood-typing; CDR;  
 KW haemolytic disease of the newborn; HDN; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT misc\_feature 67..99  
 FT /\*tag= a  
 FT /label= CDR1  
 FT misc\_feature 145..165  
 FT /\*tag= b  
 FT /label= CDR2  
 FT misc\_feature 262..300  
 FT /\*tag= c  
 FT /label= CDR3  
 PN W09107492-A.  
 PD 30-MAY-1991.  
 PF 13-NOV-1990; E01964.  
 PR 13-NOV-1989; GB-025590.  
 PA (BLOO-) CENT BLOOD LAB AUTH.  
 PI Hughes- Jones N;  
 DR WPI; 91-178104/24.  
 DR P-PSDB; R12264.  
 PT DNA encoding complementary determining regions - of human

PT	anti-rhesus D antibodies, useful in prodn. of monoclonal			
PT	antibodies and for passive immunisation			
PS	Disclosure; Fig 3; 32pp; English.			
CC	The DNA sequence of eleven monoclonal antibodies are			
CC	represented in Q119145-57. Synthetic genes, for both heavy and			
CC	light chains may be created by combining selected CDR 1, 2, and 3			
CC	regions, which may be selected from different antibody mols. having			
CC	varied binding specificity. The chimaeric anti-RhD antibodies can be			
CC	used for diagnosis and therapy, and are capable of providing blood-			
CC	typing reagents of high specificity and reliability. They can also			
CC	be used in passive immunisation to prevent haemolytic disease of the			
CC	newborn.			
SO	Sequence	333 BP;	67 A;	93 C; 108 G; 65 T;

Query Match 31.3%; Score 221; DB 2; Length 333;  
Best Local Similarity 88.0%; Pred. No. 3.98e-127;  
Matches 256; Conservative 0; Mismatches 35; Indels 0; Gaps

2	cctatgtgctga	cagccacactc	ggctcagtg	cagtgcccgagacagcagccaggatta	61
62	ccatatcaact	tgactcagccac	ccctcgctg	ctcagtgccccagacagcagccagatca	121
62	cctgtggggg	aaacaacatt	ggacgtg	aaagtgtgcactggtaccagcagaagccaggcc	121
122	ccctgtgggg	gagacaac	actagataa	tatgtctccactggtaccagcagaagccagccg	181
122	aggccctgtg	ctgtctctat	gtgtgctag	cagccagccgcccctcagggaatccctgagcaat	181
182	ggcgccctt	atacttgct	atctatg	atgtagcagccgcccctcagggaatccctgagcaat	241
182	tctctggct	ccaactct	gggaaac	agcgccaccctgaccatcagcagaggtcgagcccgagg	241
242	tcctctggct	ccaaatca	gsgaaca	accgccaccctgcacatcaacgggtcgagcccgagg	301
242	atgagccqca	ctatctg	caggtg	gggatatgtagtadgtcctatccgg	292
302	atcagcctgc	actatctat	ctcaggtg	tgggacagcagggtagctatcatccgg	352

RESULT	12	
ID	Q10674	standard; DNA; 318 BP.
AC	Q10674;	
DT	24-MAY-1991	(first entry)
DE	Feline immunoglobulin lambda chain constant region TI-62 gene.	
KW	Feline immunoglobulin; fIg; lambda chain; chimaera; antibody; ss.	
OS	Felis catus.	
PN	EP-417486-A.	
PD	20-MAR-1991.	
PF	10-AUG-1990; 115426.	
PR	10-AUG-1989; JP-208822.	
PR	30-SEP-1989; JP-255424.	
PR	28-DEC-1989; JP-344465.	
PA	(KAGA ) CHEMO-SERO-THERAPEU.	
PI	Maeda H, Eda Y, Kimachi K, Ono Y, Tokiyoshi S;	
DR	WPI; 91-081793/12.	
DR	P-PSDB; R11012.	
PT	New DNA sequences encoding constant regions of feline	
PT	immunoglobulin - and new chimeric DNA expressing mouse-cat	
PT	antibodies, useful in prevention, treatment and diagnosis of	
PT	feline disease	
PS	Claim 7; Page 15; 35pp; English.	
CC	The cDNA library of cat-mouse heterohybridoma FM-T1 cells was used	
CC	to isolate the fIg gene.	
CC	The sequence is used to produce recombinant DNA encoding the L-chain	

CC of a mouse-cat chimaeric antibody having a mouse variable  
 CC region linked at its 3'-site to a feline constant region.  
 CC The antibody expressed by cells transformed with the recombinant  
 CC DNA is useful in diagnosis, treatment and prevention of feline  
 CC disease, without showing side effects.  
 CC See also Q10674-75 and Q10945-46.  
 SQ Sequence 318 BP; 77 A; 106 C; 88 G; 47 T;

Query Match 29.1%; Score 205; DB 2; Length 318;  
Best Local Similarity 83.0%; Pred. No. 2.63e-116;  
Matches 258; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Db	1	cagcccaagtcggcccccctcaggtcacactcttcccacacctccagtcgaggaagctcagcgca	60
Qy	388	CAGCCCAAGGTCGCCCTCGGCTCACTCTGTTCCGGCCCTCTCTGAGGAGCTTCAAGCC	447
Db	61	aacaaggccacccctggtgtgtctcgtcagtgacttctaccccagcggttgacggtggcc	120
Qy	448	AACAAGGCCACACTGGTGTGTCTCATAGTGACTTCTACCGGGAGCCGTGACAGTGGCC	507
Db	121	tggaaaggaaagtggcaccocccatcaccaaggggcgtggagaccaccaagccctccagacag	180
Qy	508	TGGAAGGACGATAGACGCCCTCAAGCGCGGAGTGGAGACCAACACACCTTCCAAACA	567
Db	181	agcaacaacaagtacggcgccagcagctacctgagcctgtcaccgaaacgagtggaaatct	240
Qy	568	AGCAACACAAAGTACCGGCCGACAGCGTACTTGAGCCTTGACCCCTGACAGTGGGAATGC	627
Db	241	cacagcatatcacctgccaggtcacgcacagggagcactgtgagaagaagtgtgtc	300
Qy	628	CACAGAAGCTACAGCTGCCGGTCAAGCATGAAGGAGACCGCTGGAAAGACAGTGGCC	687
Db	301	cttgcaagatg	311
Qy	688	CCTACAGAATG	698

```

RESULT 13
ID Q64170 standard; cDNA to mRNA; 318 BP.
AC Q64170;
DC
29-DEC-1994 (first entry)
DE Sequence of feline herpes virus (FHV-1) cDNA.
KW Feline herpes virus; FHV-1; monoclonal antibody; ss.
OS Felis catus.
FH Key
FT CDS
FT /*tag= a
PN W09412661-A.
PD 09-JUN-1994.
PF 25-NOV-1993; J01724.
PR 28-NOV-1992; JP-341255.
PA (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
PI WPI; 94-200288/24.
DR P-PSDB; R54096.
PT Feline monoclonal antibody and recombinant antibodies specific
PT for FHV-1 - for detection, treatment and prevention of FHV-1
PT infection.
PS Claim 20; Page 23-24; 53pp; Japanese.
CC The inventors claim a monoclonal antibody against feline herpes
CC virus (FHV-1), the sequence of which is given in Q64168, Q64169
CC and Q64170. They also claim a recombinant antibody against FHV-1
CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
CC used in the detection, treatment and prevention of FHV-1. The

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CC' sequences of the CDRs in the VH of the recombinant anti-FHV-1  
CC antibody are given in R54092. The sequences of the CDRs in the VL of  
CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR  
CC sequences are claimed.

Query Match 29.1%; Score 205; DB 11; Length 318;  
Best Local Similarity 83.0%; Pred. No. 2.63e-116;  
Matches 258; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

**Db** 1 cagcccaagtgcggccccctcggtcacactcttcccacacctccagtgaggagctcagcgca 60  
||||||| | ||||||||| || |||| ||||| ||||| ||||| ||  
**Qv** 388 CAGCCCAAGGTCGCCCGCTGGTCACTGTCTCCGCCCGCTCCTTGAGAGGCTTCAAGCC 447

**Db**      61    aacaagccacccctggtgtgtctcgtcagtgaacttctaccccaggcgcttgacgggtgcc    120  
             |||||  
**Ov**      448    AACAAGGCACACTGGTGTCTTCATPAAGTCACTCTACCGGCGAGCCCTCAGACTGCC    507

Db      121 tgaaggaagtggcaccgccatcaccaaggcgctggagaccaccaaagccctccagacag 180  
||||| |||| | ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Ov      508 TGCACCCATCATCAGCCCCCTCACCCCGGCACTCCACACCACACACTCTTCACAA 567

[illegible][illegible]

Db 301 cctgcagagtg 311  
||| |||| ||  
502

**RESULT 14**

AC Q33036;  
DT 06-MAY-1993 (first entry)  
DE MAB 1-3-1 variable region of heavy chain.

PN EP-520499-A.

26-JUN-1992; 110841.  
28-JUN-1991; JP-158859.  
28-JUN-1991; JP-158860.

PA (MITU ) MITSUBISHI KASEI CORP.  
PI Hirakawa Y, Hosokawa S, Ito N, Nagaïke K, Tagawa T;  
DR WPI. Q3-001328/01

Human monoclonal antibody specific for a cancer cell membrane surface antigen - prepd. from a hybridoma obtd. by cell fusion between human lymphocytes derived from cancer patients and mouse

PT myeloma cells  
PS Claim 17; Page 31 + 18; 37pp; English.  
CC A human MAB specifically binding to a surface antigen of cancer

CC chains having the amino acid sequences of R30145-46 respectively,  
CC encoded by DNA sequences Q33035-36 respectively.

SQ Sequence 324 BP; 82 A; 84 C; 93 G; 65 T;

Query Match 25.8%; Score 182; DB 5; Length 324;  
Best Local Similarity 78.1%; Pred. No. 8.15e-101;  
Matches 253; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

**Db**      1    tatgagctgacacagcaccctcggtgcagtgtccccaggacagccggatcaccc    60  
         |||||    |||||    |||||    |||||    |||||    |||||    |||||    |||||  
**Qv**      64    TATGAACTCACTCAGCCACCCTCGGTGTCACTGTCCCCAGGACAGCGCCAGATCAC    128

**Db** 61 tgctctggagatgcattgcaaaagaacatatgttattggtaccagcagaagccaggccag 120  
|| ||||| ||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
**Ov** 124 TGTGGGGGACACAACTAGAAAATGAATAATTCCACTGTGTACCAGCAGAAGCGACGCCGG 183

Db            121 gcccctgtgctgtgatataatagacagtgaaggccctcagggatccctgagcgattc 180  
               ||||| ||||| |||| | ||||| ||||| ||||| ||||| ||||| |||||  
  
Ouv          184 cccccctacttcctcawtatawcatgcatactcacccgccctcagccatatccctggaccattcc 243

[illegible]

Db  
241 gaggtgactattactgtcaatcagcacagcagtggctacttatgaggtagtttcgcgcga 300

Db 301 gggaacaaagt gaccgtcctaggt 324  
||||| | ||||| ||||| |||||

RESULT 15

AC N80473;  
DT 07-DEC-1990 (first entry)  
DE Insert of clone pZ183-1.

PN	EP-269127-A.
PD	01-JUN-1988.
PF	27-NOV-1987; 117619.

PR 27-NOV-1986; GB-026453.  
PR 14-JUL-1987; GB-016497.  
PR 14-OCT-1987; GB-024100.  
PA (HOFF ) HOFFMANN-LA ROCHE AG.

PT Nucleotide sequence selectively expressed in pre-B cells - used in probes for determining non-T acute lymphoblast leukaemia and PT

CC This is the 0.7 kb insert of transcript pZ 183 which is selected for prep. of polypeptide(s) Disclosure; p; English. PS

CC strong homology to the constant (C) region of lambda-1 light (L)  
CC chains. A strong homology is also seen between posns 201-239 and  
CC the joining (J) segment sequence of the lambda-1 L-chain.

SQ Sequence 701 BP; 163 A; 188 C; 165 G; 185 T;  
Query Match 25.7%; Score 181; DB 1; Length 701;

	Matches	271;	Conservative	0;	Mismatches	78;	Indels	2;	Gaps
Db	202	gtctttggtggtgggaaccagctcacaatcctaggtcagcccaagtctgacccttggtc	261						

Qy 352 GTCTTCGAGGAGGACCGGGTGACCGTCTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTC 411







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PAPER

(TM)

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MPerch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 21:01:21 1996; MasPar time 271.01 Seconds  
935.249 Million cell updates/sec

Tabular output not generated.

Title: &gt;US-08-487-550-1

Description: (1-705) from US08487550.seq

Perfect Score: 705

N.A. Sequence: 1 ATGAGGTCGCCGCTCAGCT.....GCCCTACAGAAATCTTCATGA 705

Comp: TACTCCAGGCGCGATCGA.....GGGATGCTTACAGTACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 514334 reqs, 179763086 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-STS

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50  
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56  
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62  
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68  
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74  
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80  
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86  
87:EST87 88:EST88 89:EST89 90:EST90 91:STS1 92:STS2  
93:STS3 94:STS4 95:STS5 96:STS6 97:STS7

Database: EST-STS-TW

98:EST91 99:EST92 100:EST93 101:EST94 102:EST95  
103:EST96 104:EST97 105:EST98 106:EST99 107:EST100  
108:EST101 109:gnEST1 110:gnEST2 111:gnEST3 112:gnEST4  
113:gnEST5 114:gnEST6 115:gnEST7 116:gnEST8 117:gnEST9  
118:gnEST10 119:gnEST11 120:gnEST12 121:gnEST13  
122:gnEST14 123:gnEST15 124:gnSTS1 125:gnSTS2 126:enEST1  
127:enEST2 128:enEST3 129:enEST4 130:enEST5 131:enEST6

132:enEST7 133:enEST8 134:enEST9 135:enEST10 136:enEST11  
137:enEST12

Statistics: Mean 10.439; Variance 2.086; scale 5.004

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
c	1	319	45.2	570	136	HS777270	yw91f04.s1 Homo sapie	0.00e+00
c	2	319	45.2	570	116	N32777	yw91f04.s1 Homo sapie	0.00e+00
c	3	299	42.4	469	66	R73382	yj92a11.s1 Homo sapie	0.00e+00
c	4	297	42.1	471	67	R73492	yj93d09.s1 Homo sapie	0.00e+00
c	5	296	42.0	463	11	H25405	y146h10.s1 Homo sapie	0.00e+00
c	6	292	41.4	376	12	H26070	y152h11.r1 Homo sapie	0.00e+00
c	7	290	41.1	436	61	R55314	y77h05.s1 Homo sapie	0.00e+00
c	8	280	39.7	491	69	R83196	yp87h10.s1 Homo sapie	0.00e+00
c	9	279	39.6	329	22	H60966	yr22c08.r1 Homo sapie	0.00e+00
c	10	278	39.4	435	71	R88208	yp08b06.s1 Homo sapie	0.00e+00
c	11	277	39.3	297	124	G13531	human STS SHGC-11074.	0.00e+00
c	12	275	39.0	443	137	HS851303	za22c10.s1 Homo sapie	0.00e+00
c	13	274	38.9	428	11	H25133	y143e10.r1 Homo sapie	0.00e+00
c	14	273	38.7	487	69	R83348	yp06b01.s1 Homo sapie	0.00e+00
c	15	272	38.6	431	11	H26023	y152h11.s1 Homo sapie	0.00e+00
c	16	271	38.4	356	24	H67544	yn68e12.r1 Homo sapie	0.00e+00
c	17	271	38.4	425	59	R48172	yj66g10.r1 Homo sapie	0.00e+00
c	18	270	38.3	470	8	H15922	y127e07.s1 Homo sapie	0.00e+00
c	19	267	37.9	428	17	H45690	yp23e04.s1 Homo sapie	0.00e+00
c	20	267	37.9	445	99	T67053	ya52e05.s1 Homo sapie	0.00e+00
c	21	267	37.9	509	17	H45859	yp22e04.r1 Homo sapie	0.00e+00
c	22	266	37.7	325	60	R49901	yj58a10.r1 Homo sapie	0.00e+00
c	23	264	37.4	410	66	R72739	yj91a09.s1 Homo sapie	0.00e+00
c	24	264	37.4	516	90	T57780	ycl4a06.s1 Homo sapie	0.00e+00
c	25	263	37.3	446	13	H30137	yo59f07.r1 Homo sapie	0.00e+00
c	26	261	37.0	387	19	H51320	yp07g04.s1 Homo sapie	0.00e+00
c	27	261	37.0	451	11	H23960	y130a03.s1 Homo sapie	0.00e+00
c	28	256	36.3	365	11	H25486	y147f08.r1 Homo sapie	0.00e+00
c	29	253	35.9	379	11	H24839	y142h08.r1 Homo sapie	0.00e+00
c	30	253	35.9	428	101	T71479	yd35f06.r1 Homo sapie	0.00e+00
c	31	253	35.9	434	10	H21406	y132h05.s1 Homo sapie	0.00e+00
c	32	253	35.9	512	88	T50252	yb78h04.s1 Homo sapie	0.00e+00
c	33	249	35.3	436	107	T94334	ye31e10.s1 Homo sapie	0.00e+00
c	34	249	35.3	480	100	T70889	yc49b08.s1 Homo sapie	0.00e+00
c	35	248	35.2	277	85	T39258	ya02g12.r2 Homo sapie	0.00e+00
c	36	247	35.0	381	17	H43633	yp24a07.s1 Homo sapie	0.00e+00
c	37	245	34.8	350	12	H26778	y152g09.r1 Homo sapie	0.00e+00
c	38	245	34.8	422	12	H28778	yo30e07.s1 Homo sapie	0.00e+00
c	39	245	34.8	436	64	R64294	y121h08.r1 Homo sapie	0.00e+00
c	40	243	34.5	405	8	H14996	y126a12.s1 Homo sapie	0.00e+00
c	41	241	34.2	374	11	H25441	y147f08.s1 Homo sapie	0.00e+00
c	42	241	34.2	397	106	T92408	ye19g05.r1 Homo sapie	0.00e+00
c	43	241	34.2	406	17	H43557	yo64f09.s1 Homo sapie	0.00e+00
c	44	239	33.9	423	11	H24881	y143a04.s1 Homo sapie	0.00e+00
c	45	238	33.8	405	134	HS545221	yu68e12.s1 Homo sapie	0.00e+00

## ALIGNMENTS

RESULT 1



*Db	261	cgtactgtgtgtctgttctgttggagggtgtgtgtgtctcactccgccttgaacgggc	320
Cp	583	cctacttctgttctgttctgttggagggtgtgtgtgtctcactccgccttgaacgggc	524
Db	321	tgtatctgccttcacagn-cactgtcacggctccgggtagaaagtcaattatgagaca	379
Cp	523	tgctatctgccttcacaggccactgttcgggtccgggtgagactcatttatgacaca	464
Db	380	ccagttgagccttgttgccttgaactcctcagaggaggcggaacagagtgaacgag	439
Cp	463	ccagttgagccttgttgccttgaagctcctcagaggaggcggaacagagtgaacgag	404
Db	440	gggcanccttuggctgaacctaggacgggtcaacttgcctccgcgcgaacatcaga	497
Cp	403	gggcacaccttggcgctgacact-aggacgg-tcacccgggtgccttctccgaacggga	348

3  
RESULT LOCUS  
DEFINITION  
R73382 469 bp mRNA EST 02-JUN-1995  
Y192a11.s1 Homo sapiens cDNA clone 156188 3' similar to gb:X57809  
IG LAMBDA CHAIN C REGIONS (HUMAN);  
R73382  
ACCESSION  
NID g847414  
KEYWORDS  
SOURCE  
human clone=156188 library=Soares breast 2NbBst vector=pt7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=Promega -21m13 Reitel=Not I Reite2=Eco RI Adult  
female, 1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5' TGTTACCAATGTGAAGTGGACGGCGCCCTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pT773 vector (Pharmacia). Library went through one round  
of normalization to Cot = 230. Library constructed by Bento  
Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archontes; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 469)

REFERENCE

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le-M, Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Willson, R.

TITLE	JOURNAL	COMMENT
The WashU-Merck EST Project	Unpublished (1995)	<p>Contact: Wilson RK  WashU-Merck EST Project  Washington University School of Medicine  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  Tel: 314 286 1800  Fax: 314 286 1810  Email: est@watson.wustl.edu  High quality sequence stops: 265  Source: IMAGE Consortium, LLNL</p> <p>This clone is available royalty-free through LLNL ; contact the  IMAGE Consortium (<a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a>) for further information.</p>

NCBI gi: 847414  
Location/Qualifiers  
source 1..469

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/organism="Homo sapiens"
/clone="156188"
/note="human"

BASE COUNT      81 a  115 c  150 g  117 t      6 others

ORIGIN

Query Match          42.4%; Score 299; DB 66; Length 469;
Best Local Similarity 93.1%; Pred. No. 0.00e+00;
Matches 323; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

Db 120 atgaacattctgaggggccactgtcttccacgggtgctcccttcattcggtgacctggc 179
|||||
Cp 703 ATGACATCTCTGTAGGGGCGACACTGCTCTTCACGGTGTCTCCCTTCATGCGTGACCTGGC 644
|||||
Db 180 agctgtagcttttgggaacttcacactgctcaggcgtcaggctcaggtacgtcgtggccg 239
|||||
Cp 643 AGCTGTAGCTTCTGTGGGACTTCACATGCTCAGGCGCTCAGGCTCAGGTAGCTGCTGGCCG 584
|||||
Db 240 cgtacttgttgtcttggttggagggtgtggtgctgtccaactcccgcttgaacggggc 299
|||||
Cp 583 CGTACTTGTCTTTGCTTTGTTGAGGGGTGTGGTGTCTCCACTCCCGCCTTGACGGGGC 524
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Db 300 tgcctatctgccttcaggggcaactgtcacggtcccggttagaagtcacttatgagacac 359
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Cp 523 TGCATCTGCGCTTCAGGCCA-CTGTACGGCTCCCGGTAGAGTCACTTATGAGACAC 465
|||||
Db 360 accagtggtgcttgtgtgtgaactcctcanaggaaggtnggaacaaaataaacnag 419
|||||
Cp 464 ACCAGTGTGGCCTTGTGTGCTTGAAGCTCCTCAGAGGGCGGGAACAGTGTACCGGAG 405
|||||
Db 420 ggggcaaccttggttaacctaaaggaacggtinaacttgggncctccgc 466
|||||
Cp 404 GGGGCACTTGGGTGTACCTPAGGACGGTCAACCGGTACCCGGGTCCCTTCCTCC 358
|||||

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RESULT	LOCUS	4	R73492	471 bp	EST	02-JUN-1995
DEFINITION			yj93d09.s1	Homo sapiens cDNA clone 156305 3'		similar to gb:X57809
				IG LAMBDA CHAIN C REGIONS (HUMAN);		

R73492  
 NID  
 q847524  
 EST.  
 human clone=156305 library=Soares breast 2NBHBst vector=p7T73D  
 (Pharmacia) with a modified polyLinker host=DH10B (ampicillin  
 resistant) primer=Promega -21m3 Raite1a-Not I Raite2-Eco RI Adult  
 female. 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 [5' TGCTACCAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
 digested with Not I and cloned into the Not I and Eco RI sites of  
 modified p7T73 vector (Pharmacia). Library went through one round  
 of normalization to a Cot = 230. Library constructed by Bento  
 Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
AUTHORS

1 (Bases 1 to 471)

Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

**TITLE** The WashU-Merck EST Project





NCBI gi: 824609

Location/Qualifiers

source

1..436

/organism="Homo sapiens"

/clone="154809"

/note="human"

BASE COUNT 74 a 101 c 142 g 111 t 8 others

ORIGIN

Query Match

Best Local Similarity 97.0%; Score 290; DB 61; Length 436;

Matches 292; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 136 atgaacattctgtagggccactgtcttccacggtgctcccttcattcgtagctggc 195

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Cp 703 ATGAACATTCTGTAGGGCCACTGTCTTCCACGGTGTCCCTTCATCGCTGACCTGGC 644

|||||

Db 196 agctgagcttttgggaacttccactgctcaggcgtcaggtagctgctggccg 255

|||||

Cp 643 AGCTGAGCTTCTGTGGCACTTCCACTGCTCAGCGCTCAGGCTCAGTAGCTGGCGG 584

|||||

Db 256 cgtactgtgtgttctgttggagggtgtggtgtctccantcccgcttcacgggc 315

|||||

Cp 583 CGTACTGTGTGTGTGGAGGGTGTGGTGTCTCCACTCCCGCTTGACGGGGC 524

|||||

Db 316 tgctatctgcttcagncactntccagntccgggtagaagtcacttatgagacaca 375

|||||

Cp 523 TGCTATCTGCTTCCAGGCCACTGTCCAGGCTCCCGGTAGAGTCACTTATGAGACACA 464

|||||

Db 376 ccagtggtgcttctgttgaagctcctcagagangtnggaacagatnaccgagg 435

|||||

Cp 463 CCAGTGTGGCTTGTGGCTTGAAGCTCTCAGAGGAGGGGGGACAGTGAACGAGG 404

|||||

Db 436 g 436

Cp 403 G 403

RESULT 8

LOCUS

DEFINITION

Yp87h10.s1 Homo sapiens cDNA clone 194467 3' similar to gb:X57809

IG LAMBDA CHAIN C REGIONS (HUMAN);

ACCESSION

NID

KEYWORDS

SOURCE

human clone=194467 library=Soares fetal liver spleen INFILS  
vector=pT73D (Pharmacia) with a modified polylinker host=DH10B  
(ampicillin resistant) primer=Promega -21ml3 Reitel-Pac I  
Rs1e2-Eco RI Liver and spleen from a 20 week-post conception male  
fetus. 1st strand cDNA was primed with a Pac I - oligo (dT) primer  
[5' RACTGGAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Pac I and cloned into the Pac I and Eco RI sites of  
the modified pT73 vector. Library went through one round of  
normalization. Library constructed by Bento Soares and M.Fatima  
Bonaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choeanata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 491)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfs, T., Soares, M., Tan, F.,  
Trevaak, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE  
JOURNAL  
COMMENT

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 229

Source: IMAGE Consortium, LIND

This clone is available royalty-free through LIND; contact the

IMAGE Consortium (info@image.lind.gov) for further information.

NCBI gi: 928073

Location/Qualifiers

1..491

/organism="Homo sapiens"

/clone="194467"

/note="human"

BASE COUNT

82 a 118 c 147 g 132 t 12 others

ORIGIN

Query Match 39.7%; Score 280; DB 69; Length 491;

Best Local Similarity 91.9%; Pred. No. 0.00e+00;

Matches 318; Conservative 0; Mismatches 24; Indels 4; Gaps 4;

Db 147 atgaacattctgtagggccactgtcttccacggtgctcccttcattcgtagctggc 206

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Cp 703 ATGAACATTCTGTAGGGCCACTGTCTTCCACGGTGTCCCTTCATCGCTGACCTGGC 644

|||||

Db 207 agctntagcttctgtgggaacttccactgctcaggcgtcaggtagctgctggccg 266

|||||

Cp 643 AGCTGAGCTTCTGTGGCACTTCCACTGCTCAGCGCTCAGGCTCAGTAGCTGGCGG 584

|||||

Db 267 cgtactgtgtgttctgttggagggtntggtgtctccantcccgcttcacgggc 326

|||||

Cp 583 CGTACTGTGTGTGTGGAGGGTGTGGTGTCTCCACTCCCGCTTGACGGGGC 524

|||||

Db 327 tgctatctgcttccaggcactttcacggctccnggtagaagtcacttntgagacaca 386

|||||

Cp 523 TGCTATCTGCTTCCAGGCCACTGTCCAGGCTCCCGGTAGAGTCACTTATGAGACACA 464

|||||

Db 387 ccagntnagcctgttggcttttaagntccccagagaggcgggaacagatt-accag 445

|||||

Cp 463 CCAGTGTGGCTTGTGGCTTGA-CTCTCCTCAGAGGGGGGGAACAGTCAACCGAG 405

|||||

Db 446 ggggcagc-ttnggttancatgaagcagcagctcagttng-tccctcctc 489

|||||

Cp 404 GGGGAGGCTTGGGCTGACCTAGGACGGTCCACCGGGTCCCTCTC 359

|||||

RESULT 9

LOCUS

DEFINITION

Yr22c08.r1 Homo sapiens cDNA clone 206030 5' similar to gb:X57809

IG LAMBDA CHAIN C REGIONS (HUMAN);

ACCESSION

NID

KEYWORDS

EST.





\* Best Local Similarity 95.2%; Pred. No. 0.00e+00;  
Matches 317; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

Db 106 atgaacattctgtaggccactgtcttctccacggtgctcccttcatcggtgacctggc 165  
|||||  
Cp 703 ATCAACATTTCTGTAGGGGCACTGTCTTCCACGGGTCTCCCTTCATCGGTGACCTGGC 644  
|||||  
Db 166 agctatagctctgtgggaactccactgctcaggcgtcaggctcagatagctgctggcgg 225  
|||||  
Cp 643 AGCTGTAGCTTCTGTGGGACTTCCACTGCTCAGGCGTCAAGTCAAGTGTGCTGGCGG 584  
|||||  
Db 226 cgtactgttctgttctgttggagggtntggtgtctccactcccgcccttgacggggc 285  
|||||  
Cp 583 CGTACTTCTGTTGCTTTTGGAGGGTGTGGTCTCCACTCCGGCTTGACGGGGC 524  
|||||  
Db 286 tgcatactgctccagggaactgtcacggctcccg-tagaagtcacttatgagacaca 344  
|||||  
Cp 523 TGTATCTGCTTCCAGGCACTGTCAAGGCTCCGGGTAGAGTCACTTATGAGACACA 464  
|||||  
Db 345 ccagtgtggccttgttgggtgaagctcttagaggaaggcggaacagagatnaccca 404  
|||||  
Cp 463 CCAGTGTGG-CTTGTGGCTTGAAGCTCCTCAGAGGA-GGGCGGGAACAGAGTGACCGA 406  
|||||  
Db 405 gggggcagc-ttgggtt-acgcaggacggtaac 435  
|||||  
Cp 405 GGGGCGAGCCTTGGGTGCTAGCTAGGACGGTCAC 373  
|||||

RESULT 11  
LOCUS G13531 297 bp DNA STS 04-JAN-1996  
DEFINITION human STS SHGC-11074.  
ACCESSION G13531  
NID g1129270  
KEYWORDS STS sequence; primer; sequence tagged site.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 297)  
AUTHORS Myers, R.M.  
JOURNAL Unpublished (1995)  
COMMENT  
Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myers@shgc.stanford.edu  
Primer A: TAGTCAGCCCAAGGCTG  
Primer B: TGGGACTTCCACTGCTCAG  
STS size: 247  
PCR Profile:  
Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600  
Protocol:

Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/ul  
Total Vol: 10 ul  
Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs derived from L38563 -- Unigene.

NCBI gi: 1129270  
Location/Qualifiers  
1..297  
/organism="Homo sapiens"  
/note="human"  
29..275  
/map="22"  
primer\_bind 29..46  
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primer\_bind complement(257..275)  
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BASE COUNT 69 a 95 c 84 g 49 t  
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Best Local Similarity 96.6%; Pred. No. 0.00e+00;  
Matches 287; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
Db 1 ttccggcgaaggaccacgaactgacgcctcctagctcagcccaagcgtccccctcggtcact 60  
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Qy 355 TTCGAGGAGGGGACCGCGCTGACCGCTCTAGGTGAGCCCAAGGCTGCCCCCTCGGTCACT 414  
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Db 61 ctgtccgcctctctcaggagcttaagccaagccacacactggtgtctcata 120  
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Qy 415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTGTCTCATA 474  
|||||  
Db 121 agtgacttctacccgggagccgtgacagtggcctggaagcagatagcagcccgctcaag 180  
|||||  
Qy 475 AGTGACTTCTACCGGGAGCGCTGACAGTGGCCTTGGAGGGCAGATAGCAGCCGCTCAG 534  
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Db 181 gggggagtggagaccaccacacctccaatcaagaacacaaagtttcgpgccagcagg 240  
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Qy 535 CGGGAGTGGAGACCAACACACACCTCCAAACAAGAACACAAAGTAGTACGGCCAGCAGC 594  
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Db 241 tatctgacctgacgctgaacagtggaagtcaccacagaagctacagctgctcaggtc 297  
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Qy 595 TACCTGACGCTGACGCTGAGCAGTGGAGTCCACAGAAAGCTACAGCTCCAGGTC 651  
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RESULT 12  
ID HS851303 standard; RNA; EST; 443 BP.  
AC N64851;  
DT 02-MAR-1996 (Rel. 47, Created)  
DT 02-MAR-1996 (Rel. 47, Last updated, Version 1)  
DE za22c10.s1 Homo sapiens cDNA clone 293298 3' similar to gb:X57809  
DE IG LAMBDA CHAIN C REGIONS (HUMAN);.  
KW EST.  
OS Homo sapiens (human)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.



```

RN      [1]
* RA     1-443
RA      Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
RA      Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA      Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
RA      Trevasakis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;
RT      "The WashU-Merck EST Project";
RL      Unpublished.
CC      Contact: Wilson RK WashU-Merck EST Project Washington University
CC      School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC      MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC      est@wustl.wustl.edu High quality sequence stops: 318 Source: IMAGE
CC      Consortium, L1NL This clone is available royalty-free through L1NL
CC      ; contact the IMAGE Consortium (info@image.llnl.gov) for further
CC      information. NCBI gi: 1212680
FH      Key      Location/Qualifiers
FT      source      1..443
FT      /organism="Homo sapiens"
FT      /clone="293298"
FT      /note="human"
FT      mRNA
FT      <1..>443
SQ      Sequence 443 bp; 73 A; 108 G; 147 G; 114 T; 1 other;

Query Match      39.0%; Score 275; DB 137; Length 443;
Best Local Similarity 95.4%; Pred. No. 0.00e+00;
Matches 288; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Db 140 atgaacattctgtaggggccaactgtcttcacagtgctcccttcattgacctggc 199
      |||
Cp 703 ATGACATTCTGTAGGGCCACATGCTTCTCCAGGGTGTCTCTTATCGCTGACCTGGC 644

Db 200 agctgtagctctgtggagctccactgctcggcgctcaggctcaggtgctgctggccg 259
      |||
Cp 643 AGCTGTAGCTTCTGTGGGACTTCCACTGCTCAGCGCTCAGGCTCAGGTAGCTGTGGCGG 584

Db 260 cgtactgtgtgtgctgtgttgagggtgtgtgtgtcctcaactcccgattgacggggc 319
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Cp 583 CGFACCTGTTGCTTTGTTGGAGGTGTGTGCTCTCCACTCCCGCTGACGGGGC 524

Db 320 tgccatctgcttcaggccaactgtcacagctcccggttagaagtcactgatcacagaca 379
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Cp 523 TGCTATCTGCTTCCAGGCCACATGTCACGGCTCCCGGTAGAGTCACTTATGAGACACA 464

Db 380 ctagtgtggccttgttgcttgagctcctcagaggaaggcnggaacagagtgcaggtgg 439
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Cp 463 CCAGTGTGGCTTGTGGCTTGAAGCTCTCTCAGAGAGGGGGGGAACAGATGACCCAGG 404

Db 440 gg 441
Cp 403 GG 402

RESULT 13
LOCUS      H25133      428 bp      mRNA      EST      07-JUL-1995
DEFINITION y143e10.r1 Homo sapiens cDNA clone 161034 5' similar to gb:X57809
            IG LAMBDA CHAIN C REGIONS (HUMAN) ;.
ACCESSION  H25133
NID        g894032
KEYWORDS   EST.
SOURCE     human clone=161034 library=Soares breast 3NBBst vector=pf7T3D
            (Pharmacia) with a modified polylinker host=DH10B (ampicillin
            resistant) primer=M13RPI Raitel=Not I Rsite2=Eco RI Adult human.
            1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
```

```

TGTACCAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTT 3' ],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.

ORGANISM      Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 428)
AUTHORS      Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE      The WashU-Merck EST Project
JOURNAL      Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
High quality sequence stops: 245
Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 894032      Location/Qualifiers
source      1..428
            /organism="Homo sapiens"
            /clone="161034"
            /note="human"
BASE COUNT      104 a 129 c 113 g 71 t 11 others
ORIGIN

Query Match      38.9%; Score 274; DB 11; Length 428;
Best Local Similarity 90.9%; Pred. No. 0.00e+00;
Matches 320; Conservative 0; Mismatches 28; Indels 4; Gaps 4;

Db 10 gtctcggaactggaccaggctcacgtcctcctcaggtcagcccaaggccaacncactg 69
      |||
Cp 352 GTCTTCGAGAGGAGGACCCGGGTGACCGTCTAGGTACGCCCAAGAGTCCCGCTCGCTC 411

Db 70 actctgtcccgccctcctctgaggaggtcccaagccaagcccaactagtgtctg 129
      |||
Cp 412 ACTCTGTCGCCGCTCTCTCTGAGGAGCTTCAAGCCCAAGGCCCACTGTGTGTCTC 471

Db 130 atcagtgaacttaccgggagctgtgacagtggtgctggaanagn-atggagcccgctc 188
      |||
Cp 472 ATAGTGAATCTTACCCGGGAGCGGTGACAGTGGCTGGAGGAGATAGCAGCCCGCTC 531

Db 189 aaggcggaggtngagaccaccaaacctccaaacagacagcaacaagtcacgcggccagc 248
      |||
Cp 532 AAGCGGGAGGTGAGAGACACCCACCCCTCCAAACAAAGCAACAGTACCGCGCGAGC 591

Db 249 agctacctgaactnaccgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 308
      |||
Cp 592 AGCTACCTGACGCGCTGAGCAGTGAAGTGAAGTCCGACACAGAGCTACAGCTGCCAGGTC 651
```



Search completed: Tue Dec 17 21:06:01 1996  
Job time : 280 secs.

\*\*\*\*\*

N E S E A (TM)

\*\*\*\*\*

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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Distribution rights by IntelliGenetics, Inc.

MPerch\_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 21:26:22 1996; MasPar time 117.91 Seconds  
Tabular output not generated. 945.851 Million cell updates/sec

Title: >US-08-487-550-3  
Description: (1-1431) from US08487550.seq  
Perfect Score: 1431  
N.A. Sequence: 1 ATGAACACCTGCTGTTCTT.....CCCTGCTCCGGGTAATGA 1431  
Comp: TACTTTGTGCACCAAGAA.....GGACAGAGGCCCATTTACT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 102519 seqs, 38967980 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-genseq24  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 9.407; Variance 6.204; scale 1.516

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1201	83.9	1431	19	T18059	Monoclonal antibody D	0.00e+00
2	1032	72.1	1617	6	Q35099	Antibody D heavy chain	0.00e+00
3	1028	71.8	1135	1	N90736	DNA encoding linker	0.00e+00
4	1027	71.8	1136	1	N90779	Sequence of the linker	0.00e+00
5	1023	71.5	1549	3	Q20066	Encodes heavy chain o	0.00e+00
6	1012	70.7	9208	11	Q65629	Vector contg. TCAE 8	0.00e+00
7	1007	70.4	1576	8	Q49944	Human anti-HBs heavy	0.00e+00
8	1001	70.0	1458	4	Q23571	Reshaped CD4 antibody	0.00e+00

9	1002	70.0	1467	4	Q23570	Reshaped CAMPATH-1 an	0.00e+00
10	999	69.8	1458	4	Q23581	Reshaped CD4 antibody	0.00e+00
11	998	69.7	6557	18	T15932	Anti-IgE VH expressio	0.00e+00
12	996	69.6	1386	8	Q49834	Anti-HIV-1 recombinan	0.00e+00
13	995	69.5	1641	9	Q54655	chiT84.12 H3 heavy ch	0.00e+00
14	987	69.0	8540	11	Q65628	Vector contg. TCAE 8	0.00e+00
15	983	68.7	1412	4	Q25692	Sequence of the chime	0.00e+00
16	981	68.6	1174	9	Q51547	Human kappa immunoglo	0.00e+00
17	824	57.6	1006	17	T12663	Synthetic IgG4 cDNA.	0.00e+00
18	692	48.4	768	17	Q96101	IgG1 hinge, CH2, CH3	0.00e+00
19	689	48.1	693	15	Q87592	Human IgG1 antibody F	0.00e+00
20	689	48.1	1164	17	T12658	IL4.Y124D/IgG1 gene f	0.00e+00
21	689	48.1	6367	17	T12661	Vector COSFclink.	0.00e+00
22	689	48.1	6926	17	T12662	IL-4.Y124D/IgG1 fusio	0.00e+00
23	687	48.0	1231	15	Q87593	Human Fas/Fc fused OR	0.00e+00
24	685	47.9	699	9	Q53539	cDNA sequence for a h	0.00e+00
25	685	47.9	705	18	Q74083	Immunoglobulin G1 Fc	0.00e+00
26	686	47.9	745	9	Q55943	Polylinker/Fc fragmen	0.00e+00
27	686	47.9	745	15	Q92273	Fc cDNA.	0.00e+00
28	686	47.9	745	13	Q75425	Antibody Fc mutein co	0.00e+00
29	686	47.9	745	9	Q58428	Human IgG1 Fc-polylin	0.00e+00
30	684	47.8	740	6	Q41508	Human IgG1 Fc.	0.00e+00
31	683	47.7	705	7	Q42589	Human Fc polypeptide	0.00e+00
32	682	47.7	1050	5	Q28684	LEA-3-Ig fusion gene	0.00e+00
33	682	47.7	1347	12	Q67347	VCAM 2D-IgG.	0.00e+00
34	682	47.7	2043	9	Q55340	tICAM(453) IgG immuno	0.00e+00
35	681	47.6	1317	17	T00829	Plasmid pDC406/OX40/F	0.00e+00
36	680	47.5	1050	6	Q40423	DNA sequence of LFA3T	0.00e+00
37	675	47.2	1557	10	Q45225	Sequence encoding a r	0.00e+00
38	675	47.2	1587	10	Q63958	P-selectin ligand-IgG	0.00e+00
39	675	47.2	1587	16	T02490	P-selectin ligand/Fc	0.00e+00
40	662	46.3	884	2	N70398	Portion of plasmid pP	0.00e+00
41	658	46.0	765	2	N70257	Part of the nucleotid	0.00e+00
42	658	46.0	765	1	N82142	Immunoglobulin G Fc d	0.00e+00
43	645	45.1	6889	18	T15931	DHFR/inttron (WTrasSD)	0.00e+00
44	631	44.1	1425	6	Q41516	Human CD40-L/Fc fusio	0.00e+00
45	631	44.1	1765	10	Q71873	Sequence coding human	0.00e+00

## ALIGNMENTS

RESULT 1  
ID T18059 standard; DNA; 1431 BP.  
AC T18059;  
DT 16-AUG-1996 (first entry)  
DE Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen..  
KW Polymerase chain reaction; primer; amplify; PCR; light chain; Mab;  
KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT CDS 1..1428  
FT /\*tag= a  
FT sig\_peptide 1..57  
FT /\*tag= b  
FT mat\_peptide 58..1425  
FT /\*tag= c  
FT 3'UTR 1426..1431  
FT /\*tag= d  
PN J08038178-A.  
PD 13-FEB-1996.  
PF 20-FEB-1995; 030742.  
PR 18-FEB-1994; JP-021628.  
PA (NISHIN) NISSHINBO IND INC.  
PA (TANAKA) TANAKA H.

DR	WPI; 96-154852/16.
DR	p-PSDB; R93553.
PT	Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
PT	produced by primer amplification, used in the diagnosis of HCMV
PT	infection
PS	Claim 6; Page 16-18; 22pp; Japanese.
CC	The sequences given in T18039-60 encode the heavy and light chains
CC	respectively of a monoclonal antibody against a 65 kD antigen of human
CC	cytomegalovirus (HCMV). These sequences were amplified using the
CC	sequences given in T18040-58. The monoclonal antibody may be used
CC	in the diagnosis of HCMV.
SQ	Sequence 1431 BP; 314 A; 475 C; 379 G; 263 T;

Query Match 83.9%; Score 1201; DB 19; Length 1431;  
Best Local Similarity 93.4%; Pred. No. 0.00e+00;  
Matches 1340: Conservative 0; Mismatches 85; Indels 9; Gaps 7;

Db	1	atgaagcatctgtgggtttctctctctgtgtggcggtccccagatgggtcctgtcccag	60
Qy	1	ATGAACACCTGTGGTCTTCTCTCTCTGTGTGGCAGCTCCACAGATGGGTCTGTGCCAG	60
Db	61	ctgcagctgcaggatgcgggcccaggagctggtgaagccttcggagaccctgtccctcacc	120
Qy	61	GTGAGAGCTGCACGATGGGGCGAAGACTTTCTGCAGCCTTCGGAGACCTGTCTCGGACG	120
Db	121	tgcactgtctcgtgtgacctccatcagcaggatagttactcctgggctgcacgcgcaag	180
Qy	121	TGCGTTGTCTGTGGTGGCTCCATACG--GGT-TACT-ACCTACTGGACCTGCATCGCGCAG	177
Db	181	cccccggggaagggcctggadtggatgggactatctat--ta-tagtgaggagcaacctac	237
Qy	178	ACCCAGGGAGGGGACTGCACTGGATTGGCCATATTATTTGGTAATGGTGCACCAACCAAC	237
Db	238	tacaaccggtccctcaagtcgagtcaccatatccgtagacgcgtccacaaccagctc	297
Qy	238	TACAATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACAGCTCCAGAACCACTTC	297
Db	298	tccctgaagctgagctctgtgacgcgcgcagacacgctgtgtattactgtcgagaa--	355
Qy	298	TTCTCGACTTGAATTCCTGTGACCGACGGCGACACGGCCGTCTATTACTGTCCAGAGGC	357
Db	356	ctcctcgccagtagttacgatcttttgac-tggttctcttccctcatactgggcccaggga	414
Qy	358	CTTCGCCCTTGATTGCACAAACATTGTTATGGCGGCTGGGTGGAATGCTGGGGGCCGGGA	417
Db	415	accctgggtcaacgtctcctcaagcctccaccaagggcccacatcggtcttccccctggcaacc	474
Qy	418	GACCTGTGTACCGCTCTCTCAGCTAGCACCAAGGGGCCATCGGCTCTTCCCGCTGGCACCC	477
Db	475	tctccaaagacacctctgggggcacagggccctgggtgcctcgttcaaggaactaetic	534
Qy	478	TCTTCAAGAGCACCTCTGGGGGCACAGGGCCCTGGGCTGCCTGTGTCAAGGACTACTTC	537
Db	535	cccgaaacggtgacggtgtcgtggaactcagggccctgaccacggcgtgcacacetic	594
Qy	538	CCCGAACCGGTGACGGTGTGTGGAACTACAGGCCCTTCACCCAGCGGGCTGCACACCTTC	597
Db	595	cqggctgtcctacagctctcaggaactactcctcagcagcgtggtgacqgtgccctcc	654
Qy	598	CGGGCTGTCTTACATGCTTCAGAGACTCTACTCCCTCAGCAGCGTGTGTGACCGTGCCTCC	657
Db	655	agcagcttgggcaaccacjacctacatctgcaacgtgaatcacaagcccgacacaccaag	714
Qy	658	ACGACTTTGGGCAACCAACCTACTCTGCAACCTGAATTCAGAGCCGACCGACCAACCAAG	717

Db	715	gtggacaagaagtgtgaccccaaatctgtgacaaactcacacatgccaccgtgccca	714
Qy	718	gtggacaagaagcgagacgcccaaaTCTTGTGACAAAACCTCACATGCCACCGTCCCA	717
Db	775	gcacctgaactcctgggggaccgtcagcttctctctcccccacaaaccgaagcac	834
Qy	778	GCACCTGAACCTCTGGGGGACCGTCAGCTCTTCTCTGCCCCCAAAACCAACGACAC	837
Db	835	ctcatgatctccggaccctggagtccatgcgctggtggagctgagccacgaagac	894
Qy	838	CTCATGATCTCCGGACCCCTGAGGTGCATGCGTGGTGAGCGTGAGCCACGAAGAC	897
Db	895	octgaggtccaagtccaactggtcagtgagcggtgagagtgataatggccaagaacaag	954
Qy	898	CCTGAGGTCAAGTTCAGTGTGAGTGGACGGCGTGGAGTGCATTAATGCCAAGACAAAG	957
Db	955	ccgggggaggagcagtcacaacgacacgtaccgtgtggtcagctcctcacgctctgcac	1014
Qy	958	CCGGGGGAGGAGCAGTACAAACAGCAGCTACCGTGTGGTCAGCGTCTCACCGTCTGCAC	1017
Db	1015	caggactgctgtaatggcaaggagtacaagtgcgaagctctccacaagaagcctcccgacc	1074
Qy	1018	CAGGACTGGCTGAATGGGAGGATACAGTGCAGGCTCTCAACAAAGCCTCTCCGCGC	1077
Db	1075	cccatcgaaaaaccactctccaaagccaaaggcagcccgagaaaccacaggtgtacacc	1134
Qy	1078	CCCATCGAAGAAACCATCTCAAAAGCAAAAGGGCAGCGCCCGAGAACACAGGTGTACAC	1137
Db	1135	ctgcccaccatccgggattgagctgaccaagaacacaggtcagctcgtcgtggtcaaa	1194
Qy	1138	CTGCCCCCATCCGGGATGAGCTGACCAAGAACACAGGTGAGCTGCCTGCTGCTCAAA	1197
Db	1195	ggcttctatccagcgacatcgccgtggagctgggagagcaatggcgacgggaagaacac	1254
Qy	1198	GGCTTCTATCCAGGCAATCGCGGTGGAGTGGGAGAGCAATGGGACGCCGGAGAACAC	1257
Db	1255	tacaagaccagcctcccggtgctgactccgacggcgtccttcttctctacagcaagctc	1314
Qy	1258	TACAGACCAAGCTCCGCTGCTGACTCCGAGCGGCTCTTCTCTCTACAGCAAGCTC	1317
Db	1315	accgtggacaagcaggtggcagcagggaacgtcttctcatgctccgctgatgatgag	1374
Qy	1318	ACCGTGGCAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCGTGAATGCATGAG	1377
Db	1375	gctctgcaaaccaactacacgacgaagagcctctccctgtctccgggtaaatga	1428
Qy	1378	GCTCTGCAACCACTACACGCAAGAGAGCCTCTCCGTGTCTCCGGGTAAATGA	1431

RESULT	2	
ID	Q35099 standard; DNA; 1617 BP.	
AC	Q35099;	
DT	19-MAY-1993 (first entry)	
DE	Antibody D heavy chain.	
KW	Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;	
KW	lymphocyte; hepatitis A virus; HAV; sero; positive; patient;	
KW	murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H; ss.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	CDS	35..1465
FT	/*tag= a	
FT	sig_peptide	35..91
FT	/*tag= b	







QY 1088 AAACATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTTGCCCCCAT 1147

Db 840 cccggatgagctgaccaagaaccaggtcagctgacctgctgtgtcgaaggtctctatc 899  
|||||

QY 1148 CCGGGATGAGCTGACCAAGACACAGGTGACCTGACCTGCTGCTCAAGGCTTCTATC 1207  
|||||

Db 900 ccagcagatccgctggagtgaggagcaatggcgagccggagagaaactacaagacca 959  
|||||

QY 1208 CAGGACATGCGCGTGAGGTGGAGAGCAATGGGAGCCGCGAGACAACTACAGACCA 1267  
|||||

Db 960 cgcctccgctgctggactccagcagctctcttctcctctacagcaagctcaccctggaca 1019  
|||||

QY 1268 CGCTCCGCTGCTGACTCCGAGGCTCTTCTCTCTACAGCAAGCTCACCGTGACA 1327  
|||||

Db 1020 agagcaggtggcagcaggggaacgtctctcatgctccgctgatgcaggtctgcaca 1079  
|||||

QY 1328 AGAGCAGTGGCAGCAGGGGAACGCTTCTCATCTCCGTGATCATGAGGCTCTGCACA 1387  
|||||

Db 1080 accactacagcagaagagctctcctgtctccgggtaaatga 1123  
|||||

QY 1388 ACCACTACGCGAGAGAGCTCTCCCTGCTCCGGTAAATGA 1431  
|||||

RESULT 4

ID N90779 standard; DNA; 1136 BP.

AC N90779;

DT 14-MAY-1990 (first entry)

DE Sequence of the linked immunoglobulin gamma chain fragment

KW Immunoglobulin gamma chain; IgG heavy chain constant region.

FH Key Location/Qualifiers

FT CDS 8..1123

FT /\*tag= a

PN EP-314317-A.

PD 03-MAY-1989.

PF 03-OCT-1988; 309194.

PR 28-SEP-1988; US-250785, US-104329.

PA (GETH) Genentech Inc.

PI Capon DJ, Gregory TJ;

DR WPI; 89-131855.

DR P-PSDB; P91918.

PT Compens. contg. adhesion variants

PT - useful in therapy and diagnostics, eg CD4 variants

PT which are therapeutically useful for treating human

PT immuno-deficiency virus

PS Figure 4a-4b; 36pp; English.

CC The polypeptide it codes for may be fused to the first 180 N-terminal

CC residues of CD4 at the C-terminus. The fusion protein may be used for

CC antiviral of immunomodulatory therapy particularly in treatment of HIV

CC infection.

SQ Sequence 1136 BP; 256 A; 385 C; 303 G; 192 T;

Query Match 71.8%; Score 1027; DB 1; Length 1136;

Best Local Similarity 96.3%; Pred. No. 0.00e+00;

Matches 1079; Conservative 0; Mismatches- 40; Indels 2; Gaps 2;

Db 1 gaattctgctcaactgcgcgagcagccgctatattactgtcgagagaccacttttgcct 60  
|||||

QY 309 GAATTCGTGACCGAGCGGACAGCGGCTCTATTACTGTGCGAGAGGC-CCTCGCCCTG 367  
|||||

Db 61 atggtacagggagc-gtccccctgtgtgagctgacacctggggcctgggaaccttggtca 119  
|||||

QY 368 ATTGCACACCAATTCTTATGGCGGCTGGGTGCTGCTCTGCGGCGCGGAGACCTGTCA 427  
|||||

Db 120 cegtctctcgctccaccaagggcccatcggtcttccccctggcacctctccaaga 179  
|||||

QY 428 CCGTCTCTAGCTAGCACCAAGGGCCCATCGGTCTTCCCTTGGACACCTCTCTCAGA 487  
|||||

Db 180 gcaactctgggggacagggccctggctgcttcaaggactacttccccgaaccgg 239  
|||||

QY 488 GCACCTCTGGGGGACAGCGGCTGGGCTGCCGTGTCAGGACTACTTCCCGCAACCGG 547  
|||||

Db 240 tgaaggtgtcgtggaactcaaggccctgaccagcggcgtgcacaccttcccggtctcc 299  
|||||

QY 548 TGAAGGTGTCTGGAACCTCAGGCGCCTGACAGCGGCTGCACACCTTCCCGGCTGTCC 607  
|||||

Db 300 tacagtcctcaggactctactcctcagcagcgtggtgacctgacctccagcaggtgg 359  
|||||

QY 608 TACAGTCTCTAGGACTCTACTCTCAGCAGCGTGGTGACGCTGCCCTCCAGCAGCTTG 667  
|||||

Db 360 gacccagacactacatctgcaacgtgaatcacaagcccagcaaccacaaaggtggacaaga 419  
|||||

QY 668 GCACCCAGACCTACTCTGCAACGTGAATCAACAGCCGACACACCAAGAGGTGACAGA 727  
|||||

Db 420 aagttagcccccataatcttgtgacaaaactcacacatgccacacgtgccagcacctgaac 479  
|||||

QY 728 AAGCAGACGCCAAATCTTGTGACAAAACCTCACATGCCCCACCTGCCAGACCTGAAC 787  
|||||

Db 480 tcctgggggacgctcagctcttctcttcccccaaaacccaaggaacacctcatgatct 539  
|||||

QY 788 TCCTGGGGGACGCTCAGCTTCTCTCTCCGCCCAAAACCCAAGGACACCTCATGATCT 847  
|||||

Db 540 cccggaccttgaggtcacatgctggtggctgagctgagccacgaagacctgaggtca 599  
|||||

QY 848 CCCGGACCCCTGAGGTTCATGCGTGGTGGAGCTGAGCCAGAGACCTGAGGTCA 907  
|||||

Db 600 agttcaactggtacgtggacggcgtggaggtgcataatgccaaagacaaagccggagg 659  
|||||

QY 908 AGTTCAACTGGTGTAGTGACGGGCTGGAGTGCATTAATGCCAAGACAAAGCGCGGAGG 967  
|||||

Db 660 agcagtlacacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccaggaactggc 719  
|||||

QY 968 AGCATACACACAGCAGCTACCGGTGGTGGCTCTCTCACCGTCTCTGACACAGGACTGG 1027  
|||||

Db 720 tgaatgcaagaggtacaagtgaaggtctccaacaaagccctccagcccccatcgaga 779  
|||||

QY 1028 TGAATGCCAAGAGTACAAAGTGCAGGCTCTCCAAACAAAGCCCTCCAGGCCCATCGACA 1087  
|||||

Db 780 aaaccatctccaaagccaaaggcagcccgagaccacacaggtgtacacctgccccat 839  
|||||

QY 1088 AAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAACAGGTGTACACCTTGCCCCCAT 1147  
|||||

Db 840 cccggatgagctgaccaagaaccaggtcagcctgacctgctgtcgaaggtctctatc 899  
|||||

QY 1148 CCGGGATGAGCTGACCAAGAACCAAGTACGCTGACCTGCTGCTCAAGGCTTCTATC 1207  
|||||

Db 900 ccagcagcatccgctggagtgaggagcaatggcgagccggagaaactacaagacca 959  
|||||

QY 1208 CCAGGCACATCCCGCTGGAGTGGGACAGCAATGGGACGCCGGAACAACTACAGACCA 1267  
|||||

Db 960 cgcctccgctgctggaactccagcagcgtccttcttctctctacagcaagctcaccgtggaca 1019  
|||||

QY 1268 CGCTCCGCTGCTGACTCCGAGGCTCTTCTCTCTCTACAGCAAGCTCACCGTGACA 1327  
|||||

Db 1020 agagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcaggtctgcaca 1079  
|||||

QY 1328 AGAGCAGTGGCAGCAGGGGAACGCTTCTCATCTCTGCTCCGTGATCATGAGGCTCTGCACA 1387  
|||||

Db 1080 accactacagcagaagagcctctcctgtctccgggtaaa 1120  
|||||



Qy 1388 ACCACTACGACGAGAGACCTCTCCCTGCTCTCCGGGTAA 1428  
|||||

## RESULT 5

ID Q20066 standard; DNA; 1549 BP.  
AC Q20066;  
DT 25-MAR-1992 (first entry)  
DE Encodes heavy chain of 3D6 antibody.  
KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT sig\_peptide 101..157  
FT /\*tag= a  
FT mat\_peptide 158..1528  
FT /\*tag= b  
FT 5'UTR 1..100  
FT /\*tag= c  
FT misc\_feature 158..535  
FT /\*tag= d  
FT /label= variable\_region  
FT misc\_feature 158..247  
FT /\*tag= e  
FT /label= Framework 1  
FT misc\_feature 248..262  
FT /\*tag= f  
FT /label= CDR\_1  
FT misc\_feature 263..304  
FT /\*tag= g  
FT /label= Framework 2  
FT misc\_feature 305..355  
FT /\*tag= h  
FT /label= CDR\_2  
FT misc\_feature 356..431  
FT /\*tag= i  
FT /label= Framework 3  
FT misc\_feature 452..502  
FT /\*tag= j  
FT /label= CDR\_3  
FT misc\_feature 503..535  
FT /\*tag= k  
FT /label= Framework 4  
FT misc\_feature 536..1528  
FT /\*tag= l  
FT /label= Constant\_region  
PN W09118983-A.  
PD 12-DEC-1991.  
PE 28-MAY-1991; 100067.  
PR 29-MAY-1990; AT-001178.  
PA (JUNG/) JUNGHAUER A.  
PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;  
DR WPI; 92-007468/01.  
DR P-PSDB; R20057.  
PT Recombinant protein which binds to complex viral antigen and  
PT HIV-1 - contains variable region of antibody derived from 3D6  
PT cell line, used for detecting HIV-1 antigen  
PS Claim 2; Page 24; 52pp; German.  
CC The 5'-UTR is 100 bases long although the specification numbers it  
CC at 98 bases. It is possible that two extra bases have been inserted  
CC as a typographical error in the specification (i.e. that the 5'-UTR  
CC sequence is incorrect as printed in the specification and reproduced  
CC here). The sequence comprises a human cDNA insert encoding the 3D6  
CC heavy chain flanked by short stretches of pUC19 DNA. The variable  
CC region of the heavy chain is used in a recombinant protein with the

CC variable region from the kappa light chain of 3D6, the two V regions  
CC being joined by a linker. The recombinant protein binds to HIV gp160.  
CC See also Q20067 and Q20068.  
SQ Sequence 1549 BP; 362 A; 464 C; 416 G; 307 T;

Query Match 71.5%; Score 1023; DB 3; Length 1549;  
Best Local Similarity 86.9%; Pred. No. 0.00e+00;  
Matches 1222; Conservative 0; Mismatches 181; Indels 3; Gaps 3;

Db 126 tccttttggtattttaaaagtgctcagtgagtgagtgctggtggagtgctggggag 185  
|||||

Qy 26 TCCTGTGGCAGCTCCACATGGGTCTCTCCAGGTGAAGCTGCACGAGTGGGGCAG 85  
|||||

Db 186 gcttgtagagcctggcaggtccctgagactctctgtcagcctctgattccacttta 245  
|||||

Qy 86 GACTTCTGCAGCCTTCGAGACCTGTCCCGCACCTGCGTGTCTCTGGTGGCTCCATCA 145  
|||||

Db 246 atgatta-tgcca-tgcac-tgggtccggcaagctccagggaaggccctggagtggtct 302  
|||||

Qy 146 GCGGTTACTACTACTGACCTGCATCCGCCACCCAGGAGGGGAGCTGAGTGGATTG 205  
|||||

Db 303 caggtataagttggatagtagtataggtatcggtgactctgtgaaggccgattca 362  
|||||

Qy 206 GCCATATTTATGGTAATGTGCGACCAACCACTAGATCCCTCCCTCAAGAGTCGAGTCA 265  
|||||

Db 363 ccatctccagagacaacccaagaactccctgtatctgcaaatgaacagctctgagagctg 422  
|||||

Qy 266 CCATTTCAAAAGACAGCTCCAAAGACAGTTCTTCTGAACTTGATTTCTGTGACCGAGC 325  
|||||

Db 423 agnacaatgaccttattactgtgtaaaagcagagattactatgatagtggtgtatt 482  
|||||

Qy 326 CGGACACGGCGCTTATTACTGTGCGAGAGCGCTCGCCCTGATTGCACACCACTTTGTT 385  
|||||

Db 483 tcacggttgcttttgatctggtgggccaaggagacaatggtcacogtctcttcagctcca 542  
|||||

Qy 386 ATGCGCGTGGGTGATGTCTGGGGCCGGGAGACCTGCTCAGCTCTCTCAGCTAGCA 445  
|||||

Db 543 ccaagggcccatcggtcttcccoctggacacctctccaagagcaactctggtgggacag 602  
|||||

Qy 446 CGAAGGGCCCATCGGCTTCGCCCTGGCACCTCTCTCCAAGAGCACTCTGTGGGGCAGAG 505  
|||||

Db 603 cagcctgggtgctgctcaaggtacttccccgaaccggtgacggtgctggtggaact 662  
|||||

Qy 506 CGGCGCTGGGCTGCTGTGTAAGGACTACTTCCCGGACCCGGTGACGGTGTGTGGAAT 565  
|||||

Db 663 caggcgccctgacacagcgctgcacaccttcccgctgctctacagctctcagagctct 722  
|||||

Qy 566 CAGCGCGCTTCACACGCGCGCTGCACACCTTCCCGGCTGCTCTACAGTCTCTCAGGACTCT 625  
|||||

Db 723 actcctcagcagcggtggtgacctgacctccagcagctgggcaaccagacctcaactct 782  
|||||

Qy 626 ACTCCCTCAGCAGCGTGGTGACCTGCTCCCTCAGCAGCTGGGCGACCCAGACCTACATCT 685  
|||||

Db 783 gcaacgtgaatcacagcccagcaacccaagggtcgacaagaagttagcccaaatctt 842  
|||||

Qy 686 GCAACGTGAATCAGACGCCAGCAACCAAGGTGGACAAAGAGAGAGAGCCCAATCTT 745  
|||||

Db 843 gtgacaaaactcacatgccactgcccacgtgcccagcaactgaaactcctgggggagccgtcag 902  
|||||

Qy 746 GTGCAAAACTCAGATGCCCCACCTGCGCCAGCACCTGAACTCCTTGGGGGGAGCCGTCAG 805  
|||||

Db 903 tcttctcttcccccccaaaacccaagggacacctcatgatctccggacctctaggtca 962  
|||||

Qy 806 TCTTCTCTTCCCCCGCAAAACCCAAAGGACACCTCATGATCTCTCCCGGAGCCCTGAGGTCA 865  
|||||

Db 963 catcgctggtgacgtgagccacgaagaccctgaggtcaactgactgaactgacgtg 1022  
|||||  
Qy 866 CATCGCTGGTGGTGGACGTGAGCCACGAAGACCTCGAGGTCAAGTTCMACTGCTACGTGG 925  
Db 1023 acgcgctgaggtgcaatgacgaacgaagccgagggagagcagtgacagcaactccagct 1082  
|||||  
Qy 926 ACCGCTGGAGGTGCAATATCCCAAGCAAGAGCCGGGAGGACGAGTACACAGCACGT 985  
Db 1083 accgtgtagtcagcgtcctcaccgtcctgcaccaggaactggctgaatggcaaggagtaca 1142  
|||||  
Qy 986 ACCGTGTGGTGGACGTGCTCAGCTGCTGACACGAGACTGGCTGAATGGCAAGAGGTACA 1045  
Db 1143 agtgaaggtctccaaagaagcctccagcccccacgaagaacccatctccaaagcca 1202  
|||||  
Qy 1046 AGTGAAGGTCTCCAAAGAGCCCTCCAGGCCCCATCGAGAAAAACATCTCCAAAGCCA 1105  
Db 1203 aagggcagcccccagaaacacaggtgtacacactgcccccatccccgggatgagctgacca 1262  
|||||  
Qy 1106 AAGGCGAGCCCGAGAAACACAGGTGTACACCTGCGCCCATCCCGGATGAGCTGACCA 1165  
Db 1263 agaacaggtcagctgacctgctgtgctgaaggtcttatccagcgacatcgccgtgg 1322  
|||||  
Qy 1166 AGAACCGAGTCAGCTGACCTGGTCTGCTGTAAGGCTTCTATCCCGGACATCGCGCTGG 1225  
Db 1323 agtggaggaagcaatggcgagcggagaaacactacaagaccacgctccgtgctggact 1382  
|||||  
Qy 1226 AGTGGGAGCAAGATGGCGAGCGGAGAACTACAAAGCACCGCTCCCGTGGTGGACT 1285  
Db 1383 ccgagcgtcctcttctctctacagcaagctcaacctggacaagcagcaggtggcagcagg 1442  
|||||  
Qy 1286 CCGAGCGCTCTTCTTCTTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG 1345  
Db 1443 ggaacgtctctcatgctccgtgatgatgaggtctgcaacaacactacacacagaaga 1502  
|||||  
Qy 1346 GGAAGCTCTTCTCATGCTCGTGTATGATGAGGCTGTGCAACACCTACACGCAAGA 1405  
Db 1503 gctctcctctgctccgggtaaatga 1528  
|||||  
Qy 1406 GCCTCTCTCTGCTCGGGTAAATGA 1431  
|||||

## RESULT 6

ID Q65629 standard; DNA; 9208 BP.  
AC Q65629;  
DT 01-FEB-1995 (first entry)  
DE Vector contg. TCAE 8 DNA.  
KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;  
KW cell lysis; ss.  
OS Synthetic.  
PN W09411026-A.  
PD 26-MAY-1994.  
PF 12-NOV-1993; U10953.  
PR 13-NOV-1992; US-978891.  
PR -03-NOV-1993; US-149099.  
PA (IDEC-) IDEC PHARM CORP.  
PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;  
PI Refine;  
DR WPI; 94-183162/22.  
PT Treating B cell lymphoma with chimeric antibody - against CD20,  
PT causing rapid depletion of peripheral B cells, also new  
PT antibodies and hybridomas  
PS Disclosure; Fig 3; 101pp; English.  
CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric

CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8  
CC contains 4 transcriptional cassettes, human Ig light and heavy chain  
CC constant regions, dihydrofolate reductase, neomycin phosphotransferase  
CC and murine variable regions. The vector can be used to produce  
CC antibodies which cause depletion of peripheral blood B cells,  
CC including those associated with lymphoma. They mediate complement-  
CC dependent lysis and lyse target cells by antibody-dependent cellular  
CC cytotoxicity.  
CC See also Q65629-35.  
SQ Sequence 9208 BP; 2237 A; 2399 C; 2388 G; 2182 T;  
Query Match 70.7%; Score 1012; DB 11; Length 9208;  
Best Local Similarity 98.9%; Pred. No. 0.00e+00;  
Matches 1023; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Db 2779 tcaatgtctggggcgagggaccacggtcacccgtctctcagctagcaccgaaggcccat 2838  
|||  
Qy 398 TCGATGTCTGGGGCGGGAGACCTGGTCACTGCTCTCTCAGCTAGACCAAGGGCCCAT 457  
|||  
Db 2839 cgggtctcccccctggcacccctctccaagagcacctctgggggcacagcgccctggct 2898  
|||||  
Qy 458 CGGTCTTCCCTTGGCACCTCTCCAAAGCAGCTCTGGGGGACAGCGCGCTGGGCT 517  
Db 2899 gcttgtcaaggactactccccgaacccggtgacggtgtcgtggaactcagggccctga 2958  
|||||  
Qy 518 GCCTGGTCAAGGACTTCCCGCAACCGGTGACGGTGTCTGGAACTCAGCGCCCTGA 577  
Db 2959 ccagcggtgcaacacttcccggctgtcctacagtcctcaggactctactccctcagca 3018  
|||||  
Qy 578 CCAGCGGCTGCACACTTCCGGCTGTCTACAGTCTCTCAGGACTTACTCCCTCAGCA 637  
Db 3019 cgggtgtgacgtgcccctccagcagcttgggcacccagacctacatctgcaacgtgaac 3078  
|||||  
Qy 638 CGGTGTGACCGTGGCCCTCCAGCAGCTTGGGCAACCAGACCTTACATCTGCAACGTGAATC 697  
Db 3079 acaagccagcaacacaaaggtggacaagaagcagagcccaaatctgtgacaaaactc 3138  
|||||  
Qy 698 ACAAGCCAGCAACACCAAGGTGGAACAAGACAGAGCCCAATCTTGTGACAAAACCT 757  
Db 3139 acacatgccaccgtgcccagcactgaaactcctggggggaccgtcaagtcttctctcc 3198  
|||||  
Qy 758 ACATATGCCACCGTGCACGACCTGAACCTCTGGGGGACCGTCAGTCTTCCTCTTCC 817  
Db 3199 ccccaaaacccaaggacacctcatgatctcccggaccctgaggtcacatgctggtgg 3258  
|||||  
Qy 818 CCCCAAAACCCAGGACACCTCATATCTCCCGGACCCCTGAGGTACATCGCTGGTGG 877  
Db 3259 tggactgagccacgaagaccctgaggtcaagtccaactggtacgtggagcgtggagg 3318  
|||||  
Qy 878 TGCAGCTGAGCCAGCAAGACCTCTGAGTTCAGTTCAACTGGTGTGAGACGGCGTGGAG 937  
Db 3319 tgcaaatgccaaagaaagccgggagagcagtgacaacagcagctacctgtgtgtca 3378  
|||||  
Qy 938 TGCATAATGCCAAGCAAGCCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCA 997  
Db 3379 cgtctcactcagcgtcctgcaccaggaactggctgaatggcaacgagtagacaagtgcagtct 3438  
|||||  
Qy 998 CGGTCTCAGCGTCTGCACAGCACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCT 1057  
Db 3439 ccaacaagacctcccagcccccatcgagaaacccatctccaaagccaaaggcagcccc 3498  
|||||  
Qy 1058 CCACAAAGCCCTCCCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1117  
Db 3499 gagaaccacaggtgtacacctgccccatcccgggatgagctgaccaaagaaccaggtca 3558

1118 GAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAACACAGGTCA 1177  
3559 gcttgactgctgtgtaaggtcttatcccagcgacatcccggtgagtgagtgagagca 3618  
1178 GCCTGACCTGGCTGTGCAAGGCTTCTATCCACGGACATCGCCGTGGAGTGGGAGAGCA 1237  
3619 atgggagccgagagaacaactacaagacaacgctcccggtgctggactccgagcggtcct 3678  
1238 ATGGCAGCGGAGAACAACTACAAAGACACACGCTCCCGTGTGACTCCGACGGCTCCT 1297  
3679 tcttctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaagctctct 3738  
1298 TCITTCCTCTACAGCAAGCTCACCGTGGACACAGCAGGTGGCAGGAGGAGCTTCT 1357  
3739 catgtccggtgatgatgaggtctgcacaaccactacacgacagaagagctctccctgt 3798  
1358 CATGCTCCGTGATGCTAGGCTCTGCACACCACTACACGCGACAGAGGCTCTCCCTGT 1417  
3799 ctccgggttaataga 3812  
1418 CTCGGGTAAATGA 1431

## RESULT 7

ID Q49944 standard; cDNA; 1576 bp.  
AC Q49944;  
DT 29-APR-1994 (first entry)  
DE Human anti-HBs heavy chain.  
KW Antibody; Ab; light; heavy; chain; hepatitis B;  
KW HB; surface antigen; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 15..1394  
FT sig peptide 15..41  
FT /tag= b  
FT mat peptide 42..1391  
FT /tag= c  
FT /notes= "claim 2, page 27"  
PN W09320205-A.  
PD 14-OCT-1993.  
PE 30-MAR-1993; J00396.  
PR 30-MAR-1992; JP-074678.  
PA (SUNR ) SUNTORY LTD.  
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;  
DR WPI; 93-336913/42.  
DR P-PSDB; R42066.  
PT Human anti-hepatitis B surface antigen antibody gene - can be  
PT used to produce L and H chains of the antibody in large quantity  
PS Disclosure; Fig 6-8; 46pp; Japanese.  
CC Polynucleotides encoding the L and H chains of human anti-HBs  
CC Ab are given in Q49943-Q49944. The Ab can be easily produced in  
CC large quantities for therapeutic use.  
SQ Sequence 1576 BP; 394 A; 483 C; 426 G; 273 T;

Query Match 70.4%; Score 1007; DB 8; Length 1576;  
Best Local Similarity 99.0%; Pred. No. 0.00e+00;  
Matches 1017; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

368 ctggggcagggaacccctgtcacgctctctcagcctccacgaagggccatcggtctt 427  
405 CTGGGGCCGGGAGACCTGGTACCGTCTCTCTACGCTAGCACCAGGGGCCATCGGTTT 464

428 ccccttgacacccctctccaagagacacctctgggggacagcgccctggcctgctggt 487  
465 CCCCCCTGGCACCCCTCTCCACAGACACCTCTGGGGGACAGCGCCCTGGCTGGCTGGT 524  
488 caaggactactccccgaaccoggtgacoggtgtcgtggaactcaggcgccctggccagcgg 547  
525 CAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGAACCTCAAGCGCCCTGACCAAGCGG 584  
548 ogtgacaacctccccggtgtcctacagtcctcaggactctactccctcagcagcgtggt 607  
585 CTGCACACTTCCGGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGT 644  
608 gacggtgacctccagcagcttgggcaaccagacctacatctgcaaacgtgaatcacaagcc 667  
645 GACGCTGCCCTCCAGAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAGGCC 704  
668 cagcaacacaaggtggacaagaagttagcccaaatctgtgacaaaactcacacatg 727  
705 CAGCAACACCAAGGTGGACAGAAAGCAGAGCCCAATCTTGTGACAAAATCACACATG 764  
728 cccacogtgcacagacctgaactcctgggggagacctcagctcttctcttcccccaaa 787  
765 CCCACGCTGCCAGACCTGAACCTCTGGGGGACCGCTCAGTCTTCTTCCGCCCAAA 824  
788 acccaaggacacctcatgatctcccggacccctgaggtcacatgctggtggtgagct 847  
825 ACCCAAGGACACCTCATATCTCCCGGACCCCTCAGGTACATGCTGCTGGTGGTGGAGCT 884  
848 gagccacgaagacctgaggtcaagttcaactggtacgtggagcgctggaggtcataa 907  
885 GAGCCAGGAAGACCTGAGGTCAAGTTCAACTGTGTGAGGCGCGTGGAGGTGCATAA 944  
908 tgccaagacaaagccgggagagcagtlacaacagcagctaccgggtggtcagcgtcct 967  
945 TGCCAGACAAAAGCCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCT 1004  
968 caccgtctgcacagagactggctgaatggcaaggagtacaagtgcagggtctccaacaa 1027  
1005 CACCGTCTCGACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAA 1064  
1028 agccctccacgcccccatcgagaaaccatctccaaagccaaagggcagccccgagaacc 1087  
1065 AGCCCTCCACGCCCCCATCGAGAAAACCATCTCCAAAAGCCAAAGGGCAGCCCGAGACC 1124  
1088 acaggtgtacacctgcccccatcccggtgatgagctgaccaagaaccaggtcagcctgac 1147  
1125 ACAGGTGTACACCTTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTGAGCTGAC 1184  
1148 ctgctggtcgaaggttctatcccagcaacatcgctggagtgagagagaatgggca 1207  
1185 CTGGCTGGTCAAAAGGCTTCTATCCAGCGACATCGCCGTGAGTGGGAGCAATGGGCA 1244  
1208 gccggagacaactacaagacaacgctcccggtgctggactccgacgggtctcttctct 1267  
1245 GCGGAGAACAAAGTACAAGACCGAGCCTCCCTGCTGGACTCCGACGGCTCTTCTTCTCT 1304  
1268 ctacagaagctcacogtggacaagagcaggtggcagcagggggaacgtcttctcatgctc 1327  
1305 CTACAGCAAGCTCACCGTGGACAGACGAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC 1364  
1328 cgtgatgcaggtgctgtcaccaaccactacacgacaagaagacctctccgtgtctccggg 1387  
1365 CGTGTGTGATGAGGCTCTGCACAAACCACTACACGACGAAGAGCCCTCTCTCTCTCGGG 1424













Db	335	gacgtttggggcaaaaggacacagctcaccqgtgagctcagcctccaccaaggcccatcg	414
Qy	400	GATGTCTGGGGCCGGGAGACCTGGTCACCGTCTCCTGAGCTAGCACAAGGGCCCATCG	459
Db	415	gtcttccccctggcacccctctccaagagacacctctgggggacacagcgccctgggtgc	474
Qy	460	GTCTTCCCCCTGGCACCTCTCTCAAGAGCACCTCTGGGGGCAACAAGGGCCCTGGGTGC	519
Db	475	ctggtcaaggactaettccccgaaccggtgacggtgctggtggaactcaggcgccctgaac	534
Qy	520	CTGGTCAAGAGACTACTTTCOCGGAACCGGTGACGGGTCTCGTGGAACTCAGCGCCCTTGACC	579
Db	535	agcgcggtgcacactttcccgctgtcctacagtctctcaggactctactcctcagcagc	594
Qy	580	AGCGCGGTGCACACTTTCOCGGCTGTCTACAGTCTCAGAGCACTACTCTCTCAGCAGC	639
Db	595	gtggtgacctgtgcctccagcagcttggggcaccacagactacatctgeaagtgaaatcac	654
Qy	640	GTGGTCACCGTGGCTCTCAGCAGCTTGGGCAACCAGACCTACTCTGCAAGCTGAATCAC	699
Db	655	aagcccaagcaaaccaaggtggacaagaagtgtagcccaaatcttgtgacaaaactcac	714
Qy	700	AAGCCCAACACCAAGGTGGACAAGAACGACAGCCCAATCTTGTGACAAAACCTCAC	759
Db	715	acatgccaccagtggccagcactgaaetccctgggggagccgtcagttctctctcccc	774
Qy	760	ACATGCCCAACCGTCCCGACACTGAACTCTCTGGGGGACCGCTCAGTCTCTCTTCCCC	819
Db	775	ccaaaacccaaggacacctcatgatctccggaccctcagggtcacatcggtgggtggtg	834
Qy	820	CCAAAACCAAGAGACACTCATGATCTCCCGGACCCCTGAGGTCAATGCTGGTGGTG	879
Db	835	gacgtgagccacgaagaacctgaggtcaagttcaactggtacgtggacgcggtggaggtg	894
Qy	880	GAGTGCACCAACGAACAACCTGAGGTCAAGTTCAACTGGTACGTGACGGGTGGAGGTG	939
Db	895	cataatgccaaagcaaaagccggagagagcagtaacaacagcagctaccgtgtggtcagc	954
Qy	940	CATTAATGCCAAGACAAAGCCCGGGAGAGCAGCTACAAACACACCTACCGCTGTGGTCAGC	999
Db	955	gtctcaacctcctgcaacagagactgggtgaaatggcaagagtagcaagtgcgaagttccc	1014
Qy	1000	GTCTCACCGTCTCTGCACAGCACTGGCTGAAATGGCAAGAGTACAAGTGCAAGGTCTCC	1059
Db	1015	aacaagacctcccagcccccatctgagaaaaccaatctccaagaccaagggagccccga	1074
Qy	1060	AACAAGACCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAACCAAGGGCAGCCCGCA	1119
Db	1075	gaaccacaggtgtacacctgcccccactccggatgagctgaccaagaaccaagtcagc	1134
Qy	1120	GAACACAGGTGTACACTGCCCCCATCCCGGATGACTGTACCAAGAACCAAGTCAGC	1179
Db	1135	ctgacctgcctggtcaaaaggtctctatcccagcgacatccgctggagtgggagagcaat	1194
Qy	1180	CTGACCTGCCTGTGTAAAGGGTCTTATCCACAGCAATCCCGCTGTGATGTGGAGAGCAAT	1239
Db	1195	ggcagccggagaaacaactcaagacccacgctccggtgctggactccgagcgctctctc	1254
Qy	1240	GGGACGCGGAGAACAACTACAGACACACGCGCTCCCGCTGTGGACTCCGAGGGCTCTTC	1299
Db	1255	ttcctctcaagcaagctcaccgtggacaagagcaggtggcagcaggggaagctctctca	1314
Qy	1300	TTCTCTACAGCAAGCTACCGTGGCAAGACAGAGTGGCAAGAGGGAAGCTCTTCTCA	1359

Db	1315	tgtccgtgatgcattgaggctctgcacaaccactcaacgcagaagagcctctccctgtct	1374
Qy	1360	TCCTCCGTGATGCATGAGGCTCTGCACACCACTACCGCAGAGAGCCTCTCCCTGTCT	1419
Db	1375	cgggtaataa	1386
Qy	1420	CCGGGTAAATGA	1431
RESULT	13		
ID	Q54655	standard; cDNA; 1641 BP.	
AC	Q54655;		
DT	24-JUN-1994	(first entry)	
DE	chiT84.12 H3 heavy chain.		
KW	Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant;		
KW	region; transform; myeloma cell; light chain; tumour; ss.		
OS	Synthetic.		
FS	Key	Location/Qualifiers	
FT	CDS	52..1486	
FT	/tag= a		
FT	/product= chiT84.12 H3 heavy chain		
PN	W09325237-A.		
PD	23-DEC-1993.		
PF	15-JUN-1993; U05709.		
PR	15-JUN-1992; US-904074.		
PA	(CITY ) CITY OF HOPE.		
PA	(YANG/) YANG Y.		
PI	Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;		
PI	Yang YH;		
DR	WPI; 94-007204/01.		
DR	P-PSDB; R47453.		
PT	New chimeric T84.12 antibody active against carcinoembryonic		
PT	antigen - has murine variable and human constant regions, also		
PT	DNA encoding it and transformed myeloma cells		
PS	Claim 1; Page 22-23; 27pp; English.		
CC	The sequences (054651-52) show the light and heavy chain cDNAs		
CC	of murine T84.12. The T84.12 antibody is directed against the		
CC	tumour marker carcinoma embryonic antigen, and is useful for		
CC	tumour imaging and immunotherapy.		
SQ	Sequence 1641 BP; 370 A; 516 C; 444 G; 311 T;		
	Query Match 69.5%; Score 995; DB 9; Length 1641;		
	Best Local Similarity 98.4%; Pred. No. 0.00e+00;		
	Matches 1011; Conservative 0; Mismatches 16; Indels 0; Gaps 0;		
Db	459	ctggggcgaaggactctggccactgtctctgcagctccaccaaggccatcggtctt	518
Qy	405	CTGGGGCCGGGAGACTGGTACCCTCTCTCAGCTAGCACAGGGCCCATCGGTCTT	464
Db	519	ccccctggcacctctctccaagagcacctctgggggcacagggccctgggtcct	578
Qy	465	CCCCCTGGCACCCTCTCCAAAGACACTCTGGGGGCACAGGGCCCTGGGTGGT	524
Db	579	caaggactctcccgaccggtgacggtgctggaaactcaggcgccctgaccacgg	638
Qy	525	CAAGGACTACTTCTCCCGCAACCCGGTTCAGGGTGTCTGTGGAACTCAGCCAGCGG	584
Db	639	gtgcacacctcccgctgtctactagtcctcaggactctactccctcagcagctggt	698
Qy	585	CCTGCACAGCTTCCCGGCTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGT	644
Db	699	gacgctgcctccagcagcttgggcaccacagacctacatctgcaacgtgaatcacaagg	758

QY 645 GACCGTGGCCCTCCAGCAGCGTTGGCGACCCAGACACCTACATCTGCCAAGCTGAATCACAAGCC 704

Db 759 gacgaacacaaagtggaagaaagtggacccaattctgtgacaaaactcacacatg 818  
|||||

QY 705 CAGCACAACAAAGGTGGCAGAAACGACGCCCAATCTTGTCAGAAACTCACACATG 764  
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Db 819 ccacacgtgccagcaacctgaactcctgggggaccgtcagttcttctcttccccccaaa 878  
|||||

QY 765 CCCACGTCGCCAGCAACCTGAACCTCTGGGGGACCGTCAGTCTTCTTCTTCCCCCACA 824  
|||||

Db 879 accaaggaacacctcatgatctcccgagccctgaggtcacatgggtgtgtgtgacgc 938  
|||||

QY 825 ACCAAGGACACCTCATGATCTCCGGGACCCCTGAGGTCACTGCTGGTGGAGCT 884  
|||||

Db 939 gaccacgaagacctgaggtcaagttcaactggtacgtgagcggtggaagtgataa 998  
|||||

QY 885 GAGCCACGAAGACCTGAGGTCAAGTTCAACTGTGTAGCTGGACGGCTGGAGTGCATTA 944  
|||||

Db 999 tgcaagaacaaagccgaggagagcagtcacaacagcacgtaccgtgtgtgtcagctcct 1058  
|||||

QY 945 TGCAGAGCAAAAGCCCGCGGAGGAGCAGTACAACGACGTTACCGCTGTGTGTCAGCGTCT 1004  
|||||

Db 1059 caccgtcctgcaccagagctggtgaatgcgaagagtagcaagtgaaggtctccaacaa 1118  
|||||

QY 1005 CACCGTCTGACGACGAGCTGGTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAACA 1064  
|||||

Db 1119 agccctccagcccccacatcgagaaaaccatctccaaagccaaaggaaccccgagacc 1178  
|||||

QY 1065 AGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGCGCCCGGAAACC 1124  
|||||

Db 1179 acaggtgtacacctgcccccacatcccggtgagctgacctgacccaagaacccaggtcagctgac 1238  
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QY 1125 ACAGGTGTACACCTGCCCCATCCCGGATCCCGGGATGAGCTGACCAAGAAACGAGTCAAGCTGAC 1184  
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Db 1239 ctgctgtgcaaaaggtcttctccccagagacatcgccgtggagtggaagcaatggca 1298  
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QY 1185 CTGCTGTCAAGGCTTCTATCCAGCCACATCCCGGTGAGTGGGAGAGCATGGGCA 1244  
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Db 1299 gccggagaaacact acaagaccagcctcccggtgctggactccgacggtccttcttcc 1358  
|||||

QY 1245 GCGGGAACAACACTACAAGACCAAGCCTCCGCTCTGGACTCCGACGGCTCTTCTTCTCT 1304  
|||||

Db 1359 ctacagaagctcacgtggacaagagagtgacagcaggggaacgtcttctcatgctc 1418  
|||||

QY 1305 CTACAGCAAGCTCACGCTGGCAAGAGCAGGTGGCAGCAGGGGAAACGCTTCTCATCTC 1364  
|||||

Db 1419 cgtgatgatgaggtctgcacaaacctacacgagagaagacctctccctgtctccggg 1478  
|||||

QY 1365 GTGTGATGATGAGGCTCTGCACAACCACTACACGCAAGAGCCCTCTCCCTCTCTCCGGG 1424  
|||||

Db 1479 taaatga 1485  
|||||

QY 1425 TAAATGA 1431  
|||||

RESULT 14  
ID Q65628 standard; DNA; 8540 BP.  
AC Q65628;  
DT 01-FEB-1995 (first entry)  
DE Vector contg. TCAE 8 DNA.  
KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;  
KW cell lysis; as.  
OS Homo sapiens.  
PN W09411026-A.

PD 26-MAY-1994.  
PF 12-NOV-1993; U10953.  
PR 13-NOV-1992; US-978891.  
PR 03-NOV-1993; US-149099.  
PA (IDEC-) IDEC PHARM CORP.  
PI Anderson DR, Hanna N, Leonard JE, Newman RA, Raetetter WH;  
PI Refime;  
DR WPI; 94-183162/22.  
PT Treating B cell lymphoma with chimeric antibody - against CD20,  
PT causing rapid depletion of peripheral B cells, also new  
PT antibodies and hybridomas  
PS Disclosure; Fig 2; 101pp; English.  
CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric  
CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8  
CC contains 4 transcriptional cassettes, human Ig light and heavy chain  
CC constant regions, dihydrofolate reductase and neomycin  
CC phosphotransferase. The vector can be used to produce antibodies  
CC which cause depletion of peripheral blood B cells, including those  
CC associated with lymphoma. They mediate complement-dependent lysis  
CC and lyse target cells by antibody-dependent cellular cytotoxicity.  
CC See also Q65629-35.  
SQ Sequence 8540 BP; 2069 A; 2221 C; 2226 G; 2023 T;  
Query Match 69.0%; Score 987; DB 11; Length 8540;  
Best local Similarity 99.7%; Pred. No. 0.00e+00;  
Matches 990; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 2152 gctagacacaaaggcccatcggtcttccccctggacacctctccaagagacacctggg 2211  
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QY 439 GCTAGCACCAAGGGCCATCGCTTCCCGCTGGCACCTCTCTCAAGAGACCTCTGGG 498  
|||||

Db 2212 ggcacagcgccctgggtgctggtcaaggactactccccgaacccgtgacgtgtcg 2271  
|||||

QY 499 GCACAGCGGCCCTGGGCTGCTGCTCAAGACACTACTTCCCGAACCGGTGACGGTGTG 558  
|||||

Db 2272 tggaaactcagggcctgacacagcggtgcacaccttccccggtcctcacagtctca 2331  
|||||

QY 559 TGGAACTCAGGCGGCCCTGACAGCGCGTGACACCTTCCGGGTCTCAGTCCCTCA 618  
|||||

Db 2332 ggactctactccctcagcagcgtggtgacctgacctccagcagcttcggcaccagacc 2391  
|||||

QY 619 GGACTCTACTCCCTCAGCAGCGCTGTGACCTGCGCTTCCAGCAGCTTGGSCACCCAGACC 678  
|||||

Db 2392 tacatctgcaagtgatcaacaagccagcaacacccaaggtggacaagaagcagagccc 2451  
|||||

QY 679 TACATCTGCAACGTGAATCACAAGCCGACCAACACCAAGGTGGAAGAAGACAGAGCC 738  
|||||

Db 2452 aaatcttggacaaaactcacacatgccaccgtgccagcacctgaactcctggggga 2511  
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QY 739 AAATCTTGTGCAAAACTCACATGCCACCGTCCGCGACACCTGACTGCTCTGGGGGA 798  
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Db 2512 ccgtcagttcttcttcccccaaaacccaaggaacacctcatgatctccccgaccct 2571  
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QY 799 CCGTCAGTCTTCTCTTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCGACCCCT 858  
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Db 2572 gaggtcacatgcgtgggtggaagtgagccacgaagacctgaggtcaagttcaactgg 2631  
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QY 859 GAGGTCACTGCTGCTGGTGGAGCTGACGACCAACGACACCTGAGGTCAAGTTCAACTGG 918  
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Db 2632 taogtggacgggtggaggtgcataatgccaaagaacgcgcggggagagcagtaaac 2691  
|||||

QY 919 TACGTGGAGCGCGTGGAGGTGCATTAATGCCAAGACAAACCGCGGGAGGAGCAGTACAAC 978  
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Db 2692 agcagctaccgtgtggtcagcgtcctcaccgtcctgcaccagagactggctgaatggcaag 2751  
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Qy 979 AGCAGCTACCTGTGTGCTAGCGCTCTCACCGCTCTCGCACCAGGACTGGCTGAATGGCAAG 1038  
Db 2752 gactacaagtgaaggtctccaacaagccctccagcccccatcgaaaaaccatctcc 2811  
Qy 1039 GAGTACAGTGAAGGTCTCCACAAAGCCCTCCCGAGCCCATCGAAGAAACCATCTCC 1098  
Db 2812 aaagccaaagggcagcccgagaaacacaggtgtacacccctgcccccatcccgagatgag 2871  
Qy 1099 AAAGCCAAAGGGCAGCCCGAGAACACAGGTGTACACCTCGCCCCCATCCCGGATGAG 1158  
Db 2872 ctgaccagaacacaggtcagctgacctgcctggtcaaggtcttctatccagagacatc 2931  
Qy 1159 CTCACCAAGAACCGCTCAGCTGACCTGCCTGCTCAAGGCTTCTATCCAGCGACATC 1218  
Db 2932 gccgtggagtggagagcaatggcgagccggagagacaactacaagaccacgctccgtg 2991  
Qy 1219 GCCGTGGAGTGGGAGCAATGGCGAGCGGAGACACACTACAGACACGCGCTCCCGTG 1278  
Db 2992 ctgactccagcggtcctctctctctacagcaagctcacccgtggagagagcaggtgg 3051  
Qy 1279 CTGGACTCCGAGCGCTCTTCTCTACAGCAAGCTCACCGTGGACAGAGAGAGGTGG 1338  
Db 3052 cagcaggggaacgtcttctcatgctccgtgatgatgaggtcttgacacaccactacag 3111  
Qy 1339 CAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGAGGCTCTGCAACCACTACAGG 1398  
Db 3112 cagaagagcctcctgctctccgggtaaatga 3144  
Qy 1399 CAGCAGCGCTCTCCCTGCTCTCCGGTAAATGA 1431

## RESULT 15

ID Q25692 standard; cDNA; 1412 BP.  
AC Q25692;  
DE 28-DEC-1992 (first entry)  
DE Sequence of the chimeric H chain cDNA contained in pTB1373  
KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;  
KW antithrombotic agent; myocardial infarction therapy; ss.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT sig peptide 13..69  
FT /\*tag= a  
FT /product= Leader  
FT CDS 70..414  
FT /\*tag= b  
FT /product= VH  
FT CDS 415..708  
FT /\*tag= c  
FT /product= CH1  
FT CDS 709..753  
FT /\*tag= d  
FT /product= hinge  
FT CDS 754..1083  
FT /\*tag= e  
FT /product= CH2  
FT CDS 1084..1407  
FT /\*tag= f  
FT /product= CH3  
PN EP-491351-A.  
PD 24-JUN-1992.  
PF 17-DEC-1991; 121591.  
PR 18-DEC-1990; JP-413829.  
PR 11-NOV-1991; JP-294464.

PA (TAKE ) TAKEDA CHEM IND LTD.  
PI Iwasa S, Taka H, Matanabe T, Tada H;  
DR WPI; 92-209528/26.  
DR P-PSD3; R24812.  
PT Chimeric monoclonal antibodies - contain anti-human fibrin  
PT antibody light and heavy chain variable and constant for treating  
PT thrombotic conditions e.g. myocardial infarction  
PS Example; Figure 11; 87pp; English.  
CC Plasmid pTB1373 contains the whole length of a mouse-human  
CC chimeric anti-human fibrin heavy chain cDNA open reading  
CC frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin  
CC chimeric Ab-producing transformant FIB1-H01/X63 as a template  
CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as  
CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH  
CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding  
CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain  
CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader  
CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CH  
CC respectively as a primer for first strand cDNA synthesis and the  
CC primer combination of 5'CH and 3'C2H, of 5'EH and 3'CH and of  
CC 5'SH and 3'EH respectively as primers for PCR. The amplified gene  
CC products were isolated and used to produce plasmids. After  
CC confirmation of the cDNA sequence of each plasmid, the cDNA  
CC encoding LH, VH, CH1 and CH2CH3 were joined together to give  
CC plasmid pTB1373 contg. the whole length chimeric H chain  
CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-F1B,  
SQ Sequence 1412 BP; 325 A; 433 C; 381 G; 273 T;

Query Match 68.7%; Score 983; DB 4; Length 1412;  
Best Local Similarity 97.9%; Pred. No. 0.00e+00;  
Matches 1005; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Db 381 ctggggccaagggaccctgtgctcaccgtctcaggtgtcagcaccagggccctcggtctt 440  
Qy 405 CTGGGGCGCGGAGACCTGTGTCTCCTCAGCTAGCACCAGGGGCCATCGGTCTT 464  
Db 441 ccccttggcaccctctccaagagcactctggggcagcagggccctggctgctggt 500  
Qy 465 CCCCTCGCACCTCTCTCCAAAGACACTCTGGGGGCACAGGGCCCTGGGCTGCTCGT 524  
Db 501 caagactactctcccgaaacccggtgacggtgtcgtggaaactcaggccctgaccaggg 560  
Qy 525 CAAGGACTACTTCCCGAACCCTGACGGTGTCTGGAACCTCAGGGCCCTGACGACGG 584  
Db 561 cgtgcacacttcccggtgtcctacagtcctcaggactcactccctcagcagctggt 620  
Qy 585 CGTGCACACTTCCCGGCTGCTTACAGTCTCCTCAGGACTCTACTCTCCTCAGCAGGCTGT 644  
Db 621 gacgtgacctccagcagcttgggacccagacctacatctgcacacctgaatcacaagcc 680  
Qy 645 GACCGTGCCTTCCAGCAGCTTGGGCGACCCAGACCTACATCTCGAACGTGAATCAAGCC 704  
Db 681 cagcaacaccaaggtggacaagagagtgagcccaaatcttgtgacaaaactcacagtg 740  
Qy 705 CAGCAACCAAGGTGGACAAAGAAACAGAGCCCAATCTTGTGACAAAATCACATG 764  
Db 741 tcaacggtgcccggcgctgaactcctggggggaccgtcagctcttctcttcccccaaa 800  
Qy 765 CCCAGCTGCCACGACCTCTCCTGAGGAGCGCTCAGTCTTCTCTTCCGCCCAAA 824  
Db 801 acccaaggacacctcatgatctcccgagccctcaggtcacatgcgtggtggtggagct 860  
Qy 825 ACCCAGGAGACCCCTCATCTCTCCGGGACCCCTGAGGTACATGCTGCTGCTGGACGT 884

Db 861 gaccacgaagaccctgaggtcaagttcaactggtacgtgacggcgtgaggtgcataa 920  
|||||  
Qy 885 GAGCCACGAAGACCCTGAGGTCAGGTCAAGTTCACTGGTACGTGACGGCGTGGAGGTGCATAA 944  
  
Db 921 tgccaagacaaagccgcgggagagcagtgacaacagcaagtcaccgtgtggtcagcgtcct 980  
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Qy 945 TGCCAAGACAAAGCCGCGGAGGAGGACGTACAAACAGCAGTACCGTGTGCTCAGCGTCCT 1004  
  
Db 981 caccgtcctgcaccaggactggtgaaatgcaagagtgacaagtgaaggtctccaacaa 1040  
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Qy 1005 CACCGTCTCGACCAAGGACTGGCTGAATGGCAAGGACTACAGTGCAAGGTCTCCACAA 1064  
  
Db 1041 agccctccagcccccatcgagaaaccatctccaaagccaaaggcgagccccgagacc 1100  
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Qy 1065 AGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAGCCAAAGGGAGCCGCCGAGAAC 1124  
  
Db 1101 acaggtgtacacccctgcccccatcccgaggagagatgaccaagaaccaggtcagcctgac 1160  
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Qy 1125 ACAGGTGTACACCCCTGCCCCCATCCCGGGATGAGCTACCAAGAAACAGGTCAGCCTGAC 1184  
  
Db 1161 ctgcctggtcaaggtttctatcccagcgacatcgccgtggagtgaggagacaatgggca 1220  
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Qy 1185 CTGCTGTCAAGGCTTCTATCCAGCCACATCGCCGTGGAGTGGGAGAGCAATGGGCA 1244  
  
Db 1221 gccgagacaactacaagaccagcctcccgtgctggactccgaoggtcctcttct 1280  
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Qy 1245 GCCGAGAACAACTACAAGACACGCTCCCGTGTGGACTCCGAGGGTCTCTTCCT 1304  
  
Db 1281 ctatagaagctcaccgtggacaagcaggtggcagcagggggaacgtctctcatgctc 1340  
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Qy 1305 CTACAGCAAGCTCACCGTGGACAGAGAGGTTGGCAGCAGGGGAACGTCTTCTCATGCTC 1364  
  
Db 1341 cgtgatcatgaggtctctgcacaaccactacacgagagaagcctctccctgtcccggg 1400  
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Qy 1365 CGTGATGCATGAGGCTCTGCACAACCACTACACGCAAGAGAGCCCTCTCCCTGTCTCCGGG 1424  
  
Db 1401 taaatga 1407  
|||||  
Qy 1425 TAAATGA 1431

Search completed: Tue Dec 17 21:28:27 1996  
Job time : 125 secs.





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IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 992191

Location/Qualifiers

source

1..384

/organism="Homo sapiens"

/clone="235978"

&lt;1..&gt;384

98 a 113 c 104 g 64 t 5 others

Query Match

23.3%; Score 334; DB 20; Length 384;

Best Local Similarity 96.1%; Pred. No. 0.00e+00;

Matches 369; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

Db 1 gtgaatcacaagccagcaacacacaggtggacaagagagttgagcccaaatcttgtgac 60

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Qy 691 GTGAATCACAGCCAGCACACACAGGTGGACAGAGACGACCCCAANTCTTGTGAC 750

|||||

Db 61 aaaactcacatgcccacgctgccagcacctgaactcctgggggagcgcagctcttc 120

|||||

Qy 751 AAAACTCACATGCCCCAGCGCCAGCACACCTGAACCTCTGGGGAGACCGTCAGCTTC 810

|||||

Db 121 ctctcccccaaaacccaagacacccctcatgatctccggagccctgaggtcacatgc 180

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Qy 811 CTCTCCCCCAAAACCCAGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGC 870

|||||

Db 181 gtggtgtggagctgagccagcaagaccctgaggtcaagttcaactgtactgtgagcgc 240

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Qy 871 GTGCTGTGGAGCTGAGCCACCAAGACCCCTGAGGTCAAGTTCAACTGTACTGTGACGCG 930

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Db 241 gtgaggtgcataatgccaaagccggcgagngcagtcacacagcagctaccgt 300

|||||

Qy 931 GTGGAGGTGCATATGCCAGACAAACCGCGGGAGGAGGAGTACACAGCAGTACCCT 990

|||||

Db 301 gtggttcagctcctcacgctcctggcaccagantgctganttggcaagngtacaag 360

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Qy 991 GTGGT-CAGCGTCTCACCCTGCTG-CACCAGACTGCTGTGAAT-GGCAGGAGTACAAG 1047

|||||

Db 361 tgccaaggttttccaanaagcc 384

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Qy 1048 TGC-AAAGTCT-CCAACAAGCCC 1069

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RESULT 3 T93165 415 bp mRNA EST 22-MAR-1995

LOCUS ye24c07.r1 Homo sapiens cDNA clone 118668 5' similar to gb:M87789

DEFINITION IG GAMMA-1 CHAIN C REGION (HUMAN);

ACCESSION T93165

NID g725078

KEYWORDS EST.

SOURCE vector=pBluescript SK- host=SOLR cells (kanamycin resistant)

primer=M13RP1 Rsitel=EcRI Rsite2=XhoI Normal lung tissue from a 72

year old male. Cloned unidirectionally. Primer: Oligo dT. Average

insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:

5'-GAATTCGGACGAG-3'; 3' adaptor sequence:

5'-CTCAGTCTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 415)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

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Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevas, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

WashU-Merck EST Project

Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

High quality sequence stops: 299

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 725078

Location/Qualifiers

source

1..415

/organism="Homo sapiens"

/clone="118668"

/note="human"

BASE COUNT 104 a 134 c 103 g 71 t 3 others

ORIGIN

Query Match 22.1%; Score 316; DB 107; Length 415;

Best Local Similarity 96.9%; Pred. No. 0.00e+00;

Matches 378; Conservative 0; Mismatches 2; Indels 10; Gaps 9;

Db 1 acaaaactcaacatgccacnctgccagcacatgaactcctgggggagcagctcagtc 60

|||||

Qy 749 ACMAAACTCACATGCCACC-GTCCCAGCACCTGAACCTCTGGGGAGCCGTCAGTC 807

|||||

Db 61 ttctcttcccccaaaacccaagcacctcatgatctcccgagccctgaggtcaca 120

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Qy 808 TTCCTCTTCCCCCAAAACCCAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTGACA 867

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Db 121 tgcgtggtgtgagctgagccagcaagaccctgaggtcaagttcaactgtactgtgac 180

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Qy 868 TGCCTGTGTGGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCACTGCTAGCTGGAC 927

|||||

Db 181 ggcgtgaggtgcataatccaaagccgagcggagcagcagcagcagcagcagcagc 240

|||||

Qy 928 GCGCTGGAGGTGCATATGCCAAGACCCGCGGAGCAGTACAAACAGCAGCTAC 987

|||||

Db 241 cgtgtggtcagcgtcctcacgctcctgcaccagggacttgcttgaatggaagagagtac 300

|||||

Qy 988 CGTGTGTGTCAGCTCTCACCGCTCTGCACAGG-ACT-GGCT-GAATGCAAGGAGTAC 1044

|||||

Db 301 aagttgcaaggtcttccaacaaagccctccagcccttcgaaggaacacacatctcca 360

|||||

Qy 1045 AAGT-GCAAGGTCT-CCACAAAGCCCTCCAGCCCCCATCGA--GAATACCATCT-CCA 1099

|||||

Db 361 aagcacaagggcagcccgaggaaccacag 390

|||||

Qy 1100 AAGCAAGGGCAGCCCGCAG-AACCCAG 1128

|||||

RESULT 4

LOCUS R82750 484 bp mRNA EST 14-JUN-1995

DEFINITION YJ25c07.r1 Homo sapiens cDNA clone 149772 5' similar to gb:M87789

IG GAMMA-1 CHAIN C REGION (HUMAN);

ACCESSION R82750



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NID 9862141  
 KEYWORDS EST.  
 SOURCE human clone-149772 library-Soares placenta Nb2HP vector-p7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 Rsite1=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']  
 AACTGGAGAAATTCGGCGCGCAGGAAATTTTTTTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.  
 Homo sapiens  
 ORGANISM  
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 484)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 TITLE  
 The WashU-Merck EST Project  
 JOURNAL  
 Unpublished (1995)  
 COMMENT

NCBI gi: 862141  
 Location/Qualifiers  
 source 1..484  
 /organism="Homo sapiens"  
 /clone="149772"  
 /note="human"  
 BASE COUNT 122 a 143 c 129 g 88 t 2 others  
 ORIGIN  
 Query Match 21.7%; Score 310; DB 69; Length 484;  
 Best Local Similarity 91.9%; Pred. No. 0.00e+00;  
 Matches 442; Conservative 0; Mismatches 20; Indels 19; Gaps 19;

Db 1 cacaagccagcaacacgaagtgagagagtgaggccaaatctgtgacaaaact 60  
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 Qy 697 CACAAGCCCAACACACCAAGGTGAGAGAAAGCAGACGCAAAATCTGTGACAAAAC 756  
 Db 61 cacacatcccacgtgccagaccctgaactctctgggggaccgtcagctctctcttc 120  
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 Qy 757 CACACATCCCAACCGTCCCGACACCTGAATCTCTGGGGGACCGTCAGTCTCTCTTC 816  
 Db 121 cccccaaacccaaggaacacctgatctcccgacccttgaggtcacatgaggtg 180  
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 Qy 817 CCCCCAAACCAAGGACGACACCTCATGTCCTCCGGGACCCCTGAGGTGCATGGCGTGC 876  
 Db 181 gtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggag 240

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Qy 877 GTGCACTGAGCCAGCAACCCCTGAGTCAAGTTCACCTGCTAGCTGGACGGCGTGAG 936  
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 Db 241 gtgcataatgccaaagccgagagagcagtcacacagcagcagtcacacgtgagtt 300  
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 Qy 937 GTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACACAGCAGCTACCGTGGT- 995  
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 Db 301 cagcgtctcaccgtctctcgcacacagattgggttgatgggcaaggaggtacagt 360  
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 Qy 996 CAGCGT-CCTCACCCT-CCTG-CACCAAGCACTGGCT-GAATGG-CAAGG-AGT-ACAAGT 1048  
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 Db 361 tgaaggtttcccaaaagccctcccgagcccttttttaggaaacaccttttccaaa 420  
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 Qy 1049 -GCAAGGTCT-CCAACAAAGCCCT-CCAG-CCCCCATCG-AG-AAAACCATCT-CCAAA 1101  
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 Db 421 gccaaagggcagcccccagagacacacagtcgttacaacttgcccmctcccgaggga 480  
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 Qy 1102 GCCAAGGG-CAG-CCCCGAG-AACACAGGTGTACACCTGCCCCCAT-CCCGGGATGA 1157  
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 Db 481 g 481  
 Qy 1158 G 1158

RESULT 5  
 LOCUS H67250 364 bp mRNA EST 27-OCT-1995  
 DEFINITION yu65h03.r1 Homo sapiens cDNA clone 238709 5' similar to gb:M87789  
 IG GAMMA-1 CHAIN C REGION (HUMAN);  
 ACCESSION H67250  
 NID gi1025990  
 KEYWORDS EST.  
 SOURCE human clone=238709 primer=M13R1 library=Weizmann Olfactory Epithelium vector=pBluescript SK- host=SO1R cells (kanamycin resistant) Rsite1=EcoRI Rsite2=XhoI From 35 year old female. The cDNA was oligo (dT) primed with an XhoI restriction enzyme recognition site and an 18 base poly dT sequence. For the 5' end, the synthesized cDNA termini were treated with T4 DNA polymerase and EcoRI adaptors were ligated to the blunt ends.

ORGANISM Homo sapiens  
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 364)  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 TITLE WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT

Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 241  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 1025990

## FEATURES

source  
1..364  
/organism="Homo sapiens"  
/clone="238709"  
/note="human"

mRNA

BASE COUNT 79 a 117 c 101 g 65 t 2 others

## ORIGIN

Query Match 21.2%; Score 304; DB 24; Length 364;

Best Local Similarity 98.4%; Pred. No. 0.00e+00;

Matches 312; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 1 ccgagacacacaggtgtataccctgcccccacccgagatgagctgaccaagaacaggt 60  
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QY 1116 CCAGAACACACAGGTGTACACCCCTGCCCCCATCCCGGATAGCTGACCAAGAACAGGT 1175  
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Db 61 cagcctgacctgctggtcaaggcttctatcccagcgacatcgccgtggagtggagag 120  
|||||  
QY 1176 CAGCCTGACCTGCCCTGCTCAAAAGCTTCTATCCAGCGACATCCGCTGGAGTGGAGAG 1235  
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Db 121 caatggcagccggaagaacaactacaagacacgcctccgtgctgactccgacggctc 180  
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QY 1236 CAATGGCAGCGGAGAACAACTACAAGACACCGCTCCGCTGGTGGACTCGACGGCTC 1295  
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Db 181 cttctctctacagcaagctcaccgtggacaagagcagctngcagcaggggaacgtctt 240  
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QY 1296 CTTCTCTCTACAGCAGCTCACCCTGCAAGAGCGGTGGCAGCAGGGGAGCTCTT 1355  
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Db 241 cttactcctgctgctgaggtctgcacaacactacacgacgagagcgtctccct 300  
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QY 1356 CTCATGCTCCGCTGANGCATGAGGCTGTGCACACCACTACAGCAGAGCGCTCTCCCT 1415  
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Db 301 gtttcgggtaataqa 317  
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QY 1416 GTCT-CCGGGTAATCA 1431

## RESULT

LOCUS T59711 474 bp mRNA EST 09-FEB-1995  
DEFINITION ycl13h10.s1 Homo sapiens cDNA clone 80611 3' similar to gb:M87789 IG  
GAMMA-1 CHAIN C REGION (HUMAN);  
ACCESSION T59711  
NID 9661548  
KEYWORDS EST.  
SOURCE human clone=80611 library=Stratagene lung (#937210)  
vector=pBluescript SK- host=50LR cells (kanamycin resistant)  
primer=21ml3 Reitel-EcoRI Reite2-XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:  
5'-CTCGAGTTTTTTTTTTTTTT-3'.

## ORGANISM

Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 474)  
Hillier, L., Clark, N., Duboue, T., Elliston, K., Hawkins, M.,  
Holman, L., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevisan, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE  
WashU-Merck EST project  
JOURNAL  
Unpublished (1995)

COMMENT  
Contact: Wilson RK

## WashU-Merck EST Project

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@wustl.edu

High quality sequence stops: 353

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 661548

FEATURES  
source  
1..474  
/organism="Homo sapiens"  
/clone="80611"  
/note="human"

BASE COUNT 74 a 125 c 145 g 117 t 13 others

## ORIGIN

Query Match 21.0%; Score 300; DB 98; Length 474;  
Best Local Similarity 93.7%; Pred. No. 0.00e+00;  
Matches 341; Conservative 0; Mismatches 17; Indels 6; Gaps 6;

Db 110 tcatattaccggagacagggagaggtctctcgntagtggtntgcagagcctcatg 169  
|||||  
Cp 1431 TCATTTACCGGACAGAGGAGGCTCTTCTGGCTGTACTGTTGTGCAGAGCCTCATG 1372  
|||||  
Db 170 catcagggagcatgagaagcgttccctgctgccactgctcttntccacggttagctt 229  
|||||  
Cp 1371 CATCAGCGAGCATGAGACAGCTTCCCTGCTGCCACCTGCTCTTGTCCACGGTAGCTT 1312  
|||||  
Db 230 gctntaggaagaagagcctcgantccagcagggagcgtgctctttagtattgtt 289  
|||||  
Cp 1311 GCTGTAGGAGGAAGAGAGCGCTCGAGTCCAGACGGGAGCGCTGCTGTAGTTGTT 1252  
|||||  
Db 290 ctccggtgccccattgctctcccactccacggcgatgctcgctggggatagaagccttta 349  
|||||  
Cp 1251 CTCGGCTGCCATTGCTCTCCACTCCACGGCATGCTCGCTGG-ATAGAACCTTTGA 1193  
|||||  
Db 350 ccaggcgagtcaggtacgttcttggctcagctcatcccggtgagggcgagg 409  
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Cp 1192 CAGG-CAGGTCAGGCTGACCTGG-TTCTT-CGTCAGCTCATCCCGGATGGGGCAGGG 1136  
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Db 410 tatacactgtngtctcggggcttccctttgtttngaaatggttttcttctatggg 469  
|||||  
Cp 1135 TGTACACCTGTGTTCTCGGGCTGCCCTTTGGCTTT-CGACATGCTTTTCT-CGATGGG 1078  
|||||  
Db 470 ggcct 473  
|||||  
Cp 1077 GGCCT 1074

## RESULT

LOCUS R82945 363 bp mRNA EST 04-AUG-1995  
DEFINITION yplq03.s1 Homo sapiens cDNA clone 187156 3' similar to gb:M87789  
IG GAMMA-1 CHAIN C REGION (HUMAN);

## ACCESSION

R82945

## NID

g927913

## KEYWORDS

EST.

## SOURCE

human clone=187156 library=Soares breast 3NbHBst vector=pT7f3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=Promega -21ml3 Reitel=Eco RI Adult  
human. 1st strand cDNA was primed with a Not I - oligo(dT) primer

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11

[5' TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 363)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence starts: 1  
High quality sequence stops: 1

Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality.

NCBI gi: 927913

## FEATURES

Location/Qualifiers  
1..363  
/organism="Homo sapiens"  
/clone="187156"  
/note="human"

BASE COUNT 54 a 99 c 115 g 82 t 13 others

Query Match 20.6%; Score 295; DB 69; Length 363;  
Best Local Similarity 92.3%; Pred. No. 0.00e+00;  
Matches 308; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 31 tcattaccgggagacaggagaggtcttctgctgtagtggtntgacagcctcatg 90

Cp 1431 TCATTATCCGGACACAGAGGAGGCTCTCTGCGCTGCTAGTGGTTCGACAGCCTCATG 1372

Db 91 catcaggaagcatgagaagcgtccctgtgccaactgtcttctgtccacggtgagctt 150

Cp 1371 CATCAGGAGCATGAGAGCTTCCCTGCTGCGCCTCTCTCTGTCACAGGTGAGCTT 1312

Db 151 nctatagagaagaagagcctcgggtccagcagggagcgtggtcttctgtagtgtt 210

Cp 1311 CCTGTAGAGGAAGAAGAGCGCTCGGAGTCCAGCAGGAGCGGCTGTGTGTTGTTT 1252

Db 211 ctccgctgcccattgctctcccactccacggcgatgtcgctggatagagcctttgac 270

Cp 1251 CTCGGCTGCCCATGCTCTCCACTCCAGGCGATGCTCGCTGGGATAGAGCCTTTGAC 1192

Db 271 cagggaggtcaggctnaccgggntcttgggcanctcccccnngatgggggcaagggttna 330

Dec 17 21:23

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12

Cp 1191 CAGGCAGGTGACCTGGCTCTTGGTCAGCTATCCCGGATGGGGCAGGCTGA 1132

Db 331 cacccttggttttcngggtmnccttgcctt 363

Cp 1131 CACCTGTGTTCTCGGGGCTGCCCTTTGGGCTTT 1099

## RESULT

8

## LOCUS

H62381 473 bp mRNA EST 06-OCT-1995

## DEFINITION

yu41a02.s1 Homo sapiens cDNA clone 236330 3' similar to gb:M87789

## ACCESSION

H62381

## NID

gi1015213

## KEYWORDS

EST.

## SOURCE

clone=236330 primer=Promega -2ml3 library=Soares ovary tumor  
Nshot vector=pT7T3D (Pharmacia) with a modified polylinker  
host=DH10B (ampicillin resistant) Reitel=Not I Rsite2=Eco RI  
Female. 1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5' TGTTACCAATCTGAAGTGGAGCGCGGCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT7T3 vector (Pharmacia). Library  
constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 473)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 284  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LML; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 1015213

## FEATURES

Location/Qualifiers  
1..473  
/organism="Homo sapiens"  
/clone="236330"  
<1..>473

## BASE COUNT

77 a 114 c 158 g 116 t 8 others

## ORIGIN

Query Match 20.0%; Score 286; DB 22; Length 473;

Best Local Similarity 91.0%; Pred. No. 0.00e+00;

Matches 332; Conservative 0; Mismatches 29; Indels 4; Gaps 4;

Db 100 tcattaccggagacaggagaggtcttctgtgtagtggttgcagagcctcatg 159

Dec 17 21:23

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13

Cp 1431 TCATTTACCCGAGAGAGGAGGCTTTCTGCGTGTAGTGTGTCGACAGCCTCATG 1372  
|||||  
Db 160 catcagagagcatgagaacgttccctctgctgccacgtctcttctgacacgtgagctt 219  
|||||  
Cp 1371 CATCAGGAGCATGAGAGAGCTCCCTGCTGCCACCTGCTCTTGTGCCAGGTGAGCTT 1312  
|||||  
Db 220 gctgtagagaagaagccgtcgagtcagcatgagaggtggtgcttctgagttgt 279  
|||||  
Cp 1311 GCTGTAGAGAGAGAGAGGCGCTGGAGTCCAGACGAGGCGTGGTCTGTGTAGTGTCT 1252  
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Db 280 ctccggtcccatgctctccactccagggcgagtgctgctgggtgagagcctttna 339  
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Cp 1251 CTCGGCTGCCATTGCTCTCCACTCCACGG-CGATGTCGCTGGATAGAGCCTTTGA 1193  
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Db 340 ccaggagagtcaggctgancgttcttctggtcctctccctcccgagattggggcagggt 399  
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Cp 1192 CCAGGAGTCAAGTCACTGG-TTCTGCTCAGCTCATCCCGGATGGGGCAGGTG 1134  
|||||  
Db 400 taaaccgtngtctcggttgccttngt-ttngaaangtttt-tcgtatgggntt 457  
|||||  
Cp 1133 TACACTGTGTCTCGGGCTGCCCTTTGGCTTTGGAGATGTTTCTCATGEGGCT 1074  
|||||  
Db 458 ggaag 462  
|||  
Cp 1073 GCGAG 1069

RESULT 9  
LOCUS R66507 358 bp mRNA EST 30-MAY-1995  
DEFINITION y132f05.r1 Homo sapiens cDNA clone 140961 5' similar to gb:M87789  
IG GAMMA-1 CHAIN C REGION (HUMAN);  
ACCESSION R66507  
NID g839145  
KEYWORDS EST.  
SOURCE human clones=140961 library=Soares placenta Nb2HP vector=pT7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta  
obtained at birth (full term). 1st strand cDNA was primed with a  
Not I - oligo(dT) primer (5'  
AACTGGAGAAATCCCGCGGAGGATTTTTTTTTTTTTTTT 3'), double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the modified pT7T3  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 358)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,B., Rohlfing,T., Soares,M., Tan,F.,  
Trevisan,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.

## TITLE

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

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14

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 219  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 839145  
FEATURES  
Location/Qualifiers  
source  
1..358  
/organism="Homo sapiens"  
/clone="140961"  
/note="human"  
BASE COUNT 90 a 109 c 92 g 63 t 4 others  
ORIGIN

Query Match 19.9%; Score 285; DB 64; Length 358;  
Best Local Similarity 97.8%; Pred. No. 0.00e+00;  
Matches 310; Conservative 0; Mismatches 3; Indels 4; Gaps 4;  
Db 2 acaagtccaaggtctccaacaagccctccagcccccatcgagaaaaccatctccaaag 61  
|||||  
Qy 1043 ACAAGTCAAGGTCTCCACAAAGCCCTCCAGCCCTCCATCCGAGAAACCATCTCCAAAG 1102  
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Db 62 ccaaggagcccgagaaacacaggtgtacacccctgcccccatcccggtgagctga 121  
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Qy 1103 CCAAGGGCAGCCCGAGAACCAACAGGTGTACACCTGCGCCCATCCGGGATGAGCTGA 1162  
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Db 122 ccaagaccaggtcagctgacctgctgctcaagagcttctatcccgagacatcgccg 181  
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Qy 1163 CCAGAACACAGGTGAGCTGACCTGCTGTCAAGGCTTCTATCCGAGCAGCATCGCG 1222  
|||||  
Db 182 tggagtggagagaatggcagccgagagacaactacaagaccagcctcccggtgctgg 241  
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Qy 1223 TGGAGTGGGAGAGCAATGGCGCAGCGGAGAACAACTACAAGACCCCTCCCGTCTGG 1282  
|||||  
Db 242 gattccagagctcttctctcttcttaccagagtcacccgtgggacaagagcaggtgg 301  
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Qy 1283 -ACTCCGAGCGGCTCTCTTCTCTCT-ACAGCAAGTCAACCTGG-ACAAGAGCAGGT-GG 1338  
|||||  
Db 302 cagcaggggaacgtntt 318  
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Qy 1339 CAGCAGGGGAGCGTCTT 1355  
|||||

## RESULT 10

LOCUS H28084 421 bp mRNA EST 13-JUL-1995  
DEFINITION y156d10.s1 Homo sapiens cDNA clone 162259 3' similar to gb:M87789  
IG GAMMA-1 CHAIN C REGION (HUMAN);

## ACCESSION

H28084

## NID

g98437

## KEYWORDS

EST.

SOURCE human clone=162259 library=Soares breast 3NbHBst vector=pT7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=Promega -21m3 Rsite1=Not I Rsite2=Eco RI Adult  
human. 1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5' TGTACCAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pT7T3 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 20. Library constructed by Bento Soares  
and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

[illegible]

cp 1251 CTCGGGTGCCCATTCGCTCTCCCACTCCACGGGCAATGTCGCTGGGTAGAAGCCTTTTCAC 1192

Db 377 caggcagctgagctgcttctgtcagctcctcccggtatggggcaggt 434  
|||||  
Cp 1191 CAGGAGGTGAGGCTGAGCTGG-TTCTTGGTCAGCTCATCCGGGATGGGGCAGGCT 1135  
|||||

RESULT 12  
LOCUS T65937 436 bp mRNA EST 20-FEB-1995  
DEFINITION yc24f06.s1 Homo sapiens cDNA clone 81635 3' similar to gb:M87789 IG  
GAMMA-1 CHAIN C REGION (HUMAN);  
ACCESSION T65937  
NID g674982  
KEYWORDS EST.  
SOURCE human clone=81635 library=Stratagene lung (#937210)  
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)  
primer=21ml3 Rsite1-EcoRI Rsite2-XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:  
5'-CTCGAGTCTTTTCTTTTCTTTT-3'.  
Homo sapiens  
ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 436)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 241  
Source: IMAGE Consortium, L1NL  
This clone is available royalty-free through L1NL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 674982  
Location/Qualifiers  
source 1..436  
/organism="Homo sapiens"  
/clone="81635"  
/note="human"

BASE COUNT 74 a 113 c 140 g 104 t 5 others  
ORIGIN

Query Match 19.2%; Score 275; DB 99; Length 436;  
Best Local Similarity 94.2%; Pred. No. 0.00e+00;  
Matches 310; Conservative 0; Mismatches 15; Indels 4; Gaps 4;

Db 112 tttcccgagacagagagctcttctgctgtagtgtgtcaganc-tcattgcatc 170  
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Cp 1427 TTACCCGGACAGAGGAGGCTCTTCTCGCTGTAGTGTGTCAGAGCCTCATGCATC 1368  
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Db 171 acggagcatgagagacgttccctctgtccaccctcttctgtccacgttgagctt-ctg 229  
|||||  
Cp 1367 ACGGAGCATGAGAGACGCTTCCCTCTGCTGCCACCTGCTCTTCTGCCAGGCTGCTG 1308  
|||||  
Db 230 tagaggaagaaggagccjtcggaggtccagcagggaggcgtggtctttagttgtctcc 289

Cp 1307 TAGAGGAGAGGAGCGCTCGAGTCCAGCAGCGGCGCTGCTTGTAGTGTCTCC 1248  
|||||  
Db 290 ggtgcccctgctctcccaacttcaagcgatgctgctgggataagaagc-ttnaccag 348  
|||||  
Cp 1247 GCGTGGCCATTGCTCTCCACCTCCACGGCGATGTCGCTGGGATAGAGCCCTTGAC 1188  
|||||  
Db 349 nagtgaagctgactggtctctgtgttaa-ctcatcccgatggggcaggtatataaac 407  
|||||  
Cp 1187 CAGTCAAGCTGACCTGCTTCTGCTCAGCTCATCCGGGATGGGGCAGGCTGTACAC 1128  
|||||  
Db 408 tgtggtctcgggcttccctttgtttt 436  
|||||  
Cp 1127 TCTGCTTCTCGGGCTGCCCTTTGGCTTT 1099  
|||||

RESULT 13  
LOCUS T65912 479 bp mRNA EST 20-FEB-1995  
DEFINITION ycl1h01.r1 Homo sapiens cDNA clone 80401 5' similar to gb:M87789 IG  
GAMMA-1 CHAIN C REGION (HUMAN);  
ACCESSION T65912  
NID g674957  
KEYWORDS EST.  
SOURCE human clone=80401 library=Stratagene lung (#937210)  
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)  
primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:  
5'-CTCGAGTCTTTTCTTTTCTTTT-3'.  
Homo sapiens  
ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 479)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 273  
Source: IMAGE Consortium, L1NL  
This clone is available royalty-free through L1NL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 674957  
Location/Qualifiers  
source 1..479  
/organism="Homo sapiens"  
/clone="80401"  
/note="human"

BASE COUNT 104 a 140 c 130 g 98 t 7 others  
ORIGIN

Query Match 19.1%; Score 273; DB 99; Length 479;  
Best Local Similarity 96.7%; Pred. No. 0.00e+00;

Matches 323; Conservative 0; Mismatches 3; Indels 8; Gaps 8;

Db 1 cagcccccacgagaaacaccatctccaaagcaaaagcagcccccagagacacaggtgt 60  
|||||  
Qy 1073 CAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGACACAGGTGT 1132  
|||||  
Db 61 ataccctgcccccatcccgagatgagctgaccaagaaccaggtcagctgacctgctgtg 120  
|||||  
Qy 1133 ACACCTGCCCCCATCCCGGATGAGCTGCACCAAGAACAGGTGAGCTGACCTGGCTGG 1192  
|||||  
Db 121 tcaagagcttctatccagagacatccgctggagtgaggagagcaatggcagcggagaa 180  
|||||  
Qy 1193 TCAAAAGGCTTATCCAGCAGCATCGCGTGGAGTGGAGAGCAATGGCGAGCGGAGA 1252  
|||||  
Db 181 acaactacaagaccacgctccgctgctggactccagcagcgtctcttctctctacagca 240  
|||||  
Qy 1253 ACACCTACAGACACGCGCTCCGCTGGACTCCGAGCGGCTCTTCTCTCTACAGCA 1312  
|||||  
Db 241 agctcaccgtgggacaagagcaggtggcagcaggggaaacgtcttcttctctctcgt 300  
|||||  
Qy 1313 AGCTCAGCTGG-ACAAAGCAGCTGG-CACAGCGGAGACGTCTT-CT-CATGCT-CCGT 1367  
|||||  
Db 301 tgatcatggaggtcttgacacattacacg 334  
|||||  
Qy 1368 -GATCATG-AGGCTCT-GCAACCACTACACG 1398  
|||||

## RESULT 14

LOCUS H61373 297 bp mRNA EST 06-OCT-1995  
DEFINITION yu41d01.r1 Homo sapiens cDNA clone 236353 5' similar to gb:M87789  
IG GAMMA-1 CHAIN C REGION (HUMAN);.

## ACCESSION

H61373

## NID

g1014205

## KEYWORDS

EST.

SOURCE  
clone=236353 primer=M13RP1 library=Soares ovary tumor NBR0T  
vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B  
(ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Female. 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT7T3 vector (Pharmacia). Library  
constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 297)

## REFERENCE

AUTHORS  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaekie,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, L1NL  
This clone is available royalty-free through L1NL; contact the  
IMAGE Consortium (info@image.l1nl.gov) for further information.  
Trace considered overall poor quality.

NCBI gi: 1014205

Location/Qualifiers

1..297

/organism="Homo sapiens"

/clone="236353"

<1..>297

BASE COUNT 81 a 92 c 75 g 41 t 8 others

## ORIGIN

Query Match 18.9%; Score 271; DB 22; Length 297;  
Best Local Similarity 94.3%; Pred. No. 0.00e+00;  
Matches 280; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
Db 1 caggactngcgaatggcaaggnacaaagtgcgaagtctccaacaagccctccagcc 60  
|||||  
Qy 1018 CAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGCTCTCCAACAAGCCCTCCAGCC 1077  
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Db 61 cagatcgagaaacacatctccaaagcgaagggcagcccccagagaccacaggtgtacacc 120  
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Qy 1078 CCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACC 1137  
|||||

Db 121 ctgccccctccgggagagatgaccaagaaccaggtcagcctgacctgacctgcctgcctcaaa 180  
|||||

Qy 1138 CTGCCCCCATCCCGGATGAGCTGACCAAGAACACAGGTGAGCTGAGCTGCTGGTCAAA 1197  
|||||

Db 181 ggtcttctatcccaagcagatcgctggagtgagagcaatggcagcggcgagcanc 240  
|||||

Qy 1198 GCTTCTATCCCGGACATCGCGTGGAGTGGGAGCAATGGCGAGCGGAGCAAC 1257  
|||||

Db 241 tacaagaccagacttccgtgctgagctnccagcgtctctatttactatagaag 297  
|||||

Qy 1258 TACAAGACCGAGCTCCGCTGCTGGAGTCCGAGCGCTCTCTCTCTACAGCAAG 1314  
|||||

## RESULT 15

## LOCUS

T59950 418 bp mRNA EST 09-FEB-1995

DEFINITION y001g07.e1 Homo sapiens cDNA clone 79452 3' similar to gb:M87789 IG  
GAMMA-1 CHAIN C REGION (HUMAN);.

## ACCESSION

T59950

## NID

g661787

## KEYWORDS

EST.

## SOURCE

human clones=79452 library=Stratagene lung (#937210)  
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)  
primer=-21m13 Rsitel=EcoRI Rsite2=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:  
5'-CTCAGTGTGTGTGTGTGTGTGTGT-3'.

## ORGANISM

Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 418)

## REFERENCE

AUTHORS  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaekie,E.,  
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.  
WashU-Merck EST Project

## TITLE























Db	550	caatcgggttaactccacgagagtggtcacagagcagcagcagcagcagcactacagc	609
Qy	538	CAATCGGCTAACTCCACGGAGAGTGTACACAGCAGCAGCAAGCAGCAGCTACAGC	597
Db	610	ctcagcagcaccctgacgtctgagcaaaagcagactacgagaacacacaaagtctacgcctgc	669
Qy	598	CTCAGCAGCAGCCCTGACCTTCAGCAAAACGACAGCTACGAGAAACACAAGACTTCACGCCTGC	657
Db	670	gaagtcacccatcagggcctgagctgcgcctgcacaaagagcttcaacaggggagagtggt	729
Qy	658	GAACTACCCATCAGGGCCTGACCTCGCCCTCAGAAAGACTTTCACAGCGGAGAGTGT	717
Db	730	t 730	
Qy	718	T 718	
RESULT	12		
LOCUS	MAC1GKVCDS	499 bp mRNA	PRI 13-MAY-1994
DEFINITION	Macaca fascicularis immunoglobulin kappa light chain variable region, constant region mRNA.		
ACCESSION	L13314		
NID	g293132		
KEYWORDS	constant region; immunoglobulin kappa-chain; variable region.		
SOURCE	Macaca fascicularis cDNA to mRNA.		
ORGANISM	Macaca fascicularis		
REFERENCE	Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Cercopithecoidea; Cercopithecinae; Papionini.		
AUTHORS	1 (bases 1 to 499) Lewis,A.P., Barber,K.A., Cooper,H.J., Sims,M.J., Worden,J. and Crowe,J.S.		
TITLE	Cloning and sequence analysis of kappa and gamma cynomolgus monkey immunoglobulin cDNAs		
JOURNAL	Dev. Comp. Immunol. 17 (6), 549-560 (1993)		
MEDLINE	94131152		
COMMENT	NCBI gi: Location/Qualifiers		
FEATURES	source		
CDS	1..499 /organism="Macaca fascicularis" /note="putative; NCBI gi: 293132" /codon_start=1 /product="immunoglobulin kappa-chain" /db_xref="PID:g293132" /translation="QPLIYEVNRSACVDFRSGSGSDFTFIKISRVEADVGWYCYMQYTHIPFTFGGPTKLDIKRAVAPSVFIIPPSEQVKSGTGVVCLIANEYPREASVWKVDGALKTDNSQESVTFQDSKUNFTYLSLSTFLSTSDYQSHVYACEVTHQGLGSPVTKSFN"		
BASE COUNT	129 a 136 c 127 g 107 t		
ORIGIN			
Query Match	51.8%; Score 373; DB 56; Length 499;		
Best Local Similarity	87.5%; Pred. No. 0.00e+00;		
Matches	435; Conservative 0; Mismatches 62; Indels 0; Gaps 0;		
Db	3	gcccttgattatgaggtttcaacacggcctctgagttccagacaggttcagtgagcag	62
Qy	210	GCTCTGATTTATAGGTTTCTAAACCGGACTCTGGGTCGCCAGACATTCAGCGGCAG	269
Db	63	tggttcgacactgatttcacactcaaatcagcagagtgaggagcttgaggttgagggt	122
Qy	270	TGGGCGAGGACAGATTTACACTGAAATCAGCGACTGAGCGCTGAAGATCTTGGGCT	329

Db	123	ttattactgcatgaataacacacattccattcacttctggccgggacccaaactgga	182
Qy	330	TTATTTCTCGGGCAAGGTACRAGGACTCTCCACTTTCCGGGAGGACCAAGGTGCA	389
Db	183	Latcaaacgagctgtggctgcacacatctgtcttcacatctcccgccatctgaggtcaggt	242
Qy	390	RATCAACGTACGTGGCTGGCGACCATCTGTTCTCATCTTCCGCCCATCTGATGAGCAGTT	449
Db	243	gaaatctgaaactgtctctgttgtgtgcctgcgtgaataactctatcccagagagccag	302
Qy	450	GAATACTGGAACTGCCTCTCTTGTCTGCCTGCTGGAATAACTTCTATCCCAGAGAGCCAA	509
Db	303	cgtaaagtggaaagtggatggctgcctcctcaaaacggataactcccagagagatgtcacaga	362
Qy	510	AGTACAGTGGAAAGTGGATAAGCGCCTCCAAATCGGGTAACCTCCAGGAGACTGTACAGA	569
Db	363	gcagcacagaagggacacacacctacagctgagcagcagccctgacgctgagcagcacaga	422
Qy	570	GCAGCACAGGAGACAGCACTACAGCTCAGCAGACCCCTGACGCTGACGAAAGCA	629
Db	423	ctaccagagtcaaatgtctatgctgcgaggtcacccatcaggcctgagctcgccgt	482
Qy	630	CTACGAGAACACAAAGTCTACGCCTCGGAAGTCAACCTCAGCGGCTGAGCTGCGCCGT	689
Db	483	caccaagagcttcaaca	499
Qy	690	CACMAAGAGCTTCAACA	706
RESULT	13		
LOCUS	107074	468 bp	PAT 14-NOV-1994
DEFINITION	Sequence 18 from patent EP 0314317.		
ACCESSION	107074		
NID	g590385		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 468)		
AUTHORS	Capon, D.J. and Gregory, T.J.		
TITLE	Adhesion variants, nucleic acid encoding them and compositions comprising them		
JOURNAL	Patent: EP 0314317-A1 18 03-MAY-1989;		
COMMENT	NCBI gi: 590385		
FEATURES	Location/Qualifiers		
source	1..468		
	/organism="unknown"		
BASE COUNT	126 a 131 c 118 g	93 t	
ORIGIN			
Query Match	51.1%	Score 368;	DB 37; Length 468;
Best Local Similarity	92.2%;	Pred. No. 0.00e+00;	
Matches	402; Conservative	0; Mismatches 34; Indels	0; Gaps 0;
Db	1	gaattcactctcacatcatcagcgctgcagcctgaagcttttgcgaacttattactgccaa	60
Qy	283	GATTCACACTGAAATFACGCGAGCTGGAGGCTGAAGATGTTGGGCTTTATTTCTCGGG	342
Db	61	cagtatagaagtgttcgtctcacitcttcgctggcggaggaccaggtggagatcaaacgaact	120
Qy	343	CAAGGTACAAAGACTCTCCCACTTTTCGGGGAGGACCAAGGTGGAATCAAACTGACG	402

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19

Db 121 gtggctgaccatctgtctcatctcccgccatctgatgacagttgaaatctggaact 180  
Qy 403 GTGGCTGCACACATCTGTCTTCTCTCCGCCATCTGTATGAGCATTTGAAATCTGGAAC 462  
Db 181 gctctgtgtgtgctctgaataacttctatccagagagagcccaagtacagtgaag 240  
Qy 463 GCCTCTGTGTGTGCTCTGAATAACTTTCTATCCAGAGAGGCCAAAGTACAGTGAAG 522  
Db 241 gtgataaacgccctccaatcgggtaaactccagagagagtgctcacagagcagcagcaag 300  
Qy 523 GTGATAAACGCCCTCCAATCGGTTAACTCCAGGAGAGTGTCTACAGAGCAGCAGCAAG 582  
Db 301 gacagcaactacagcctcagcagcaccctgacgtgagcaagcagactacgagaacac 360  
Qy 583 GACAGCACTACAGCCTCAGCAGCCTCTGACCTGAGCAAGCAGACTACAGAAACAC 642  
Db 361 aaagtctacgctgcgaagtcaacctcagggcctgagctgcgccgtcacaaagagcttc 420  
Qy 643 AAAGTCTACGCCCTGCGAAGTCCCATCAGGGCCTGAGCTGCCCGCTCACAAAGAGCTTC 702  
Db 421 aacagggagagtggt 436  
Qy 703 AACAGGGAGAGTGTT 718

RESULT 14  
LOCUS I09304 468 bp PAT 14-NOV-1994  
DEFINITION Sequence 7 from patent WO 8902922.  
ACCESSION I09304  
NID g587990  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 468)  
AUTHORS Capon,D.J. and Gregory,T.J.  
TITLE ADHESON VARIANTS  
JOURNAL Patent: WO 8902922-A 7 06-APR-1989;  
COMMENT NCBI gi: 587990  
FEATURES  
source  
location/Qualifiers  
1..468  
/organism="unknown"  
BASE COUNT 126 a 131 c 118 g 93 t  
ORIGIN

Query Match 51.1%; Score 368; DB 37; Length 468;  
Best Local Similarity 92.2%; Pred. No. 0.00e+00;  
Matches 402; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
Db 1 gaattcaactctcaaccatcagcgctcagcctgaagattttgcaacttattactgcaa 60  
Qy 283 GATTTACACTGAATAACAGCGCAGTGGAGGCTCAAGATGTTGGGGTTTATTTCTCGGG 342  
Db 61 cagtaagaagtttgcgtcactcttcgcgagggagccaaagtgagatcaaacgaact 120  
Qy 343 CAGGTACAGAGACTCTCTCCACTTTCGGCGGAGGACCAAGGTGGAATCAAACTAGC 402  
Db 121 gtggctgcaccatctgtctcatcttcccgccatctgatgagcagttgaaatctggaact 180  
Qy 403 GTGGCTGCACACATCTGTCTTCTCTCCGCCATCTGTATGAGCATTTGAAATCTGGAAC 462  
Db 181 gctctgtgtgtgctctgaataacttctatccagagagagcccaagtacagtgaag 240

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20

Qy 463 GCCTCTGTGTGTGCTCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAG 522  
Db 241 gtgataaacgccctccaatcgggtaaactccagagagagtgctcacagagcagcagcaag 300  
Qy 523 GTGATAAACGCCCTCCAATCGGTTAACTCCAGGAGAGTGTCTACAGAGCAGCAGCAAG 582  
Db 301 gacagcaactacagcctcagcagcaccctgacgtgagcaagcagactacgagaacac 360  
Qy 583 GACAGCACTACAGCCTCAGCAGCCTCTGACCTGAGCAAGCAGACTACAGAAACAC 642  
Db 361 aaagtctacgctgcgaagtcaacctcagggcctgagctgcgccgtcacaaagagcttc 420  
Qy 643 AAAGTCTACGCCCTGCGAAGTCCCATCAGGGCCTGAGCTGCCCGCTCACAAAGAGCTTC 702  
Db 421 aacagggagagtggt 436  
Qy 703 AACAGGGAGAGTGTT 718

RESULT 15  
LOCUS A07738 754 bp DNA PAT 02-AUG-1993  
DEFINITION Synthetic nucleotide sequence of the Y22 light chain.  
ACCESSION A07738  
NID g413214  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 754)  
AUTHORS  
JOURNAL Patent: WO 8912098-A 39 14-DEC-1989;  
COMMENT NCBI gi: 413214  
FEATURES  
source  
location/Qualifiers  
1..754  
/organism="Artificial sequences"  
CDS  
10..720  
/note="NCBI gi: 413215"  
/codon\_start=1  
/product="Y22 light chain"  
/db\_xref="pid:g413215"  
/translation="MTMLSLAPLLSLLLCVSDSRSTTTVTQSPISLSVATGKVTIR  
CITTTDIDDDMKWYQKPGEPKLLISEGNTLRPGVPSRSSSGYGSDFVTIETLS  
EDVADYYCQSDNMWFTFGSGTKLEIRTVAAPSVFIIPPSPDEQ IASGTASVWCLLN  
FYPREAKVQWRYDNLALQSGNSQSVTEQDSKDSYLSSTLTLSKADYKHKRYACEV  
THQGLSSPVTKSFNRGEC"  
BASE COUNT 203 a 207 c 174 g 170 t  
ORIGIN

Query Match 50.6%; Score 364; DB 35; Length 754;  
Best Local Similarity 83.3%; Pred. No. 0.00e+00;  
Matches 455; Conservative 0; Mismatches 91; Indels 0; Gaps 0;  
Db 173 tgaagtggtaaccaacagagcggggaacctccaaagctctatttcagaaggaata 232  
Qy 173 TGAGTTGGTATCAGCAGAGAGCCAGGCCAACCTCCAGAGGCTCTGATTTAAGTTTCTA 232  
Db 233 ctcttgctcctggagtcctccatcccagattctccagcagtggtatggctcagattttgttt 292  
Qy 233 ACCGGCACTCTGGGGTCCACAGAGATTTCAGCGGAGGCGAGGACAGATTCACAC 292  
Db 293 ttacaattgaaaacacgctctcagaagatgttcagattactactgttgcgaagtgata 352  
Qy 293 TGAANAATCAGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTCGCGGCAAGGTACAA 352



\*\*\*\*\*

Result No.	Score	Match	Query Length	DB Length	ID	Description	Pred. No.
1	525	72.9	726	19	T18060	Monoclonal antibody D	0.00e+00
2	484	67.2	729	16	T03380	Anti-IL-8 chimeric G6	0.00e+00
3	481	66.8	737	4	Q25619	Sequence of the chime	0.00e+00
4	415	57.6	9208	11	Q55629	Vector contg. TCAB 8	4.38e-263
5	411	57.1	924	10	Q71872	Sequence coding human	2.71e-260
6	405	56.3	1066	8	Q49943	Human anti-HBs light	4.16e-256
7	402	55.8	4691	16	Q92546	pComb3 expression vec	5.15e-254
8	402	55.8	6166	16	Q92547	Expression vector, pP	5.15e-254

## ALIGNMENTS

RESULT	1
ID	Tl8060 standard; DNA; 726 BP.
AC	Tl8060;
DT	20-AUG-1996 (first entry)
DE	Monoclonal antibody DNA light chain against 65 kD hCMV antigen.
KW	Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;
KW	65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.
OS	Synthetic.
FF	Key
FT	Location/Qualifiers
FT	CDS
FT	1..717
FT	/tag= a
FT	sig_peptide
FT	1..60
FT	/tag= b
FT	mat_peptide
FT	61..714
FT	/tag= c
FT	3'UTR
FT	715..726
FT	/tag= d
PN	J08038178-A.
PD	13-FEB-1996.
PF	20-FEB-1995; 030742.
PR	18-FEB-1994; JP-021628.
PA	(NISN ) NISSHINO IND INC.
PA	(TANA) TANAKA H.

DR WP1; 96-154852/16.

DR P-PSDB; R93554.

PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -  
PT produced by primer amplification, used in the diagnosis of hCMV  
PT infection

PS Claim 7; Page 19; 22pp; Japanese.

CC The sequences given in T18059-60 encode the heavy and light chains  
CC respectively of a monoclonal antibody against a 65 kD antigen of human  
CC cytomegalovirus (hCMV). These sequences were amplified using the  
CC sequences given in T18040-58. The monoclonal antibody may be used  
CC in the diagnosis of hCMV.

SQ Sequence 726 BP; 177 A; 192 C; 199 G; 158 T;

Query Match

72.9%; Score 525; DB 19; Length 726;

Best Local Similarity 87.6%; Pred. No. 0.00e+00;

Matches 629; Conservative 0; Mismatches 86; Indels 3; Gaps 2;

Db 1 atgaagggtccccgcgtgctctctcctggtggtgctgaatgctgtgatacctggtatgtgca 60

Qy 1 ATGAGCCTCCCTGCTCAGCTCTCCGGGCTGCTATGCTGCTGCCGGCTCCAGTGGG 60

Db 61 gatattgtatgaccagactccactctctgtcgtccgaccctggacagccggtctcc 120

Qy 61 GAAGTGTGTGATGACCTCTCCAGCTGTCCTTCCCATCACACCTGGAGCGCGCTCC 120

Db 121 atctctcgaagtctagtccagagctctctgcatgatgaggaagacctattgtatgg 180

Qy 121 ATCTCTGTAGGTCAGTCAAGAGCCTTAACACAGTAATGAGACACCTTCTCAGTGG 180

Db 181 tatttcagaagccagccagctccacagctcctgactgtatgaggtttccaacggcttc 240

Qy 181 TATCAGCAAGACCGAGCAACCTCCAGGCTCTGATTTATAAGGTTTCTAACCGGGAC 240

Db 241 tctggaagtgcagataggttcadgtggcagcgggtcaggagacagattccactgaaatc 300

Qy 241 TCTGGGGTCCACAGACAGATTCCAGCGCAGTGGGCGAGGACAGATTTCACACTCAAAATC 300

Db 301 agccgggtgaggtgagatgttggtgtttattactgcatgcaagtatacagt-tcg- 358

Qy 301 ACCGACGTGAGGCTGAGATGTTGGGTTTATTTCTCGGGGCAAGGTACAGACTCT 360

Db 359 -cgacttttggccagggaccagactggagatcaaacgaactgtggtgcacactgttc 417

Qy 361 CCCACTTTCGGCGGAGGACCAAGGTGGAATCAAAACGTACGGTGGCTGCACCATCTGTC 420

Db 418 ttcatcttcgccatctgatgagcagttgaaactctggaactgctctgtgtgctgtg 477

Qy 421 TTCACTTTCGGCCCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGCTGTG 480

Db 478 ctgaaactttctatccccagagggccaaagtgcagtggaaggtggataacgccctccaa 537

Qy 481 CTGAATAACTTCTATCC\*AGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAA 540

Db 538 tcgggttaactccagagaggtgtcacagagcagcagcagcaagagacagcactacagctc 597

Qy 541 TCGGGTAACTCCCAAGAGTGTACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCTC 600

Db 598 agcagaccctgacgtgagcaagcagactacgagaacacaaagtctacgcctcgcaa 657

Qy 601 AGCAGACCCCTGACGCTCAGCAAGAGCAGCTACGAGAAACACAAAGTCTACGCCCTCGAA 660

Db 658 gtccaccatcagggtgactgctgcgcctcacaaagactttcaacaggggagagtggt 715

Qy 661 GTCCCAATCAGGGCTT\*AGCTCGCCGCTCACAAGAGAGCTTTCAACAGGGGAGAGTGTT 718

RESULT 2

ID T03380 standard; DNA; 729 BP.

AC T03380;

DT 12-MAR-1996 (first entry)

DE Anti-IL-8 chimeric 6G4.2.5 light chain DNA.

KW Monoclonal antibody 6G4.2.5; MAb; interleukin-8; IL-8;

KW chimeric antibody; Fab; antibody engineering; inflammation;

KW inflammatory bowel disease; ulcerative colitis; bacterial pneumonia;

KW ds.

OS Chimeric Mus sp.;

OS Chimeric Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..729

FT /\*tag= a

FT /product= fusion protein

FT sig\_peptide 1..69

FT /\*tag= b

FT /function= STII signal peptide

FT mat\_peptide 70..726

FT /\*tag= c

FT /product= mouse-human chimeric Fab

PN W09523865-A1.

PD 08-SEP-1995.

PF 01-MAR-1995; U02589.

PR 03-MAR-1994; US-205864.

PA (GETH ) GENENTECH INC.

PA (INDV ) UNIV INDIANA FOUND.

PI Doerschuk CM, Fong S, Herbert CA, Kim KJ, Leong SR;

DR WP1; 95-320580/41.

DR P-PSDB; R86323.

PT New anti-interleukin-8 monoclonal antibodies - useful for treating

PT inflammatory disorders, partic. ulcerative colitis, and bacterial

PT pneumonia

PS Example G; Fig 27A-B; 114pp; English.

CC A cDNA insert (T03380) in vector pchimFab codes for a mouse-human

CC chimeric Fab light chain (R86323) consisting of the light chain

CC variable region of anti-interleukin-8 mouse MAb 6G4.2.5 and the

CC light chain constant region of human IgG1. A chimeric Fab vector,

CC plasmid p6G425chim2 (ATCC 97055), was constructed that encoded the

CC murine-human variable/constant regions of both the light and heavy

CC chains of 6G4.2.5.

SQ Sequence 729 BP; 192 A; 192 C; 174 G; 171 T;

Query Match

67.2%; Score 484; DB 16; Length 729;

Best Local Similarity 87.1%; Pred. No. 0.00e+00;

Matches 568; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Db 76 gtgatgacagacacaccactctcctgctgctgctgagatcaggtcctccatctct 135

Qy 67 GTGATGACTCAGTCTCCACTCTCCCTTCCCATCACACCTGGAGAGCGGCTTCCATCTCC 126

Db 136 tgcagatctagtcagagcttgttacacggtattggaacacacctattacattggtactg 195

Qy 127 TGTAGTCTAGTCAAGCCCTTAACACAGACTAATGGACACACCTTCTCTGAGTTGTATCAG 186

Db 196 cagaagccagccagctctccaaagctctgactacaaagtttccaacgactttctggg 255

Qy 187 CAGAAGCCAGGCCAACCTCCAAAGGCTCTCTGATTTATAGGTTTCTAACCGGAGCTCTGGG 246

Db 256 gtccagacaggttctcagtggtgagtgatcagggacagatttcacactcaggtacagaga 315

Qy 247 GTCCACAGACAGATTTCAGCGGCGAGTGGGCGGAGGACAGAGATTTCACACTGAAATCAGCGCA 306





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Qy 610 CTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAGTACCCAT 569  
Db 681 caggcgctgagctcgccgtcacaaagagcttcaacgcggagagtggt 729  
Qy 670 CAGGGCCTGAGCTCGCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGTT 718

## RESULT 4

ID Q65629 standard; DNA; 9208 BP.  
AC Q65629;  
DT 01-FEB-1995 (first entry)  
DE Vector contg. TCAE 8 DNA.  
KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;  
KW cell lysis; ss.  
OS Synthetic.  
PN W09411026-A.  
PD 26-MAY-1994.  
PF 12-NOV-1993; U10953.  
PR 13-NOV-1992; US-978891.  
PR 03-NOV-1993; US-149099.  
PA (IDEC-) IDEC PHARM CORP.  
PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;  
PI Refine;  
DR WPI; 94-183162/22.  
PT Treating B cell lymphoma with chimeric antibody - against CD20,  
PT causing rapid depletion of peripheral B cells, also new  
PT antibodies and hybridomas  
PS Disclosure; Fig 3; 101pp; English.  
CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric  
CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8  
CC contains 4 transcriptional cassettes, human Ig light and heavy chain  
CC constant regions, dihydrofolate reductase, neomycin phosphotransferase  
CC and murine variable regions. The vector can be used to produce  
CC antibodies which cause depletion of peripheral blood B cells,  
CC including those associated with lymphoma. They mediate complement-  
CC dependent lysis and lyse target cells by antibody-dependent cellular  
CC cytotoxicity.  
CC See also Q65629-35.  
SQ Sequence 9208 BP; 2237 A; 2399 C; 2388 G; 2182 T;  
Query Match 57.6%; Score 415; DB 11; Length 9208;  
Best Local Similarity 88.2%; Pred. No. 4.38e-263;  
Matches 479; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
Db 1143 tggttccagcagaagccagagctctcccaaacctggatttatgccacatccaaactg 1202  
Qy 178 TGGTATCAGCAGAACGCCAGCAACTCCAGGCTCTGATTATAAGGTTTCTAACC 237  
Db 1203 gcttcggagtcctgttcgcttcagtgagctgggtctgggactcttaactctctcaac 1262  
Qy 238 GACTCTGGGCTCCAGACAGATTACAGGGCAGTGGGGCAGGACAGATTTCACACTGAAA 297  
Db 1263 atcagcagatggaggtgaagtgtgccacttattactccagcagtggaactagtaac 1322  
Qy 298 ATACGCCACTGAGCGCTGAAGATGTGGGGTTATTCTCGGGGCAAGCTACAGGACT 357  
Db 1323 ccaccacgttcgaggggggagcagctggaatcaaacgtacggtgctgcacatct 1382  
Qy 358 CTCCCACTTTCGGCGGAGGCAAGGTGGGAATCAAACTACGGTGGCTGCACACTCT 417  
Db 1383 gcttcctatctcccgcaatctgatgagcagttgaaatctggaactgctctgtgtgtgc 1442  
Qy 418 GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGC 477

Dec 17 21:42

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Db 1443 ctgctgaataacttctatccccagagagccaaagtacagtggaggtggataacgcctc 1502  
Qy 478 CTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTC 537  
Db 1503 caatcggtgaactccccagagagtgctcacagagcaggacagcaaggacagcactacag 1562  
Qy 538 CANTCGGGTAACTCCCGAGGAGTGTCACAGAGCAGACAGCAGAGGACGACCTACAGC 597  
Db 1563 ctacagcagccacctgacgtgagcaagcagactacgagaaacacaaagtctacgcctgc 1622  
Qy 598 CTACGAGAGCCCTGACGCTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCCCTGC 657  
Db 1623 gaagtcacccatcagggtcgtgagctcgccctcaaaaagcttcaacaggggagagtg 1682  
Qy 658 GAAGTCACCCATCAGGGCCTGAGCTCGCCCTCACAAGAGGTTCAACAGGGGAGAGTGT 717  
Db 1683 tga 1685  
Qy 718 TGA 720

## RESULT 5

ID Q71872 standard; cDNA; 924 BP.  
AC Q71872;  
DT 27-OCT-1994 (first entry)  
DE Sequence coding human anti-IgE MAb light chain.  
KW Human IgE; CH4 region; triggers mediator release;  
KW Mast cells; Monoclonal antibody; allergy; Immunoglobulin; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT misc feature 4..6  
FT /\*tag= a  
FT /note= "C or G, illegible sequence."  
FT misc feature 908..910  
FT /\*tag= b  
FT /note= "N is an unidentified base"  
FT misc feature 71..394  
FT /\*tag= c  
FT /note= "L-chain variable region"  
FT CDS 11..715  
FT /\*tag= d  
FT /product= antibody light chain  
FT /note= "Human monoclonal anti-IgE antibody"  
PN EP-592230-A.  
PD 13-APR-1994.  
PF 07-OCT-1993; 308006.  
PR 07-OCT-1992; JP-293800.  
PA (SNOW) SNOW BRAND MILK PROD CO LTD.  
PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;  
PI Yoshida T;  
DR WPI; 94-120330/15.  
DR P-PSDB; R52951.  
PT Human monoclonal anti-IgE peptide antibody - inhibits histamine  
PT release from mast cells by allergen stimulation, useful for  
PT preventing allergies  
PS Claim 4; Page 17; 21pp; English.  
CC Q71872 encodes the light chain of a human type anti-IgE peptide  
CC monoclonal antibody which inhibits the signal transmission for  
CC the release of chemical mediator from mast cells and basophils  
CC stimulated with allergen. The antibody can be used for the  
CC prophylaxis and the therapy of allergy.  
SQ Sequence 924 BP; 230 A; 277 C; 216 G; 195 T;

	Query Match	57.1%	Score 411;	DB 10;	Length 924;	
	Best Local Similarity	88.0%;	Pred. No. 2.71e-260;			
	Matches	476;	Conservative	0;	Mismatches 65;	Indels 0; Gaps 0;
Db	173	tgttaccagcagaacctgccagggtcccagggtccctcatctatggtgcgtccaccagg	232			
Qy	178	TGTFATCAGCAGAGAGCCAGGCCAACCTCCAGGCTCTGATTATAAGGTTTCTTAACCGG	237			
Db	233	gccactggatccccgccagggttcagtgccagtggtctgggacagacttcaactctcaac	292			
Qy	238	GACTCTGGGTCCCGACACAGATTACGGCGGCACTGGGGCAGGGACACATTTCACACTGAAA	297			
Db	293	atcagcagctcacagttctgaagatttttgcgaattttattactgtcagcaatatagtagctgg	352			
Qy	298	ATACGCGCAGTGGAGGCTGAAGTGTGGGGTTTATTTTCGGGGCAGAGGTACAGGACT	357			
Db	353	cttcgagagtttcgccaagggaccaaggttgacctcaaaaggaactgtggtgcacctct	412			
Qy	358	CCTCCCACTTTTCGGCGGAGGGCAAGGTCGAAATCAAACTACGTGGCTGGCTGCACCATCT	417			
Db	413	gtcttcactctccggccactctgatgagcagdtgaaactctggaaactgcctctgtgtgtgc	472			
		-				
Qy	418	GTCTTCATCTTCCCGGCATCTGATGAGCAGTTGAAATCTGGAATCGCCTCTGTTGTGTC	477			
Db	473	ctgtgtaataactctatccccagagggccaaagtacagtggaggtggataaagccctc	532			
Qy	478	CTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGTGCGATGAGCGCCCTC	537			
Db	533	caatcgggttaactccagagagaggtgtcacagagcaggagcagcagcagcactcacagc	592			
Qy	538	CAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACGACGACGACGACCTACAGC	597			
Db	593	ctcagcagcacacctgacgctgagcaaaagcagactacgagaaacacaaaagtctacgctgc	652			
Qy	598	CTACGACGACCCCTGACGCTGAGCAAAAGACGACTACGAGAAACACAAAGTCTAGCGCTGC	657			
Db	653	gaagtcaccctacagggctcgagctcgcccgctcacaagagcttcaacagggagagtgct	712			
Qy	658	GAAAGTCACCCATCAGGCGCTGAGCTCGCCCGCTCACAAGAGAGCTTCACAGGGGAGAGTGT	717			
Db	713	t 713				
Qy	718	t 718				

RESULT	6	
ID	Q49943 standard; cDNA; 1066 BP.	
AC	Q49943;	
DT	29-APR-1994 (first entry)	
DE	Human anti-HBs light chain.	
KW	Antibody; Ab; light; heavy; chain; hepatitis B;	
OS	HB; surface antigen; ss.	
OS	Homo sapiens.	
FK	Key	Location/Qualifiers
FT	CDS	33..743
FT	/*tag= a	
FT	sig_peptide	33..98
FT	/*tag= b	
FT	mat_peptide	99..740
FT	/*tag= c	
FT	/*note= "claim 1, page 26"	
PN	W09320205-A.	
PD	14-OCT-1993.	
PF	30-MAR-1993; J000396.	

[illegible]

RESULT	7
ID	Q92546 standard; DNA; 4691 BP.
AC	Q92546;
DT	11-MAR-1996 (first entry)
DE	pComb3 expression vector.
EW	pComb3; phagemid expression vector;
KW	bacteriophage; coat protein 3;









SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T;  
Query Match 55.6%; Score 400; DB 12; Length 646;  
Best Local Similarity 88.4%; Pred. No. 1,28e-252;  
Matches 478; Conservative 0; Mismatches 60; Indels 3; Gaps 2;  
Db 100 tggatccagcagaacctggccaggtccacaggtcctcatctatggtacatccagcagg 159  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 178 TGTATACAGCAAGAGCGGCGCAACCTCCAGGCTCTGATTTATAGGTTTCTTAACCGG 237  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 160 gccactggcatccacagacagctccagtggcagtggtctgggacagacttcactctcacc 219  
|| ||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 238 GACTCTGGGGTCCCGACAGATTCAGCGCAGTGGGCGAGGACAGATTTCACACTGAAA 297  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 220 atcagcagactggagcctgaagattttgacgtgtactactgtcagca--gtatggtgct 277  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 298 ATCAGCGCAGTGGAGGCTCAAGATGTTGGGTTTATTTCTGGGCGCAAGGTACAGGACT 357  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 278 ca--ccgtggttcggcccaagggtggaactcaaacgaactgtggctgcaccatct 336  
|| || ||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| |||||  
Qy 358 CTCCCACTTTCCGGCGGAGCACCAGGTGGAAATCAAACTACGCTGGCTGCACATCT 417  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 337 gtcttcactttcccgccatctgatgagcagttgaaatctggaactgcctctgtgtgc 396  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 418 GTCTTCATCTTCCCGCCATCTGTATGAGAGTTGAAATCTGGAACTGCTCTGTGTGTGC 477  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 397 ctgctgaataactctatccagagaggccaaagtacagtggaaagtgataacgcccctc 456  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 478 CTGCTGAATAACTTTATCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTC 537  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 457 caatcgggttaactccagagaggtgtcacagagcagcagcagcagcagcagcagcagc 516  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 538 CAATCGGTAACTCCAGGAGAGTGTACAGAGGAGGACAGCAAGAGGAGCAGCCTACAGC 597  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 517 ctgagcagcactgacgtgagcgaagcagactacgagaacacaaagtctacgctgc 576  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 598 CTGAGCAGCCTCTGAGCTGCAAGAGCAGACTTCGAGCAACAAAGTCTACGCCCTGC 657  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 577 gaagtcacccatcagggcctgagtcgcccgtcacaaagagcttcacagggagagtggt 636  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 658 GAAGTCACCCATCAGGGCTCAGCTCGCCCGTCAAAAAGAGCTTCAACAGGGAGAGTGT 717  
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Db 637 t 637  
Qy 718 T 718

## RESULT 12

ID Q67894 standard; cDNA to mRNA; 645 BP.  
AC Q67894;  
DT 07-AUG-1995 (first entry)  
DE cDNA contg. an ORF for a globulin kappa chain for an antibody to SLE.  
KW globulin kappa chain; light chain; antibody; treatment; nephritis;  
KW systemic lupus erythematosus; SLE; ds.  
OS Homo sapiens.  
PN J06296490-A.  
PD 25-OCT-1994.  
PF 14-APR-1993; 109783.  
PR 14-APR-1993; JP-109783.  
PA (LTKR-) LFT KENKYUSHO KK.  
PA (TAIH ) TAIHO PHARM CO LTD.  
DR WPI; 95-010856/02.  
PT DNA coding SLE nephritis-causing positive charge antibody - and  
PT it's use in treating nephritis

PS Claim 2; Page 4-5; 6pp; Japanese.  
CC Q67894-7 are cDNA sequences contg. an open reading frame encoding a  
CC globulin kappa chain for an antibody causing systemic lupus erythematosus  
CC (SLE). The nucleotide sequences can be used to aid in the treatment of  
CC nephritis caused by SLE.  
SQ Sequence 645 BP; 179 A; 178 C; 158 G; 130 T;  
Query Match 55.4%; Score 399; DB 13; Length 645;  
Best Local Similarity 86.9%; Pred. No. 6.36e-252;  
Matches 470; Conservative 0; Mismatches 71; Indels 0; Gaps 0;  
Db 103 tggatccagcagaacacaggaagccctcaagcctgacatctatctatctgcatccagctcg 162  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 178 TGGTATACAGAGAGCGGCAACCTCCAGGCTCTGATTTATAAGTTTCTTAACCGG 237  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 163 caaagtgggtgccatcaaggttcagcggcagtgatctgagacagaattcactctcaca 222  
|| ||||| || ||||||| || ||||||| || ||||||| || ||||||| || ||||||| || |||||  
Qy 238 GACTCTGGGGTCCCGACAGATTTCAGGCGCAGTGGGCGAGGACAGATTTCACACTGMA 297  
||||| ||||||| || ||||||| || ||||||| || ||||||| || ||||||| || ||||||| || |||||  
Db 223 atcaacagcgtcgagcctgaagattttgcaacttattactgtctgcagcagaatagttac 282  
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Qy 298 ATCAGCGCATGCGAGGCTCAAGATGTTGGGTTTATTTCTCGGGCGAAGGTACAGGACT 357  
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Db 283 ccgtggactcaagcccaagggaccgaaggtggaatcaaacgaactgtggctgcacacatct 342  
||||| || || ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||  
Qy 358 CTCCCACTTTCCGGCGGAGGACCAAGGTGGAAATCAAACTGGAAGTACGCTGCACCATCT 417  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 343 gtcttcactttcccgccatctgatgagcagttgaaatctggaactgcctctgtgtgtgc 402  
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Qy 418 GTCTTCATCTTCCCGCCATCTGTATGAGAGTTGAAATCTGGAAGTCTGCTCTGTGTGTGC 477  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 403 ctgctgaataactttatccagagaggccaaagtacagtggaaagtgataacgcccctc 462  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 478 CTGCTGAATAACTTTATCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTC 537  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 463 caatcgggttaactccagagaggtgtcacagcagcagcagcagcagcagcagcagcagc 522  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Qy 538 CAATCGGTAACTCCCGAGCAGTGTACAGAGCAGGACAGCAAGAGCAGCCTACAGC 597  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 523 ctgagcagcactgcctgacgtgagcaagcagactacgagaacacaaagtctacgctgc 582  
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Qy 598 CTCAGCAGCACCTCTGAGCTGAGCAAGCAGACTTACGAGAAACACAAAGTCTACGCCCTGC 657  
||||| ||||||| || ||||| ||||| ||||||| || ||||| ||||| ||||| ||||| |||||  
Db 583 gaagtcacccatcagggcctgagctcgcctgcacaaagagcttcacagggggagagtggt 642  
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Qy 658 GAAGTCACCCATCAGGGCTCAGCTCGCCCGTCAAAAAGAGGTTCAACAGGGGAGAGTGT 717  
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Db 643 t 643  
Qy 718 T 718

## RESULT 13

ID Q67895 standard; cDNA to mRNA; 645 BP.  
AC Q67895;  
DT 07-AUG-1995 (first entry)  
DE cDNA contg. an ORF for a globulin kappa chain for an antibody to SLE.  
KW globulin kappa chain; light chain; antibody; treatment; nephritis;  
KW systemic lupus erythematosus; SLE; ds.  
OS Homo sapiens.  
PN J06296490-A.  
PD 25-OCT-1994.  
PF 14-APR-1993; 109783.  
PR 14-APR-1993; JP-109783.





AC T03363;  
DT 03-APR-1996 (first entry)  
DE Anti-IL-8 MAB 5.12.14 VL/human IgG1 CL cDNA.  
KW Monoclonal antibody 5.12.14; Mab; interleukin-8; IL-8;  
KW chimeric antibody; Fab; antibody engineering; inflammation;  
KW inflammatory bowel disease; ulcerative colitis; bacterial pneumonia;  
KW ds.  
OS Chimeric - Mus musculus.  
OS Chimeric - Homo sapiens.  
FH Key Location/Qualifiers  
FT sig\_peptide 1..69  
FT /\*tag= a  
FT /product= STII signal peptide  
FT mat\_peptide 70..396  
FT /\*tag= b  
FT /product= Murine 5.12.14 light chain variable region  
FT mat\_peptide 397..713  
FT /\*tag= c  
FT /product= Human IgG1 light chain constant region  
PN W09523865-A1.  
PD 08-SEP-1995.  
PF 01-MAR-1995; U02589.  
PR 03-MAR-1994; US-205864.  
PA (GETH ) GENENTECH INC.  
PA (INDV ) UNIV INDIANA FOUND.  
PI Doerschuk CM, Fong S, Herbert CA, Kim KJ, Leong SR;  
DR WPI; 95-320580/41.  
DR P-PSDB; R86319.  
PT New anti-interleukin-8 monoclonal antibodies - useful for treating  
PT inflammatory disorders, partic. ulcerative colitis, and bacterial  
PT pneumonia  
PS Example E; Fig 19; 114pp; English.  
CC A cDNA insert (T03363) in vector pA51214VL' codes for the light  
CC chain variable region of anti-human interleukin-8 mouse monoclonal  
CC antibody 5.12.14 and human IgG1 light chain constant region. The  
CC cDNA was obtd. by amplification of cDNA derived from 5.12.14-producing  
CC hybridoma cells using primers (T03352-55) based on light chain  
CC sequences. It is used with cDNA (T03364) coding for the heavy chain  
CC variable region in the prodn. of anti-IL-8 mouse-human chimeric Fab.  
SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T;

Query Match 54.3%; Score 391; DB 16; Length 714;  
Best Local Similarity 86.1%; Pred. No. 2.41e-246;  
Matches 466; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Db 172 tggatcaacaagacagggaactctctaagacgtgatttactcgtcatcctaccgg 231  
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Qy 178 TGGTATCAGCAGAAGCAGCGCAACCTCCAGGCTCTCAITTAAGGTTTCTAACCGG 237

Db 232 tacagtggagtcctcgtcctccacaggcagtgatctgggacagatttcactcacc 291  
|| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 238 GACTCTGGGGTCCACAGAGATTTCAGGCGCAGTGGGGCAGGACAGATTTCACATCGAAA 297

Db 292 atcagccatgtcagctcgaagactggcagactatttctgtcagcaataacatctat 351  
||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
Qy 298 ATCAGCGCAGTGGAGGCTGAAGATGTTGGGCTTTATTTCTGGGGCAGGTACAGGACT 357

Db 352 cctctcagcttcggtcctgggacacagctggagcttcgaagagctgtggctgacacctct 411  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 358 CTTCCCACTTTCGGCGGAGGAGCAAGGTGGAATCAAACTACGGTGGCTGCACCAATCT 417

Db 412 gctctcatctccgccalctcgtgagcagttgaaatctggaactgctctctgttgtgc 471  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 418 GTCTTCATCTTCGCCCATCTCTGATGACAGTGTGAATCTGGAACCTGCCTCTGTTGTGTC 477

Db 472 ctgctgaataacttctatccccagagagggcaaaagtacagtggaggtggataaacgcctc 531  
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Qy 478 CTGCTGAATAACTTCTATCCACAGAGAGGCCAAAGTACAGTGCAGAGGTGGATAACGCCCTC 537

Db 532 caatcgggtaactccccaggagagtggtcacagagcaggacagcaaggacagcactacagc 591  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 538 CAATCGGGTAACTCCACAGGAGGTGTCACAGAGCAGCAGCAGCAAGGACAGCAGCTACAGC 597

Db 592 ctcagcagcacctctgacgtgagcaagcagactacgagaaacacaaagtctacgcctgc 651  
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Qy 598 CTACAGCAGCCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGC 657

Db 652 gaagtcacccatcagggtcgtgactcgccctcacaagagcttcaacagggagagagt 711  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 658 GAAGTCAACCCATCAGGGCTGAGGTCGCCCGCTCAAAAGAGGCTTCAACAGGGGAGAGTGT 717

Db 712 t 712  
Qy 718 T 718

Search completed: Tue Dec 17 21:56:29 1996  
Job time : 69 secs.

2

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MPsrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 21:56:52 1996; MasPar time 276.50 Seconds  
936.193 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-550-5

Description: (1-720) from US08487550.seq

Perfect Score: 720

N.A. Sequence: 1 ATGAGCTCCCTGCTCAGCT.....TCAACAGGGAGAGTGTGA 720  
Comp: TACTCGAGGGAGCAGTCTCAACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0: Querv 0

Searched: 514334 seqs, 179763086 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-STS

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST11 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50  
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56  
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63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68  
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74  
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93:EST93 94:EST94 95:EST95 96:EST96 97:EST97

Database:

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103: EST96 104: EST97 105: EST98 106: EST99 107: EST100  
108: EST101 109: gNEST1 110: gNEST2 111: gNEST3 112: gNEST4  
113: gNEST5 114: gNEST6 115: gNEST7 116: gNEST8 117: gNEST9  
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Statistics: Mean 10.582; Variance 1.910; scale 5.541

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query			DB	ID	Description	Pred. No.	
	No.	Score	Match Length					
1	331	46.0	391 11	H25972	y156d07.r1	Homo sapie	0.00e+00	
2	324	45.0	448 68	R79141	y186c11.r1	Homo sapie	0.00e+00	
3	313	43.5	418 15	H39556	y168ef11.r1	Homo sapie	0.00e+00	
4	311	43.2	398 69	R83107	ypl1a08.r1	Homo sapie	0.00e+00	
5	308	42.8	378 11	H25329	y146c07.r1	Homo sapie	0.00e+00	
6	307	42.6	451 17	H44560	yo75g10.r1	Homo sapie	0.00e+00	
7	303	42.1	432 17	H45568	yo72g01.r1	Homo sapie	0.00e+00	
8	301	41.8	488 11	H25625	y148g05.r1	Homo sapie	0.00e+00	
9	299	41.5	429 12	H28387	y152e01.r1	Homo sapie	0.00e+00	
c	10	297	41.3	403 69	R83659	ypl16c10.s1	Homo sapie	0.00e+00
c	11	297	41.3	475 65	R69391	yf93b12.r1	Homo sapie	0.00e+00
c	12	296	41.1	489 106	H79330	yel3a01.s1	Homo sapie	0.00e+00
c	13	294	40.8	429 17	H44320	yo04d12.r1	Homo sapie	0.00e+00
c	14	293	40.7	520 67	R76323	y123g12.r1	Homo sapie	0.00e+00
c	15	284	39.4	407 69	R83657	ypl1610.s1	Homo sapie	0.00e+00
c	16	281	39.0	435 69	R83590	ypl16b03.r1	Homo sapie	0.00e+00
c	17	280	38.9	366 12	H27048	yf65f06.r1	Homo sapie	0.00e+00
c	18	280	38.9	400 107	T93145	yel2a02.r1	Homo sapie	0.00e+00
c	19	275	38.2	493 90	T58152	yb98g11.s1	Homo sapie	0.00e+00
c	20	273	37.9	405 8	H16015	y127c03.r1	Homo sapie	0.00e+00
c	21	270	37.5	576 99	T64667	yf25h07.s1	Homo sapie	0.00e+00
c	22	268	37.2	441 99	T64100	yc05g09.r1	Homo sapie	0.00e+00
c	23	267	37.1	329 107	T94914	yf3e2e07.r1	Homo sapie	0.00e+00
c	24	267	37.1	498 106	T89966	ye13e12.r1	Homo sapie	0.00e+00
c	25	266	36.9	456 11	H24569	y140b02.s1	Homo sapie	0.00e+00
c	26	263	36.5	438 65	R69535	yf92d12.r1	Homo sapie	0.00e+00
c	27	262	36.4	395 106	T89943	yf12d09.r1	Homo sapie	0.00e+00
c	28	261	36.3	482 67	R73415	yj92g10.s1	Homo sapie	0.00e+00
c	29	261	36.3	514 106	T89673	yf66f007.s1	Homo sapie	0.00e+00
c	30	260	36.1	392 17	H45129	yo66g03.r1	Homo sapie	0.00e+00
c	31	259	36.0	284 15	H39534	y168a07.r1	Homo sapie	0.00e+00
c	32	255	35.4	521 67	R76324	y123g12.s1	Homo sapie	0.00e+00
c	33	252	35.0	520 8	H15909	y127c02.s1	Homo sapie	0.00e+00
c	34	251	34.9	438 64	R64693	yi22f09.r1	Homo sapie	0.00e+00
c	35	251	34.9	508 17	H44507	yo75h08.r1	Homo sapie	0.00e+00
c	36	250	34.7	425 64	R66359	yi34g12.r1	Homo sapie	0.00e+00
c	37	250	34.7	542 65	R69401	yj93d09.s1	Homo sapie	0.00e+00
c	38	249	34.6	488 98	T62514	yo04a07.s1	Homo sapie	0.00e+00
c	39	247	34.3	340 11	H24540	y130f05.r1	Homo sapie	0.00e+00
c	40	247	34.3	344 99	T64374	yc47b03.r1	Homo sapie	0.00e+00
c	41	247	34.3	467 12	H27034	yf65d05.r1	Homo sapie	0.00e+00
c	42	246	34.2	433 10	H22016	y134c05.s1	Homo sapie	0.00e+00
c	43	246	34.2	474 99	T63859	ycl16e03.s1	Homo sapie	0.00e+00
c	44	244	33.9	411 8	H16042	y127g01.r1	Homo sapie	0.00e+00
c	45	243	33.8	453 68	R79142	y186f10.s1	Homo sapie	0.00e+00

## ALIGNMENTS

## RESULT 1



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1..448      /organism="Homo sapiens"
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            /note="human"
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BASE COUNT	122 a	117 c	116 g	92.t	1 others
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Query Match 45.0%; Score 324; DB 69; Length 448;  
Best Local Similarity 96.7%; Pred. No. 0.00e+00;  
Matches 355; Conservative 0; Mismatches 8; Indels

Db 61 ctncgctcactttcggcgaggaggaccaagtgagatgaacgaactgtggctgcacat 120

Qy 356 CTCTCCGACTTTCGGCGGAGGACCAAGGTGGAAATCAAAAGCTACGGTGGGTGCACCAT 415

Db 121 ctgtcttcattcccccatctgatgagcagttgaaatctggaactgcctctgttgt 180

Qy 416 CTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT 475

Db 181 gcctgctgaataacttctatcccagagaggccaaagtacagtggaagtgataacgccc 240

Qy 416 GCCTGCTGAATAAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAAACGCC 533

[illegible][illegible]

361 tgcgaagt taccat cagggcct agct cggcct tcaaaaagat ttaacaggga 420

[illegible]

Db 421 qagtttt 427

Qv 712 GAGTGT 718

RESULT	LOCUS	3	H39556	418 bp	mRNA	EST	31-JUL-1995

DEFINITION y168c11.r1 Homo sapiens cDNA clone 163412 5' similar to gb:S49999.1 IG KAPPA CHAIN C REGION (HUMAN);.

ACCESSION	H39556
NID	g915572

EST: human clone=163412 library=Soares breast 3NHBst vector=p7T73D

pharmacia) with a modified polylinker host=PH10B (ampicillin resistant) primer=M13Rpl Rsite1=Not I Rsite2=Eco RI Adult human 1st strand cDNA was combined with a Not I cta1cc/(m) primer 157

18T strand cDNA was primed with a Not I - oligo(dT) primer [5'-GTTACCAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adapters (Pharmacia

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia) digested with Not I and cloned into the Not I and Eco RI sites modified pT7T3 vector (Pharmacia). Library went through one round of screening.

of normalization to a Cot = 20. Library constructed by Bento S. and M. Fatima Ronaldo.

ORGANISM	Homo sapiens
Eukaryotae:	Metazoa:
Eumetazoa:	Bilateria:
Coelomata:	

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 418)

AUTHORS	Hillier, L., Clark, N., Dubuque Holman, M., Hultman, M., Kucal Parsons, J., Rifkin, L., Rohlf Trevaskis, E., Waterston, R., Wilson, R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 367  
Source: IMAGE Consortium, LINL  
This clone is available royalty-free through LINL ; contact the  
IMAGE Consortium ([info@image.linnl.gov](mailto:info@image.linnl.gov)) for further information.

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NCBI gi: 915572
FEATURES
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                /note="human"

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ORIGIN					

Query Match 43.5%; Score 313; DB 15; Length 418;  
Best Local Similarity 95.8%; Pred. No. 0.00e+00;  
Matches 343; Conservative 0; Mismatches 11; Indels 4; Gaps 4;

Db 22 acgtcggccaaagg-ccaaggtggaattaaacgaacttggtgcaccatctcttc 80

Qy 364 ACTTTCGGCGGAGGACCAAGGTGGAAATCAACGTACGGTGGCTGCACCATCTGTCTTC 423

Db 81 atcttcgcccatctgatgagcagctgaaatctgganctgcctctgttgtgtgcctgctg 1400

424 ATCTCCCGCACTCTGATGACGAGTTGAAATCTGAACTGGCTCTGTTCTGTGCCCTCTG 483

Db 141 aataactttatcccagagaggcccaagtacagtgaaggtgataaacgccctccaatcg

Qy 484 AATAACTTCTATCCAGAGAGGCCAAACTACACTGGAAGGTGGATAACGCCCTCCCAATCG 543

[illegible]

544 GGTAACCTCCCAGGAGAGTGTACACAGGAGGACAGCAAGGACACCTACAGCCCTCAGC

[illegible]

321 accatcagggggtt gaggc cagcctt cacaagagaggtt tt caacaggggagaggt nt 378

**Qv** 664 ACCCATCAGGGCGCT-GAGCTTCCCCGCT-CACAAAGAGCTT-CAACAGGGGAGAGCTGT 718

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RESULT	4
LOCUS	R83107 398 bp mRNA EST 04-AUG-1995
DEFINITION	yplaa08.r1 Homo sapiens cDNA clone 187094 5' similar to gb:M63438
	IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.
ACCESSION	R83107
NID	g927984

**KEYWORDS**  
**SOURCE**

**KEYWORDS**  
SOURCE

**EST.**  
human clone=187094 library=Soares breast 3NbHst vector=p7T73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13P1 Rsite1=Not I Rsite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACCAATCTGAAGTCGGAGCGCCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fátima Bonaldo.

## ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
AUTHORS

**AUTHORS** Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

**TITLE** The WashU-Merck EST Project  
**JOURNAL** Unpublished (1995)

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8500  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
High quality sequence stops: 297  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-  
free from the IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov))

## NCBI ai: 927984

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ORIGIN					

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Best Local Similarity 96.8%; Pred. No. 0.00e+00;  
Matches 335; Conservative 0; Mismatches 8; Indels

**Db** 3 gggacgaagctggagatcaaacgaaactgtgctgcaccatctgtctcatnttcccgcca 62  
||||| ||| |||| | ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||  
**Qv** 376 GGGACCAAGCTGGAATCAACGTGCGGTGGCTGCACCATCTGCTTCATCTTCCGCCA 435

Db	63	tctgatgagcagttaaattctggaaactgcctctgttgtgcctgctgaataacttctat	122
Ov	436	TCTCATCAGACATTGAAAATCTCCGAATCCCTCTCTCTCTGCCTCGTCAATAAATTTCTAT	495

[illegible]

Db 123 cccagagagcccaagtacagtggaagtggaataacgcccctccaatcgggtaactccag 182  
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Qy 496 CCCAGAGAGGCCAAAGTACAGTGGAGGTGCAACGCCCTCCCAATCGGGTAACTCCAG 555

[illegible]

Db 183 gagagtgtcacagagcaggacagcaagcacctacagcctcagcagcacctgacg 242

QY	556	GAGAGTGTTCACAGAGCAGCAGCAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTCAGC	615
Db	243	ctgagcaagcagactacgagaacacacaactctacgctcgcaagtcacccattcagg                         	302
QY	616	CTGACCAACGACACTACACGAACACAAAGTCTACGCTCGCAAGTCACCAT-CAAGG	674

Db 303 cctgagcttgcgcgtcacaaagagctttcaacaggggagagintt 348  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Qv 675 cctgagct-cgcccctcacaaagagctt-caacaggggagagcttt 718

## RESULT

LOCUS	H25329	378 bp	mRNA	EST	10-JUL-1995
DEFINITION	y146c07.r1 Homo sapiens cDNA clone 161292 5' similar to gb:S49006 IG KAPPA CHAIN C REGION (HUMAN) ;.				

ACCESSION	H25329
NID	g894452

**KEYWORDS** EST.

SOURCE

human clone=161292 library=Soares breast 3NbHst vector=ptT3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M3SRP1 Rsite2=Eco RI Adsite2=Eco RI Adsite1 human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTCAAGTGGAGGCGCGCCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified ptT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chloanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
AUTHORS

**AUTHORS**  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, N., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Willson, R.

TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
ABSTRACT	
KEYWORDS	
DESCRIPTION	
REFERENCES	
NOTES	
REMARKS	

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence steps: 337  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL ; contact  
IMAGE Consortium (info@image.lnl.gov) for further information

NCBI gi: 894452

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Best Local Similarity 97.9%; Pred. No. 0.00e+00;  
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Db 2 atcaaacgaactgggtgaccatctgtcttcatcttccgcctatctgatgagcagtt 61  
||||||| 11 |||||  
Qy 391 ATCAACGTCAGCGTGG-CTGACCATCTGTCTTATCTTCCGCCCATCTGATGACGATT 449  
|||||||  
Db 62 gaaactcgaactcctgtgtgtgctgctgaataaacttctatccagagagccaa 121  
|||||||  
Qy 450 GAAATCTGAACACTGCCCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGCCAA 509  
|||||||  
Db 122 agtacagtggaagtggataaacgacctcaatcgggttaactccagagagagtgctcacaga 181  
|||||||  
Qy 510 AGTACAGTGAAGGTGATGATAAGCCCTCCAAATCGGGTAACCTCCAGGAGAGTCTCACAGA 569  
|||||||  
Db 182 gcaggacagcagcagcactcagcctcagcagcaccctgacgtgagcaagcaga 241  
|||||||  
Qy 570 GCAGGACAGCAGCAGCAGCACTACAGCTCAGGAGCACCCTGACGCTGAGCAAGAGCAGA 629  
|||||||  
Db 242 ctacgagaacacaaagtctacgncctgcgaagtcaacctcagggcctgagctcgcccg 301  
|||||||  
Qy 630 CTAGAGAAACACAAAGTCTAGGCTCGGAGCTCAGCCATCAGGCCCTGAGCTGCCCGGT 689  
|||||||  
Db 302 nacaagaagttcaacaggggagagtggt 331  
|||||||  
Qy 690 CACAAAGAGCTTCAACAGGGG-AGAGTGT 718  
|||||||

RESULT 6  
LOCUS H44560 451 bp mRNA EST 31-JUL-1995  
DEFINITION yo75g10.r1 Homo sapiens cDNA clone 183810 5' similar to gb:549006  
IG KAPPA CHAIN C REGION (HUMAN);  
ACCESSION H44560  
NID G920612  
KEYWORDS EST.  
SOURCE human clones=183810 library=Soares breast 3NbH8st vector=p7T73D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=M13RP1 Rsite=Not I Rsite2=Eco RI Adult human.  
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTT 3']  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pT7T3 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 20. Library constructed by Bento Soares  
and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonaria; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 451)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, B., Rohlfing, F., Soares, M., Tan, F.,  
Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Willson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

Fax: 314 286 1810  
Email: est@wustl.edu  
High quality sequence stops: 340  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 920612  
FEATURES  
Location/Qualifiers  
source 1..451  
/organism="Homo sapiens"  
/clone="183810"  
/note="human"  
BASE COUNT 106 a 142 c 102 g 98 t 3 others  
ORIGIN

Query Match 42.6%; Score 307; DB 17; Length 451;  
Best Local Similarity 99.7%; Pred. No. 0.00e+00;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1 caccatctgtcttcatcttccgcctatctgatgagcagttgaaatctggaactgcctcg 60  
|||||||  
Qy 410 CACCATCTGTCTTTCATCTTCCGCCCATCTCATGACGAGTTGAAATCTGGAATCTGCTCTG 469  
|||||||  
Db 61 ttgtgtcctgctgaataacttctatcccgagagggccaaagtacagtgaagtgata 120  
|||||||  
Qy 470 TTGTGTGCTGTGTAATACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATA 529  
|||||||  
Db 121 acgcctccaactcgggttaactcccgagagagtgctcacagcagcagcagcagcagcaga 180  
|||||||  
Qy 530 AGCCCTCCAAATCGGGTACTCCAGGAGAGTGTCCAGAGCAGCAGCAGCAGCAGCAGCA 589  
|||||||  
Db 181 cctacagctcagcagcacctgacgtgagcaagcagcagcagcagcagcagcagcagcagc 240  
|||||||  
Qy 590 CCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 649  
|||||||  
Db 241 acgctcgaagtcacccatcagggcctgagctcgccctcacaagagagcttcaacagg 300  
|||||||  
Qy 650 AGCGCTCGCAAGTCACCATCAGGCGCTGAGCTCGCCCGCTCACAAGAGAGCTTCAACAGGG 709  
|||||||  
Db 301 gagagtggt 309  
|||||||  
Qy 710 GAGAGTGT 718  
|||||||

## RESULT 7

LOCUS H45568 432 bp mRNA EST 31-JUL-1995  
DEFINITION yo72g01.r1 Homo sapiens cDNA clone 183504 5' similar to gb:007989  
IG KAPPA CHAIN V-I REGION (HUMAN);

## ACCESSION

H45568

## NID

G921620

## KEYWORDS

EST.

SOURCE human clones=183504 library=Soares breast 3NbH8st vector=pT7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=M13RP1 Rsite=Not I Rsite2=Eco RI Adult human.  
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTT 3']  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pT7T3 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 20. Library constructed by Bento Soares  
and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;



Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marta, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
High quality sequence stops: 322  
Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

NCBI q1: 921620

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FEATURES
source
Location/Qualifiers
1..432
/organism="Homo sap
/clone="183504"
/note="human"
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BASE COUNT	114 a	107 c	116 g	90 t	5 others
ORIGIN					

Query Match 42.1%; Score 303; DB 17; Length 432;  
Best Local Similarity 95.4%; Pred. No. 0.00e+00;  
Matches 335; Conservative 0; Mismatches 12; Indels 4; Gaps 4;

**D**b      54    acgttcggccaaggaccaaagtggaatcaaacgaaactggctgcaccatctgttcc 113  
         ||||| |  
  
**Ov**     364   ACTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGCCCTGCACCACGTGTTCTC 423

Db 114 atcttccgcgcacatctgatgagcagttgaaatctggaactgcctctgttgtatgcctgctg 173  
|||||  
Ov 424 ATCTTCCCGGCATCTGATGACACATCAATCTGGAACCTGCCTCTCTCTCTCTCTCTCTG 483

Db 174 aataactctatcccagagagccaaagtacagtgaagtggtataacgcctccaatcg 233

Qy	484	ANAACTTCTATCCAGAGAGGCCAAGTACAGTGGAGGTGGATAACGCCCTCCAATCG
Db	234	qdtaaactccaggagaqaqtgtcacagacgacgagcagcaggaqqacagcaacctacagqctcagc

Qy 544 GGTAATCCAGGAGTGTACACAGCAGGACAGCAAGGACACCTACAGCCTCAGC 603

Qy 604 AGCACCCCTGACGGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCT-ACGCCCTGGGAAGT 662

Db 354 tcaccttcaggggcntyagtttcgcccgtcacaagagnttcaacagggg 404

[illegible]

LOCUS	H25625	438 bp	mRNA	EST	10-JUL-1995
8					

DEFINITION y148q05.r1 Homo sapiens cDNA clone 161528 5' similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);.

ACCESSION	H25625
NID	g894748

KEYWORDS	EST.
SOURCE	human

(Pharmacia) with a modified polylinker host=DHI0B (ampicillin resistant) primer=M3R91 Rstel=Not I Rsite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTCAAGTCGGAGCGCGCCCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soa and M.Fatima Bonaldo.

## ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Arcnonta; Primates; Catarrhini; Hominoidea; Homo.

## REFERENCE

**AUTHORS**  
Hillier, L., Clark, N., Dubucq, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and  
Wilson, R.

TITLE	JOURNAL	COMMENT
The WashU-Merck EST Project	Unpublished (1995)	

**Contact: Wilson RK**

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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
High quality sequence stops: 362

Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 894748

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FEATURES
source
Location/Qualifiers
1..488
/organism="Homo sapiens"
/clone="161528"
/note="human"
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BASE COUNT	99 a	130 c	128 g	127 t	4 others
ORIGIN					

Query Match 41.8%; Score 301; DB 11; Length 488;  
Best Local Similarity 83.3%; Pred. No. 0.00e+00;  
Matches 405; Conservative 0; Mismatches 76; Indels 5; Gaps 5;

db 3 atgaggctccctgctcagctcctgggctgctaatactctgggtctctggatccagtgagg 62

QY 1 ATGAGCCTCCCTGCCTCAGCTCTCGGGCTGCTATTGCTCTCCGCTCCCGGGTCCAGTGG 60

Db 63 gatattgtgatgactcagtcctccactctccagcccgctcacccctggagagccggctcc 122

QY 61 GAAGTTGTGATGACTCACTCTCCACTGTCCCTTCCCATCACACTGGAGACCGGGCTTC 120

Db 123 atctcctgcaagtctagtcagagcctcctacatagtaatggatacagttatttggattgg 182



REFERENCE  
AUTHORS

Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 403)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project  
Unpublished (1995)

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence stops: 191  
Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Possible reversed clone: poly\* not found.

NCBI gi: 928536

FEATURES  
source Location/Qualifiers

1..403  
/organism="Homo sapiens"  
/clone="187602"  
/note="human"

BASE COUNT 78 a 95 c 126 g 102 t 2 others

Query Match 41.3%; Score 297; DB 69; Length 403;  
Best Local Similarity 98.7%; Pred. No. 0.00e+00;  
Matches 304; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Db 89 acaactctccccgttggaagctcttggagggcgagctcaggccctgatgggtgactt 148  
|||||

Cp 718 AACACTCTCCCTGTGAAGCTCTTTCTGACGGCGAGCTCAGCCCTGATGGGTGACTT 659  
|||||

Db 149 cgcaggcgtagagtgtgtttctcgtagctgtcttctcagcgtcagggtgctgcta 208  
|||||

Cp 658 CGACGGGTAGACTTTGTTCTCTGCTAGCTTGGCTGAGCTCAGGGTCTGCTGA 599  
|||||

Db 209 ggctgtaggctgctctctgctctctctctgacactctctggaggtaccgatt 268  
|||||

Cp 598 GGCTGTAGGTCTGCTCTGCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 539  
|||||

Db 269 ggagggcgttatccactccactgaacttggcctctntggatagaaagtattacga 328  
|||||

Cp 538 GGAGGGCGTTATCCAGCTTCCAGCTGACTTTGGCTCTCTGGATAGAGTATTTCAGCA 479  
|||||

Db 329 ggcacacacagaggcaggtccagatttcaactgctcatcagatngccgggaagatgaag 388  
|||||

Cp 478 GGACACACAGAGGAGGAGTCCAGATTTCACTGCTCATCAGATGCC-GGGAGATGAAC 420  
|||||

Db 389 acagatgg 396  
|||||

Cp 419 ACAGATGG 412

RESULT 11  
LOCUS R69391 475 bp mRNA EST 01-JUN-1995

DEFINITION yj83b12.r1 Homo sapiens cDNA clone 155327 5' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.

ACCESSION R69391

NID g842908

KEYWORDS EST.

SOURCE human clones=155327 library=Soares breast 2NBHbst vector=p7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13p1 Reitel=Not I Rsite2=Eco RI Adult female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTCAAGTGGAGCGCCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo.

#### ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

#### REFERENCE

##### AUTHORS

1 (bases 1 to 475)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

#### TITLE

##### JOURNAL

##### COMMENT

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Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence stops: 340  
Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 842908

FEATURES  
source Location/Qualifiers

1..475  
/organism="Homo sapiens"  
/clone="155327"  
/note="human"

BASE COUNT 117 a 124 c 126 g 104 t 4 others

#### ORIGIN

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Best Local Similarity 89.9%; Pred. No. 0.00e+00;  
Matches 393; Conservative 0; Mismatches 33; Indels 11; Gaps 11;

Db 1 tgaacatcagcagggtggaggtcagcatcttggctttattactgcagcaggttcaac 60  
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Cy 293 TGAATAATCAGCGCAGTGAGGCTCAACATGTTGGGGTTTATTTCTGCGGCAAGGTACAA 352  
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Db 61 actggctccacttttggcagggggacacagctggagatcaaacgaactgtggctgac 120  
|||||

Cy 353 GGACTCTCCCACTTTCCGGCGGAGGACCAAGGTGGAATCAACAGCTACGTCGTCAC 412  
|||||

Db 121 catctgtcttcattctccgcgcctcatctgatgagcagttgaaatctggaaactgctctgtt 180  
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17

Qy 413 CATCTGCTTCATCTCCCGCATCTGATCAGCAGTTGAAATCTGGAATCGCTCTGTG 472

Db 181 tgtgctgtgaataaactctatccagagagcgcaagtacagtgaagtggaataacg 240  
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Qy 473 TGTGCTGCTGAATTAATCTTATCCAGAGAGGCCAAGTACAGTGAAGTGGATAACG 532  
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Db 241 ccctccaatcgggtgaactccagggagaggtgtcacagagcagcagcagcagcagc 300  
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Qy 533 CCTTCATTCGGGTAACTCCAGG-AGAGTGTCAAGCAGCAGCAGCAGCAGCAGC 591  
|||||

Db 301 tacagctcagcagcaccctggagcgtgagcaaaacagcagcagcagcagcagc 360  
|||||

Qy 592 TACAGCCTCAGCAGCACCCTG-ACGCTGAGCAGCAGCAGCAGCAGCAGCAGC 648  
|||||

Db 361 ttaagcctgnaaggtcaacccctcagggccttgagctnctcagtcagcaagagcttt 420  
|||||

Qy 649 T-ACGCTCGCAAGT-CACCAT-CAGGGCCT-GAGCT-CGCCCGT-CACAAAGAGCTT- 701  
|||||

Db 421 caacaggggagagtttt 437  
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Qy 702 CAACAGGGGAGAGTGT 718  
|||||

RESULT 12 789330 489 bp mRNA EST 20-MAR-1995

LOCUS yel3ell.61 Homo sapiens cDNA clone 117644 3' similar to gb:M63438

DEFINITION IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);

ACCESSION 789330

NID g717843

KEYWORDS EST.

SOURCE human clones-117644 library-Stratagene lung (#937210)  
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)  
primer=-21m13 Rsite=EcoRI Rsite2=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-CAATTCGCAGCAGCAG-3'; 3' adaptor sequence:  
5'-CTCAGCTTTTTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 489)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaaskis, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 420  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

FEATURES  
source NCBI gi: 717843  
Location/Qualifiers  
1..489  
/organism="Homo sapiens"

Dec 17 21:47

US-08-487-550-5.rst

18

BASE COUNT 104 a 114 c 151 g 116 t 4 others

ORIGIN

Query Match 41.1%; Score 296; DB 106; Length 489;  
Best Local Similarity 99.3%; Pred. No. 0.00e+00;  
Matches 303; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Db 168 aacactccccctgtgaagctctttgtgacggcgagctcagggcctgatgggtgactt 227  
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Cp 718 AACACTCTCCCTGTTGAAGCTCTTTGTACGGCGAGCTCAGGCCCTGATGGGTGACTT 559  
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Db 228 qcagcggcgaactttgtttctcgtagctcgtttgttcagcgtcagggtgctgctga 287  
|||||

Cp 658 CCGAGCGGTAGACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599  
|||||

Db 288 ggctgtaggtgctgctccttgctgctgctgctgctgctgctgctgctgctgctg 347  
|||||

Cp 598 GGCTGTAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
|||||

Db 348 tggaggcgcttatccacttccactgtactttggcctctctgggataagattattcagc 407  
|||||

Cp 539 TCGAGGGCGGTATCCACCTTCCACTGTACTTTGGCCTCTCGGATAGAGTTATTACG 480  
|||||

Db 408 aggcacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 467  
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Cp 479 AGGCACACACAGCAGCAGCTCCAGATTCAACTGCTCATCATGCGCGGAAGATGAAG 420  
|||||

Db 468 acaga 472  
|||||

Cp 419 ACAGA 415  
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RESULT 13 H44320 429 bp mRNA EST 31-JUL-1995

LOCUS YP04d12.rl Homo sapiens cDNA clone 186455 5' similar to gb:M63438

DEFINITION IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);

ACCESSION H44320

NID g920372

KEYWORDS EST.

SOURCE human clones-186455 library-Soares breast 3NbHbSt vector=p77T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=M13R1 Rsite=Not I Rsite2=Eco RI Adult human.  
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TCTTACCAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified p77T3 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 20. Library constructed by Bento Soares  
and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 429)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)



Dec 17 21:47

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21

RESULT 15

LOCUS R83657 407 bp mRNA EST 04-AUG-1995  
DEFINITION ypl6b10.s1 Homo sapiens cDNA clone 187579 3' similar to gb:S49006  
IG KAPPA CHAIN C REGION (HUMAN);

ACCESSION R83657

NID 9928534

KEYWORDS EST.

SOURCE

human clones=187579 library=Soares breast 3NbHst vector=pT7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=F3 Rsite1=Not I Rsite2=Eco RI Adult human. 1st  
strand cDNA was primed with a Not I - oligo (dT) primer [5'  
TCTTACCATCTCAAGTGGAGCGGCCCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pT7T3 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 20. Library constructed by Bento Soares  
and M.Fatima Bonaldo.

ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 407)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 239  
Source: IMAGE Consortium, ILNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: polyt not found.

NCBI gi: 928534

Location/Qualifiers

1..407

/organism="Homo sapiens"

/clone="187579"

/note="human"

BASE COUNT 77 a 96 c 125 g 107 t 2 others

ORIGIN

Query Match

Best Local Similarity 39.4%; Score 284; DB 69; Length 407;

Matches 304; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

Db

94 aacactctccctgtgaagctcttctgtgacggcgagctcaggccctgatgggtgactt 153

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Cp

718 AACACTCTCCCTGTTGAGAGCTCTTTGTGACGGCGAGCTCAGGCCCTGATGGGTGACTT 659

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154 cgcaggcgtagactttgtttctctgtctgtctgtcagcgtcagggtgctgctga 213

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Cp

658 CGCAGGCGTAGACTTTGTTCTTCGTAGTCTGCTTTGCTCAGCGCTCAGGGTCTGCTGA 599

Dec 17 21:47

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22

Db 214 ggcgtgtaggtgctgtccttgctgtcctgtcctgtgtgacactctcctggggagttaccgcat 273

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Cp 598 GGCTCTAGGTGCTGTCTTGTCTGCTGCTGTGACACTCTCTCTGGG-AGTTACCGCAT 540

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Db 274 tggaggcgtttatccaccttccactgtactttggcctctctgggatagaagttattcagc 333

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Cp 539 TGGAGGGCGTTATCCACCTTCCACTGTACTTTGGGCTCTCTGGGATAGAGTTATTTCAGC 480

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Db 334 aggcacacacagagcgagttccacagattttccactgctcatcatcagatngcgggaagatta 393

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Cp 479 AGGCACACACAGAGGCGAGTTC-AGATT-CAACTGCTCATCAGATGGCGGGAAGATGA 422

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Db 394 agacagattgt 404

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Cp 421 ACACAGATGGT 411

Search completed: Tue Dec 17 22:01:37 1996

Job time : 285 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

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Run on: Tue Dec 17 22:07:24 1996; MasPar time 850.41 Seconds
1284.318 Million cell updates/sec
Tabular output not generated.
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09-097 550 7

Description: (1-1437) from US08487550.seq  
Perfect Score: 1437

1 ATGGTTGGAGCCTCATCTT.....CCTGTCTCGGGTAATGA 1437  
TACCAACCTGGAGTAGAA.....GGGACAGGCCCATTTACT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 270440 seqs. 380027776 bases x 2

Post-processing: Minimum Match 0%

Database: emb1-new3

1: BCT 2: FUN 3: INV1 4: INV2 5: INV3 6: MAM 7: ORG 8: PLN  
9: PRI1 10: PRI2 11: PRO 12: ROD 13: SYN 14: UNC 15: VRT  
16: VIR1 17: VIR2

Database: aenbank92

98:BNK071  
18:BCIT1 19:BCI2 20:BCI3 21:BCI4 22:BCI5 23:BCI6 24:BCI7  
25:BCI8 26:BCI9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5  
32:INV6 33:MAM1 34:MAM2 35:PAT1 36:PAT2 37:PAT3 38:PHG  
39:PLN1 40:PLN2 41:PLN3 42:PLN4 43:PLN5 44:PLN6 45:PIN7  
46:PLN8 47:PRI1 48:PRI2 49:PRI3 50:PRI4 51:PRI5 52:PRI6  
53:PRI7 54:PRI8 55:PRI9 56:PRI10 57:PRI11 58:PRI12  
59:PRI13 60:ROD1 61:ROD2 62:ROD3 63:ROD4 64:ROD5 65:ROD6  
66:ROD7 67:STR 68:SYN 69:UNA 70:VRL1 71:VRL2 72:VRL3  
73:VRL4 74:VRL5 75:VRL6 76:VRL7 77:VRT1 78:VRT2 79:VRT3  
genbank-neal

Database:

Database:

Database: u-embl45\_92 93:part1

Statistics: Mean 11.574; Variance 4.914; scale 2.355

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1114	77.5	1549	36	A21385	Plasmid DNA with huma	0.00e+00
2	1045	72.7	1599	56	HUM1GHEPAH	Human (hybridoma H210	0.00e+00
3	1008	70.1	1135	37	I09303	Sequence 5 from paten	0.00e+00
4	1008	70.1	1135	37	I07069	Sequence 15 from pate	0.00e+00
5	1007	70.1	1465	59	S79307	Ig gamma =Immunoglobu	0.00e+00
6	998	69.5	1341	35	A07562	DNA sequence of chime	0.00e+00
7	762	53.0	1359	38	MAC1GHWCDR	Macaca fascicularis i	0.00e+00
8	695	48.4	768	51	HS1GQ4FCA	H.sapiens mRNA for Im	0.00e+00
9	693	48.2	1163	51	HS1GQVDJ1	H.sapiens rearranged	0.00e+00
10	608	42.3	1089	56	HUM1GHAF	Human Ig gamma3 heavy	0.00e+00
11	588	40.9	1547	34	MVI1GVDVJ3	Mink immunoglobulin q	0.00e+00
12	585	40.7	1551	34	PIG1GHVCA	S.domesticus immunogl	0.00e+00
13	494	34.4	1594	34	OA1GGISA	O.aries mRNA for immu	0.00e+00
14	489	34.0	1235	34	RAB1IGHAD	Rabbit Ig active gamma	0.00e+00
15	479	33.3	1179	34	MVI1GGJC	Mink immunoglobulin g	0.00e+00
16	468	32.6	1563	34	PIG1GHVGC	S.domesticus immunogl	0.00e+00
17	466	32.4	1581	33	BT1GIG1HCX	B.taurus mRNA for imm	0.00e+00
18	456	31.7	1079	34	SSU03779	Sus scrofa Ig gamma 2	0.00e+00
19	454	31.6	1079	34	SSU03780	Sus scrofa Ig gamma 2	0.00e+00
20	442	31.2	1079	34	SSU03781	Sus scrofa Ig gamma 3	0.00e+00
21	440	30.8	1093	34	PIG1GHVGB	S.domesticus IgG chai	0.00e+00
22	443	30.8	1488	75	PVY1B	Potato virus Y immuno	0.00e+00
23	443	30.8	1544	63	MUS1GIB1H1	Mouse mRNA for immuno	0.00e+00
24	440	30.6	1079	34	SSU03778	Sus scrofa Ig gamma 1	0.00e+00
25	418	29.1	1581	60	MM1GHC2AA	M.musculus mRNA for m	0.00e+00
26	414	28.8	1092	66	R1G1G2C	R.rattus mRNA for Ig	0.00e+00
27	414	28.8	1106	63	MUS1GEG3ALL	Mus musculus germline	0.00e+00
28	414	28.8	1341	37	I07390	Sequence 4 from paten	0.00e+00
29	397	27.7	1095	60	MM1G66	Mouse mRNA for gamma-	0.00e+00
30	397	27.6	1347	37	I08674	Sequence 2 from paten	0.00e+00
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35	384	26.7	928	34	SSU03782	Sus scrofa Ig gamma 4	0.00e+00
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44	341	23.7	711	36	HUM1GHZZA	Mouse Ig rearranged g	2.00e-302
45	341	23.7	1492	63	MUS1GHBAS	Homo sapiens Ig rearr	1.66e-294
46	341	23.7	1492	63	MUS1GHBAS	Mouse germline immuno	1.66e-294

## ALIGNMENTS

RESULT	1	
LOCUS	A21385	1549 bp RNA PAT
DEFINITION	Plasmid DNA with human cDNA insert.	
ACCESSION	A21385	
NID	g583507	
KEYWORDS	.	
SOURCE	unidentified.	
ORGANISM	unidentified.	
	unclassified.	



Dec 17 22:07

US-08-487-530-7.rge

3

REFERENCE 1 (bases 1 to 1549)  
AUTHORS  
TITLE RECOMBINANT PROTEIN WHICH BINDS TO A COMPLEX VIRAL ANTIGEN OF HIV-1  
JOURNAL Patent: WO 9118983-A 1 12-DEC-1991;  
COMMENT NCBI gi: 583507  
FEATURES Location/Qualifiers  
source 1..1549  
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101..1528  
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BASE COUNT 362 a 463 c 417 g 307 t  
ORIGIN

Query Match 77.5%; Score 1114; DB 36; Length 1549;  
Best Local Similarity 90.3%; Pred. No. 0.00e+00;  
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Qy 361 TACATTTCAGATTGTCGGGGTGTGCTGTATGAGAGTTACTTCGAATTCGTGGGGCCAG 420  
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Qy 421 GCGGCCCTGGTCACCTCTCTCAGTAGCACCACCAAGGGCCCATCGGTCTTCCCTCGGA 480  
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Dec 17 22:07

US-08-487-530-7.rge

4

Qy 481 CCCTCTCTCAAGAGCACCTCTGGGGGCACAGCGCCCTGGCTGCCTGGTCAAGGACTAC 540  
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Qy 1381 GAGGCTCTGCACAAACCTACTACACAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1437

RESULT 2



Qy 841 ACCCTCATGATCTCCCGGACCCCTGAGGTACATCGGTGGTGGACGCTGAGCCACGAA 900  
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RESULT 3 109303 1135 bp PAT 14-NOV-1994

LOCUS 109303 Sequence 5 from patent WO 8902922.

DEFINITION 109303

ACCESSION 109303

NID g587989

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1135)

AUTHORS Capon,D.J. and Gregory,T.J.

TITLE ADHESON VARIANTS

JOURNAL Patent: WO 8902922-A 5 06-APR-1989;

COMMENT NCBI gi: 587989

FEATURES Location/Qualifiers

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BASE COUNT 255 a 385 c 303 g 192 t

ORIGIN

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Db 270 ccagcggtgcaacacctcccggtgtcctacagtcctcaggactctactccctcaaga 329  
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Qy 884 TGGAGCTGAGCCACCAAGCAACCCCTGAGGTCAGTTCAACTGGTACGTGGACGGCGTGGAG 943  
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RESULT 4  
LOCUS 107069 1135 bp PAT 14-NOV-1994  
DEFINITION Sequence 15 from patent EP 0314317.  
ACCESSION 107069  
NID g590384

## KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

1 (bases 1 to 1135)

Capon,D.J. and Gregory,T.J.

Adhesion variants, nucleic acid encoding them and compositions

comprising them

Patent: EP 0314317-A1 15 03-MAY-1989;

JOURNAL

NCBI gi: 590384

Location/Qualifiers

1..1135

/organism="unknown"

BASE COUNT 255 a 385 c 303 g 192 t

ORIGIN

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Best Local Similarity 98.7%; Pred. No. 0.00e+00;

Matches 1021; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 1424 CTCGGGTAAATGA 1437

RESULT 5

LOCUS S79307 1465 bp mRNA PRI 10-JUL-1992

DEFINITION Ig gamma =immunoglobulin heavy chain [rats, humanized lympholytic

MoAb CAMPATH-IH, mRNA, 1465 nt].

ACCESSION S79307

NID 9243865

KEYWORDS human humanized lympholytic MoAb CAMPATH-IH.

SOURCE Homo sapiens

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1465)

AUTHORS Crowe,J.S., Hall,V.S., Smith,M.A., Cooper,H.J. and Tite,J.P.

TITLE Humanized monoclonal antibody CAMPATH-IH: myeloma cell expression

of genomic constructs, nucleotide sequence of cDNA constructs and

comparison of effector mechanisms of myeloma and Chinese hamster

ovary cell-derived material

CLIN. Exp. Immunol. 87 (1), 105-110 (1992)

JOURNAL 92127884

MEDLINE

REMARK GenBank staff at the National Library of Medicine created this

entry [NCBI gibbsq 79307] from the original journal article.

This sequence comes from Figure 2.a.

## COMMENT

NCBI gi: 243865

## FEATURES

Location/Qualifiers

## source

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/note="human"

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/gene="IgGgamma"

/note="This sequence comes from Figure 2.a. NCBI gi:

243866"

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/product="immunoglobulin heavy chain"

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BASE COUNT 352 a 466 c 383 g 264 t

## ORIGIN

Query Match 70.1%; Score 1007; DB 59; Length 1465;

Best Local Similarity 98.6%; Pred. No. 0.00e+00;

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Qy 463 TCGGTCTTCCCGCTGSCACCTCTCCAAGAGACCTCTGGGGGCACAGCGCCCTGGGC 522

Db 534 tgcctggcgaagactacttccccgaacgggtgacggtgctggaactcagggccctg 593

Qy 523 TGCCTGGTCAGAGACTACTTCCCGGACCGGTGACGGTCTCGTGAACCTCAGCGGCCCTG 582

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Qy 1303 TTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGAGGGGAAAGCTCTTC 1362

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RESULT 6

LOCUS A07562 1341 bp DNA PAT 28-JUN-1993

DEFINITION DNA sequence of chimeric monoclonal TSH antibody, gamma chain.

ACCESSION A07562

NID g413075

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified

REFERENCE 1 (bases 1 to 1341)

AUTHORS Kaluza, B. and Lenz, H.

TITLE Diagnostic method using chimeric antibodies

JOURNAL Patent: EP 0378175-A 13 18-JUL-1990;

COMMENT BOEHRINGER MANNHEIM GMBH

FEATURES NCBI gi: 413075

source Location/Qualifiers

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Qy	466	GTCTTCCCTTGGCACCCCTCTCTCAAGAGACCTCTGGGGGGACAGCGCCCTTGGGCTGC	525	
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Qy	526	CTGGTCAAGGACTACTTTCGCCGAACCGGTGACGGTGTCTGGMACTCAGCGCGCCCTGACC	585	
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Qy	586	AGCGGCTGCACCTTTCGGCGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGC	645	
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Qy	706	AAGCCACGACACACAGTAGTGTGACAAAGACAGAGCGCCAAATCTTTGTGCAAAACTCAC	765	
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Qy	766	ACATGCCACCCTGCCCGACCTGAACTCTCTGGGGGGACCGTCAGTCTTCTCTTCCCC	825	
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Qy	946	CATAATGCCAAGCAAGCCGGGGAGCGAGTACAAAGCAGCAGTACCTGCTGGTCTAGC	1005	
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7

RESULT

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

FEATURES

MAC1GHVCDR

1359 bp

mRNA

PRI

13-MAY-1994

Macaca fascicularis immunoglobulin gamma variable region, constant region, complementarity-determining region 1 (CDR1), complementarity-determining region 2 (CDR2), complementarity-determining region (CDR3) mRNA.

L13307

q293118

immunoglobulin gamma; variable region.

Macaca fascicularis cDNA to mRNA.

Macaca fascicularis

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Cercopithecoidea; Cercopithecinae; Papionini.

1 (bases 1 to 1359)

Lewis,A.P., Barber,K.A., Cooper,H.J., Sims,M.J., Worden,J. and Crowe,J.S.

Cloning and sequence analysis of kappa and gamma cynomolgus monkey immunoglobulin cDNAs

Dev. Comp. Immunol. 17 (6), 549-560 (1993)

9413152

NCBI gi: 293118

Location/Qualifiers

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BASE COUNT
ORIGIN

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Qy	1114	GGGACGCCCGAGAACACACAGGTTGATACACCTCCGCCATCCCGGGATGAGCTGCACAG	1173
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Qy	1174	AACCAAGGTCAAGCTGACCTGCTGGTCAAAAGGCTTATCCAGCGCATCGCCGTCGAG	1233
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Qy	1234	TGGGAGACGAATGGCAGCGAGAACAACTACAAGACACCGCTCCGCTGCTGGACTCC	1293
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Qy	1294	GACGGCTCCTTCTTCTCTACACAACTACCGTGGACAGAGCAGGTGGCAGCAGGGG	1353
Db	1279	aacgtctctctatgctccgctgatgatgagctctgcacaaccactacaccagaagagc	1338
Qy	1354	AACGCTTCTCATGCTCCGCTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC	1413
Db	1339	ctctccgtgtctccgggtaaa	1359
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RESULT	8		
LOCUS		768 bp	RNA
DEFINITION		H.sapiens mRNA for Immunoglobulin G1, Fc fragment.	PRI 21-JAN-1994
ACCESSION		X70421	
NID		g33068	
KEYWORDS		immunoglobulin; protein A binding.	

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ORGANISM      Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Cathartini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 768)
AUTHORS      Filipula,D.
TITLE        H. sapiens mRNA for immunoglobulin G1, Fc fragment
JOURNAL      Unpublished
REFERENCE     2 (bases 1 to 768)
AUTHORS      Filipula,D.R.
TITLE        Direct Submission
JOURNAL      Submitted (10-FEB-1993) to the EMBL/GenBank/DBJ databases. D.R.
              Filipula, Enzon Labs, 16020 Industrial Drive, Gaithersburg, Maryland
              20877, USA
COMMENT       NCBI gi: 33068
FEATURES
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RESULT	13			
LOCUS	OAGGISA	1594 bp	RNA	MAM 16-FEB-1993
DEFINITION	O.aries mRNA for immunoglobulin gamma chain secreted form.			
ACCESSION	X69797			
NID	g1268			
KEYWORDS	Ig heavy chain; immunoglobulin gamma-1.			
SOURCE	sheep.			
ORGANISM	Ovis aries			
	Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;			
	Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;			
	Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;			
	Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Artiodactyla;			
	Ruminantia; Pecora; Bovoidae; Bovidae; Caprinae; Ovis.			
REFERENCE	1 (Bases 1 to 1594)			
AUTHORS	Nau,F.			
TITLE	Direct Submission			
JOURNAL	Submitted (15-DEC-1992) to the EMBL/GenBank/DBJ databases. F. Nau,			
	CNRS/Universite de Poitiers, IMIG, Lab d'Immunologie Molculaire,			
	Faculte des Sciences de Poitiers, 40 avenue du Recteur Pineau,			
	86022 Poitiers Cedex, FRANCE			
REFERENCE	2 (Bases 1 to 1594)			
AUTHORS	Patri,S. and Nau,F.			
JOURNAL	Unpublished			
COMMENT	NCBI gi: 1268			
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	Qy	1301	CCTTCTCTCTACACAGCTCACCGTGCAGACAGAGCAGGTGGCAGCAGGGGAACTCT	1360
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	Qy	1361	TTCATGCTCGGTGATGATGAGGCTTCGACAAACCCTACACGCAAGAAGCGCTCTCCC	1420
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RESULT	13			
LOCUS	OAGGISL	1594 bp	RNA	MAM
DEFINITION	O.aries mRNA for immunoglobulin gamma chain secreted form.			16-FEB-1993
ACCESSION	X69797			
NID	g1268			
KEYWORDS	Ig heavy chain; immunoglobulin gamma-1.			
SOURCE	sheep.			
ORGANISM	Ovis aries			
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;			
AUTHORS	Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;			
JOURNAL	Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;			
	Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Artiodactyla;			
	Ruminantia; Pecora; Bovoidae; Bovidae; Caprinae; Ovis.			
REFERENCE	1 (Bases 1 to 1594)			
AUTHORS	Nau,F.			
TITLE	Direct Submission			
JOURNAL	Submitted (15-DEC-1992) to the EMBL/GenBank/DBJ databases. F. Nau,			
	CNRS/Universite de Poitiers, IMIG, Lab d'Immunologie Molculaire,			
	Faculte des Sciences de Poitiers, 40 avenue du Recteur Pineau,			
	86022 Poitiers Cedex, FRANCE			
REFERENCE	2 (Bases 1 to 1594)			
AUTHORS	Patri,S. and Nau,F.			
JOURNAL	Unpublished			
COMMENT	NCBI gi: 1268			
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Qy	1419	CTGTCTCCGGTAAATGA	1437
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DEFINITION	Rabbit Ig active gamma H-chain		MAM 23-MAR-1995
ACCESSION	K00752	M12187	M24226
NID	g165127		
KEYWORDS	C-region; D-region; J-region; V-region; heavy chain allotype Vha2; heavy chain allotype de12,14; immunoglobulin gamma-chain; immunoglobulin heavy chain; processed gene.		
SOURCE	Rabbit (haplotype F-I; Vha2 de12,14 allotype) spleen, cDNA to mRNA, clone p-gamma-BI-12,14.		
ORGANISM	Oryctolagus cuniculus		
REFERENCE	Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Lagomorpha; Leporidae.		
AUTHORS	1 (bases 1 to 1235)		
TITLE	Bernstein,K.E., Alexander,C.B. and Mage,R.G.		
JOURNAL	Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplotype		
MEDLINE	Immunogenetics 18 (4), 387-397 (1983)		
COMMENT	84030930		
	Original entry prepared by Dr. Rose Mage. The V-region is compared [1] with the Vha2 allotype p-mu-3 and the human genomic VH26 sequence. The two rabbit V-regions are 89.5% homologous, and this sequence is 77% homologous with the human segment. This sequence, as well as the p-mu-3 sequence, shows remarkable homology with two human CDR2 and D minigenes. The C-region is compared [1] with two rabbit C-regions, one of de11,15 allotype and the other of e15 and unknown d allotype.		
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ORIGIN          9 bp upstream of Avail site.

Query Match      34.0%; Score 489; DB 34; Length 1235;
Best Local Similarity 78.9%; Pred. No. 0.00e+00;
Matches 811; Conservative 0; Mismatches 196; Indels 21; Gaps 9;

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Db 323 tcaaggctacctccccggagcagtgacctgacctggaactcgggcaacctcaccaatg 382
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RESULT 15
LOCUS      MVIIGGJC 1179 bp mRNA MAM 14-DEC-1992
DEFINITION Mink immunoglobulin gamma heavy chain (IGHG) joining region and
            hinge region mRNA, 3' end.
ACCESSION 107788
NID        gl64255
KEYWORDS   J-region; gamma chain; heavy chain; hinge region; immunoglobulin;
            serum protein.
SOURCE      Mustela vison spleen cDNA to mRNA.
ORGANISM   Mustela vison
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Carnivora; Caniformia; Musteloidae; Mustelidae.
REFERENCE  1 (bases 1 to 1179)
AUTHORS    Belousov, J.S., Alabyev, B.Y., Najakshin, A.M., Christensen, J., Stor
            Gaard, T., Aasted, B. and Taranin, A.V.
TITLE       Molecular cloning of cDNA encoding mink immunoglobulin gamma chain
JOURNAL     Unpublished (1992)
COMMENT     NCBI gi: 164255
FEATURES    Location/Qualifiers
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BASE COUNT 243 a 423 c 313 g 200 t
ORIGIN
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Query Match 33.3%; Score 479; DB 34; Length 1179;  
Best Local Similarity 76.0%; Pred. No. 0.00e+00;  
Matches 787; Conservative 0; Mismatches 236; Indels 12; Gaps 4;



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Qy	469	TTCCGCTGGCAGCCTCTCTCAAGACGACCTCTGGGGGACAGCGGCCCTGGGTGCTG	528
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Qy	529	GTCAAGGACTACTTCCCAGAACGGGTGACGGTGTCTGTGAACTCAGGGCCCTGACCA	588
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Qy	709	CCCAACAACCAAGGTGGACAGAAAGCAGAGCCCAATCTTGTGACAAAATCACA	768
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Qy	829	AAACCCAGGACACCTCATGATCTCCCGGACCCCTGAGTCACTGCTGTGGTGGAC	888
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Qy	949	AATGCCAAGACAAAGCCCGGAGGAGCAGTACAAACGACGCTACCGTGTGTGACGGCT	1008
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Qy	1129	CCACAGGTGTACACCTTGGCCCCCATCCCGGAGTCACTGACCAAGAACCGGTGACGGCTG	1188
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Qy	1189	ACCTGCCTGTCAAAGGCTTCTATCCCAAGACGACATCCGCTGTGAGTGGGAGAGCAAT	1248
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Qy	1249	CAGCGGG-----AGAA--CAACTACAAAGACA--CGCCTCCGCTCTGCACTCGACGGCTCC	1302
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Search completed: Tue Dec 17 22:21:53 1996  
Job time : 869 secs.

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US-08-487-550-7

(TW)

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MPsrch mn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 22:22:12 1996; MasPar time 118.25 Seconds  
Tabular output not generated. 947.093 Million cell updates/sec

Title: &gt;US-08-487-550-7

Description: (1-1437) from US08487550.seq

Perfect Score: 1437

N.A. Sequence: 1 ATGGGTCGAGCCTCATCTT.....CCCTGTCTCCGGGTAAATCA 1437

Comp: TACCCACCTCGGAGTAGAA.....GGGACAGAGCCCATTTACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 102519 seqs, 38967980 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-genseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 9.414; Variance 6.114; scale 1.540

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1144	79.6	1386	8	Q49834	0.00e+00
2	1112	77.4	1549	3	Q20056	0.00e+00
3	1043	72.6	1617	6	Q35099	0.00e+00
4	1032	71.8	1576	8	Q49944	0.00e+00
5	1014	70.6	1431	19	T18059	0.00e+00
6	1012	70.4	9208	11	Q65629	0.00e+00
7	1007	70.1	1467	4	Q23570	0.00e+00
8	1006	70.0	1135	1	N90736	0.00e+00

9	1005	69.9	1136	1	N90779	Sequence of the linker	0.00e+00
10	1005	69.9	1458	4	Q23571	Reshaped CD4 antibody	0.00e+00
11	1003	69.8	1458	4	Q23581	Reshaped CD4 antibody	0.00e+00
12	1001	69.7	6557	18	T15932	Anti-IgE VH expressio	0.00e+00
13	1000	69.6	1641	9	Q54655	chiT84.12 H3 heavy ch	0.00e+00
14	988	68.8	1412	4	Q25692	Sequence of the chime	0.00e+00
15	987	68.7	8540	11	Q65628	Vector contg. TCAE 8	0.00e+00
16	981	68.3	1174	9	Q51547	Human kappa immunogl	0.00e+00
17	824	57.3	1006	17	T12663	Synthetic IgG4 cDNA.	0.00e+00
18	692	48.2	768	17	Q96101	IgG1 hinge, CH2, CH3	0.00e+00
19	689	47.9	693	15	Q87592	Human IgG1 antibody F	0.00e+00
20	689	47.9	1164	17	T12658	IL4.Y124D/IgG1 gene f	0.00e+00
21	689	47.9	6367	17	T12661	Vector COSFclink.	0.00e+00
22	689	47.9	6926	17	T12662	IL-4.Y124D/IgG1 fusio	0.00e+00
23	687	47.8	1231	15	Q87593	Human Fas/Fc fused OR	0.00e+00
24	685	47.7	699	9	Q35339	cDNA sequence for a h	0.00e+00
25	685	47.7	705	18	Q74083	Immunoglobulin G1 Fc	0.00e+00
26	686	47.7	745	9	Q55943	Polylinker/Fc fragmen	0.00e+00
27	686	47.7	745	15	Q92273	Fc cDNA.	0.00e+00
28	686	47.7	745	13	Q75425	Antibody Fc mutein co	0.00e+00
29	686	47.7	745	9	Q58428	Human IgG1 Fc-polylin	0.00e+00
30	684	47.6	740	6	Q41508	Human IgG1 Fc.	0.00e+00
31	683	47.5	705	7	Q42589	Human Fc polypeptide	0.00e+00
32	682	47.5	1050	5	Q28684	LFA-3-Ig fusion gene	0.00e+00
33	682	47.5	1347	12	Q67347	VCAM 2D-IgG.	0.00e+00
34	682	47.5	2043	9	Q55340	TICAM(453)IgG immuno	0.00e+00
35	681	47.4	1317	17	T00829	Plasmid pDC406/OX40/F	0.00e+00
36	680	47.3	1050	6	Q40423	DNA sequence of LFA3T	0.00e+00
37	675	47.0	1557	10	Q45225	Sequence encoding a r	0.00e+00
38	675	47.0	1587	10	Q63958	P-selectin ligand-IgG	0.00e+00
39	675	47.0	1587	16	T02490	P-selectin ligand-pb	0.00e+00
40	662	46.1	884	2	N70398	Portion of plasmid pC	0.00e+00
41	658	45.8	765	2	N70257	Part of the nucleotid	0.00e+00
42	658	45.8	765	1	N82142	Immunoglobulin G Fc d	0.00e+00
43	645	44.9	6889	18	T15931	DHFR/intron (WTrasSD)	0.00e+00
44	631	43.9	1425	6	Q41516	Human CD40-L/Fc fusio	0.00e+00
45	631	43.9	1765	10	Q71873	Sequence coding human	0.00e+00

## ALIGNMENTS

RESULT 1  
ID Q49834 standard; cDNA; 1386 BP.  
AC Q49834;  
DT 27-APR-1994 (first entry)  
DE Anti-HIV-1 recombinant antibody 447-52D heavy chain coding sequence.  
KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;  
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;  
KW acquired immune deficiency syndrome; chimeric antibody;  
KW surface glycoprotein gp120, V3 loop; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS  
FT /tag= a  
FT /note= "encodes recombinantly modified 447-52D  
FT heavy chain"  
FN M09319785-A.  
PD 14-OCT-1993.  
PF 23-MAR-1993; U02629.  
PR 01-APR-1992; US-861701.  
PA (MERI ) MERCK & CO INC.  
PA (JOHN/) JOHNSON L.S.  
PA (PFAR/) PFAR D S.  
PI Conley AJ, Emami EA, Johnson LS, Mark GE, Pfarr DS;

DR WP1; 93-336600/42.  
 DR P-PSDB; R42162.  
 PT New recombinant human antibody - with HIV neutralising activity  
 PT against at least two isolates, useful for preventing or treating  
 PT infection in diagnosis, etc.  
 PS Example 9; Fig 2A; 154pp; English.  
 PS CC EBV-transformed cell lines and mouse-human heterohybridomas  
 CC producing human MBs specific for the gp120 V3 loop of HIV-1 MN  
 CC isolate were obtained. Mab 447-52D was found to recognise the  
 CC tetrapeptide motif GPCR, i.e. the Principal Neutralising  
 CC Determinant common to the V3 loop of different HIV isolates.  
 CC A recombinant Ab was produced in which the H chain V region was  
 CC derived from 447-52D and to which a signal sequence and a H chain  
 CC intronic sequence are appended, fused to a fragment contg. a short  
 CC intronic segment of the human gamma 1 C region and the human gamma  
 CC 1 encoding domain in its genomic form.  
 CC Sequence 1386 BP; 333 A; 429 C; 377 G; 247 T;  
 SQ

Query Match 79.6%; Score 1144; DB 8; Length 1386;  
 Best Local Similarity 92.4%; Pred. No. 0.00e+00;  
 Matches 1280; Conservative 0; Mismatches 100; Indels 6; Gaps 4;

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 Db 61 acctgtagcctctgttttcaactcagtcgaatgctcggctgaactgggtccgcagcgt 120  
 Qy 118 TCCTGTGCAGTCTCTGGATTCACTTCCAGTGCACATACATGTATTGTTCCGCCAGGCT 177  
 Db 121 ccagggaaagggtcgtgagtcgggtcggcgctattaaagcagaactgatggtggacaaca 180  
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 Db 181 gactacgtcgtcgtcgtgaaaggcagattcacctcctaagagatgactcaaaaacacg 240  
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 Db 241 ctatctcgaatgaatagctcaaacagagacacacgcgtttattcctgcaccaca 300  
 Qy 298 GCCTATCTGCAATTCAGCAGCTGAAATTCGAGACACGCCGCTCTATTACTGTACTACA 357  
 Db 301 gatggtttattatgatccggggagctcccgaggactactactactactacatgacgtt 360  
 Qy 358 TCCTACATT-TCAC-ATTTCGGGGTG---GTGT-CTGCTATGGAGGTTACTTCGAATTC 411  
 Db 361 tggggcaaggagcacggtcacgctgagctcagctccaccaaggccactcggtcttc 420  
 Qy 412 TGGGGCCAGGGCGGCTGTGTCACGCTCTCCTCAGTACGACCAAGGGCCCATCGGTC TTC 471  
 Db 421 cccctggcacctcctccaaagcacctctggggcagacgcccctgggtcgctcggtc 480  
 Qy 472 CCCCCTGGACCCCTCTCCAGAGCACCTCTGGGGGGCACCAGGCCCTGGGCTGCTGTC 531  
 Db 481 aaggactactcctccgaacacggtgacggtgctggtgaactcaggcgccctgaccagcgc 540  
 Qy 532 AAGGACTACTTCCCGCAACCGGTGACGGGTGCTGCGAATCTCAGGGCGCCTGACCAAGCGGC 591  
 Db 541 gtgcacacctcccggtcgtcctacagtcctcaggactctactcctccagcagcgtggtg 600  
 Qy 592 GTGCACACCTTCCCGGCTGCTCTACGCTCTCAGGACTCTACTGCTCCTCAGCAGCGTGTG 651  
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Qy	712	AGCAACACCAAGGTGGACGAAGAAGCAGACCCAAATCTTGTGACAAACTCACATGC	771
Db	721	ccacqgtgccagcaacctgaaactcctgggggagacqgtcagttctctctccccccaaaa	780
Qy	772	CCACCTGCCCAGACCTCAACTCCTGGGGGACCGTCAGTCTTCTTCCCTCCCCCAAA	831
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Qy	832	CCCAAGGACCCCTCATGATCTCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTG	891
Db	841	agccacgaagaccctgaggtcaagttcaactggtacgtggcgcggtggagtcgaat	900
Qy	892	AGCCAGGAAGACCTGAGGTCAAGTCAACTGTGAGTGGACGGCGTGAGGTGCAATAT	951
Db	901	gccaagacaagccggggaggaagcagtcacaacagcagctaccgttgtgtcagcgtccct	960
Qy	952	GCCACGAAGAAGCGGGGAGGAGCAGTACAACGACGCTACCGTGTGTCAGCGCTCTC	1011
Db	961	accgtctgcacaggacctggctgaatggcaagagatcaagtgcaaggtctccaacaa	1020
Qy	1012	ACCGTCTCCACGAGSACTGGCTGAATGGCAAGAGTCAAGTCCAAGSTCTCCAACAA	1071
Db	1021	gcoctccagcccccatcgagaaaaacatctccaaagccaaagggcagcccgagaaaca	1080
Qy	1072	GCCTCTCCAGCCCCCATCGACAAAACCATCTCCAAGCCAAAAGGCAGCCCGAGAACA	1131
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Qy	1132	CAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAGAACCGTCAGCCTGACC	1191
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Qy	1252	CCGGAGAACAACTACAAGACACGCTCCCGTCTGGACTCCGACGGCTCTTCTTCCTC	1311
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Qy	1312	TACAGCAAGCTCACCTGGCAAGAGCAGGTGGCAGCAGGGGAAACGCTTCTCACTGC	1371
Db	1321	gtgatgatgaggtctgtcaaacaccatcacgcagagaagcctctccctgtctccgggt	1380
Qy	1372	GTGATCATGAGGCTCTGCACAAACCACTTACACGCAGAGAGCCTCTTCCCTGTCTCG	1431
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Qy	1432	AAATGA 1437	
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ID	Q20066	standard; DNA; 1549 BP.	
AC	Q20066;		
DT	25-MAR-1992	(first entry)	
DE	Encodes heavy chain of 306 antibody.		
KW	Plasmid pUC36HC; human immunodeficiency virus; AIDS; ss.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	seq peptide	101..157	

## RESULT 2

RESULT	2
ID	Q20066 standard; DNA; 1549 BP.
AC	Q20066;
DT	25-MAR-1992 (first entry)
DE	Encodes heavy chain of 3D6 antibody.
KW	Plasmid pUC3D6HC; human immunodeficiency virus; AIDS; ss.
OS	Homo sapiens.
FN	Key
FT	Location/Qualifiers
	FT seq peptide
	101..157



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Db 1112 caccaggactgctgaatggcaagagtcacagtgcaaggtctccaaagaagccctccca 1171
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Qy 1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTCCAAGTCTCCAACAAGCCCTCCCA 1080
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Db 1172 gcccccatcgagaaacacatctccaaagccaaagggcagcccccagagaccacaggtgtac 1231
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Qy 1141 ACCCTGCCCATCTCCGGGATGACCTGACCAAGAACCCAGGTGAGCTGACCTGCCCTGTC 1200
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Qy 1381 GAGGCTTGGCAACACCATACACCCAGAGAGCCTCTCCCTGTCTCCGGGTAATGA 1437
|||||

RESULT 3
ID Q35099 standard; DNA; 1617 BP.
AC Q35099;
DE 19-MAY-1993 (first entry)
DE Antibody D heavy chain.
KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;
KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;
KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 35..1465
FT /*tag= a
FT sig peptide 35..91
FT /*tag= b
FT misc_RNA 92..181
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FT TATA signal
FT /*tag= n
PN EP-523949-A.
PD 20-JAN-1993.
PF 14-JUL-1992; 306420.
PR 15-JUL-1991; GB-015284.
PR 01-AUG-1991; GB-016594.
PR 23-MAR-1992; GB-006284.
PA (WELL ) WELLCOME FOUND LTD.
DR Crowe JS, Lewis AP;
PI WPI; 93-019951/03.
DR P-PSDB; R31024.
PT Prodn. of recombinant primate antibodies - useful for treating
infections caused by hepatitis A, B and C, herpes,
PT cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
PT arthritis etc.
PS Disclosure; Fig 2; 35pp; English.
CC The sequences given in Q35099-100 encode the heavy and light chains
of Antibody D respectively. Antibody D is a monoclonal antibody which
was derived from peripheral blood lymphocytes from a hepatitis A virus
(HAV) sero positive patient. Antibody D is closely related in nature
CC to murine antibody B5B3. Total RNA was isolated from antibody D
expressing cells and polyadenylated RNA was extracted. These polyA
RNA's were used to prepare a cDNA library which was screened for human
CC kappa light (L) chains and two positive clones were detected.
CC Further heavy (H) chain clones were also isolated.
SQ Sequence 1617 BP; 375 A; 526 C; 441 G; 275 T;

Query Match 72.6%; Score 1043; DB 6; Length 1617;
Best Local Similarity 87.3%; Pred. No. 0.00e+00;
Matches 1255; Conservative 0; Mismatches 176; Indels 6; Gaps 3;

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Qy 1 ATGGGTTGGAGCGCTCACTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
|||||
Db 95 atgcaggtggtgcagctctggggctgaagtaagagcctgggtcctcgggtgacggtctcc 154
|||||
Qy 61 GTGCAACTGGTGGAGCTCTCGGGGAGGCTTGTGTCAGCCTGGCGGGTCCCTCAGAGTCTCC 120
|||||
Db 155 tgaaggcatctggaggcacccttcgaactatgctatcagctgggtggcagacagggccct 214
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Qy 121 TGTGCAGTCTCTGGATTCACTTCACCTTCAGCTGACCACTACATGTATTGGTTCCGCCAGGCTCCA 180
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Db 215 ggacaaggcttgagtgatggg----agg-gat-catccctcttttggtaacacaacc 268
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Qy 181 GGGAGGGGGCGGAATGGGTAGTTTTTATTAGAACAACACCGAACCGTGGGACACAGAA 240
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Db 269 tactcacagaacttccagggcagagtcacgattaccggcgagacaatccaccagcacagcc 328
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Qy 241 TAGCCCGCGTGTGTGAAGACAGATGATCCCATCTCCAGACATGATTTCCAAAAGCATGCC 300
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```

Db 329 cacatggagctgactagctgagatctgaggaacagcggtgtattactgtgcgacgat 388  
Qy 301 TATCTGCAATTCAGACGCTGAAATTCGAGGACACGGCGCTTATTACTACTACATCC 360  
Db 389 cgtacaggaagcaaatatttgacccggccgggtgtgctggttcgacccctggggccag 448  
Qy 361 TACATTTTCATTTGTCGGGGTGGTGTCTGCTATGAGGCTTACTTCGAATTCGTGGGGCCAG 420  
Db 449 ggcacccctgggtcacgctctcctcagcctccacaaagggcccaatcggtctccccctggca 508  
Qy 421 GGGCGCCCTGCTACCGCTCTCTCAGTACACACCAAGGGCCCATCGGTCTTCCCGCTGGCA 480  
Db 509 cccctcctcaagagacacctctggggccacagcgccctgggtgctgctggtcaaggactac 568  
Qy 481 CCCCTCTCAAGAGACCTCTGTGGGGGCAACGGGCCCTGGGTGCTGCTGAGGACTAC 540  
Db 569 ttcccgaaacccgtgacggtgtcgtggaactcagcgccctgaccagcggtgcacacc 628  
Qy 541 TTCCCGGAACCGGTGACGGTGTCTGTGGAATCTCAGGGCCCTGACCAAGCGGTGCACACC 600  
Db 629 ttccggctgtcctacagtcctcagactcctactcctcagcagcggtggtgacgctgcc 688  
Qy 601 TTCCGGGCTGTCTACAGTCTCAGGACTCTACTCTCCTCAGCAGCGTGGTGCACGTCGCC 660  
Db 689 tccagcagcttgggaccac 748  
Qy 661 TCCAGCAGCTTGGGACCCAGACCTTACATCTGCAAGCTGATCATCAGCCGACGACACC 720  
Db 749 aaggtggacaagaaagtgtagcccaaatctgtgacaaaactcacacatgccacccgtgc 808  
Qy 721 AAGGTGGACAAGAAAGACAGACCCCAATCTTGTGCAAAATCTCACATGCCCCACCGTGC 780  
Db 809 ccagcactgaactcctgggggagcgctcagctcttctctcccccacaaacccaaagac 868  
Qy 781 CCAGCACCTGAATCTCTGGGGGACCGCTCAGTCTCTCTTCCCGCCCAAAACCAAGGAC 840  
Db 869 accctcatgatctcccgacccttgggtcacatgacgtggtggtggagtgagccacgaa 928  
Qy 841 ACCCTCATGATCTCCGGACCCCTTGAGGTTCATGCGTGGTGGTGAGCTGAGCCACGAA 900  
Db 929 gacctgaggtcaagttcaactggtacgtggacggcggtgaggtgcataatgccaaagaca 988  
Qy 901 GACCTGAGGTCAAGTTCACTGTTAGTGCAGCGCGTGGAGTGCATATGCCAAGACA 960  
Db 989 aagccggggaggaagcagtcacaacagcacgtaccgtgtggtcagcgtcctcacgctcgtg 1048  
Qy 961 AAGCCGGGGAGGAGGACGATACACAGCAGCTACCGTGTGTGTCAGCGCTCTCAGCGTCCG 1020  
Db 1049 caccagactggctgaatggcaagagntacaagtgaaggtctccaaagacccctccca 1108  
Qy 1021 CACCAGCACTGGCTGAATGGCAAGAGTACAAGTGCAAGGTCTCCAAAGAACCCCTCCCA 1080  
Db 1109 gccccctcagaaaaacacatctccaaagccaaagggcagcccgagaaacccaggtgtac 1168  
Qy 1081 GCCCCCATCAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGCCGAGAACCAAGGTGTAC 1140  
Db 1169 accctgccccctcccggtgagctgaccaaagaccaggtcagcctgacctgacctgctgtc 1228  
Qy 1141 ACCCTGCCCCCATCTCCGGGATGAGCTGACCAAGAACCGAGGTGACGCTGACCTGCCGTGCT 1200  
Db 1229 aaagcttctatccag-gacatccgctggagtgagagcaatgggagcgccagagaac 1288  
Qy 1201 AAAGGCTTATCTCCCGACATCCCGCTGGAGTGGGAGCAATGGGACGCGCGGAGAC 1260

Db 1289 aactacaagaccagcctccgctgactgagctccgagcagcgtcctctctctctacaagaag 1348  
Qy 1261 AACTTACAAGACACCGCTCCGCTGCTGGACTCCGACGGGTCCCTTCTCTCTACAGCAAG 1320  
Db 1349 ctacacgctggacaagagcaggtggcagcaggggaacgctctctctcctcctcgatgatcat 1408  
Qy 1321 CTCACCGTGGCAAGAGCAGGTGGCAGCAGGGGAACGCTCTTCTCATGCTCCGCTGATGAT 1380  
Db 1409 gaggctctgcacaaccactacacgacgaagagcctctcctgctgtccgggtaaatga 1465  
Qy 1381 GAGGCTCTGCACAACCACTACACGCGACGACGCTCTCCCTGTCTCCGGGTAAATGA 1437  
RESULT 4  
ID Q49944 standard; cDNA; 1576 BP.  
AC Q49944;  
DT 29-APR-1994 (first entry)  
DE Human anti-HBs heavy chain.  
KW Antibody; Ab; light; heavy; chain; hepatitis B;  
KW HB; surface antigen; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 15..1394  
FT /\*tag= a 15..41  
FT sig\_peptide  
FT /\*tag= b  
FT mat\_peptide 42..1391  
FT /\*tag= c  
FT /note= \*claim 2, page 27\*  
FN W09320205-A.  
PD 14-OCT-1993.  
PF 30-MAR-1993; J00396.  
PR 30-MAR-1992; JP-074678.  
PA (SUNR) SUNTORY LTD.  
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;  
DR WPI; 93-336913/42.  
DR P-PSDB; R42066.  
PT Human anti-hepatitis B surface antigen antibody gene - can be  
PT used to produce L and H chains of the antibody in large quantity  
PS Disclosure; Fig 6-8; 46pp; Japanese.  
CC Polynucleotides encoding the L and H chains of human anti-HBs  
CC Ab are given in Q49943-Q49944. The Ab can be easily produced in  
CC large quantities for therapeutic use.  
SQ Sequence 1576 BP; 394 A; 483 C; 426 G; 273 T;  
Query Match 71.8%; Score 1032; DB 8; Length 1576;  
Best Local Similarity 91.9%; Pred. No. 0.00e+00;  
Matches 1279; Conservative 0; Mismatches 85; Indels 27; Gaps 16;  
Db 31 ggtccagctcaggtgcagctggtggagctctgggggagggcggtggccagcctgggaggt 90  
Qy 47 GTGTCCAGTGTGAGGTGCAATGGTGGAGTCTGGGGGAGGCTTGTCCAGCCTGGCGGCT 106  
Db 91 cccgtgagactctcctgtcagcctctgagttcaccttcagtagcaattctatgcactggg 150  
Qy 107 CCCTGAGAGTCTCCTGTGCGACTCTCTGATTCACCTTCAGTCACCACTACATGTTGGT 166  
Db 151 tccgccagctccagcaaggggttgagtggtggcgagttatattatgatg-gaaa- 208  
Qy 167 TCCGCCAGGCTCCAGGGAAGGGGGCCGAATGGGTAGTGGTTTCATTAGAAACAAACCGAAC 226  
Db 209 -tc--ataa-attctacgacagctccgtgaagggccgattccaccatttccagagacaatt 264  
Qy 227 GTGGCAACAAGAAATACGCCCGCTCTGTCAAGAGACAGATTTCACCATCTCCAGAGATGATT 286





Qy 468 CTTCCCCCTGGCACCTCTCTCAAGAGCAGCTCTGGGGGCAACAGCGGCTGGGTGCTCCT 527

Db 519 ggtcaaggaactacttcccgaaacccgtgacgggtgctcgtggaactcagggccctgaccag 578  
|||||

Qy 528 GGTCAAGACTACTTCCCGACCGGTGACGGTCTGTGGAACTCAGCGCCCTGACCAG 587  
|||||

Db 579 cggcgtgcacaacttcccggtgtcctacagtcctcaggactctactccctcagcagcgt 638  
|||||

Qy 588 CGCGGTGCACACTTCCGGCTGTCTAGAGTCTAGGACTTCTCCCTCAGCAGCGT 647  
|||||

Db 639 ggtgacctgccctccagcagcttgggaccagacctacatctgaacygaatacaaa 698  
|||||

Qy 648 GGTGACCGTGCCTCAGCAGCTTGGGACCCAGAGCTACATCTGCAAGCTGAATCAAA 707  
|||||

Db 699 gcccagcaacccaagtggaagaagaagtggagcccaaatcttgacaaactcacac 758  
|||||

Qy 708 GCCAGCAACACCAAGGTGGAAGAAAGCAGAGGCCAAATCTTGTGACAAAATCAGAC 767  
|||||

Db 759 atgccaccgtgccagcagcactgaactcctgggggaccgtcagttctctcttcccccc 818  
|||||

Qy 768 ATGCCACCGTCCCGACGACCTGACTCTCTGGGGGACCGCTCAGTCTCTCTTCCCCC 827  
|||||

Db 819 aaaccccaaggaacacctcatgatctcccgaccctgaggtcacatgctggtgga 878  
|||||

Qy 828 AAAAAACCAAGGACACCTCATGATCTCCGGGACCCCTGAGGTCAATGGCTGGTGA 887  
|||||

Db 879 cgtgaccaggaagacctgaggtcaagttcaactggtacgtgacggctgaggtgca 938  
|||||

Qy 888 CGTGAGCCACGAAGACCTTGAGGTCAAGTTCACTGGTACGTGGAGCGGTGGA 947  
|||||

Db 939 taatgccaagaacaaagccgggagagcagtgacacagcagctacggtggtcagcgt 998  
|||||

Qy 948 TAATGCCAAGCAAAAGCCGGGAGGAGCAGTACAAACAGCAGCTACCGTGTGTCAGCGT 1007  
|||||

Db 999 cctcaccgtcctgcaccagactggctgaatggcaaggagtacaagtcaaggtctccaa 1058  
|||||

Qy 1008 CTTACCGTCTCCACGAGCTGGCTGATGGCAGAGGAGTACAGTGCAAGGTCTCCA 1067  
|||||

Db 1059 caaagccctcccagcccctcagagaaaaccatctccaaagccaaagggcagcccgaga 1118  
|||||

Qy 1068 CAAAGCCCTCCAGCCGCCCATTCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGA 1127  
|||||

Db 1119 accacaggtgtacacccctgccccatcccgggatgagtgaccaagaacacaggtcagcct 1178  
|||||

Qy 1128 ACCACAGGTGTACACCTGCCCCCATTCCTGGGATGAGCTGACCAAGAACAGGTACGCT 1187  
|||||

Db 1179 gacctgacctcaaggtctctatcccagcagacatcgccgtggagtggagagacaatgg 1238  
|||||

Qy 1188 GACCTGCCTGTCAAAGCTTCTATCCAGGCAATCGCGGTGGAGTGAGGAGCAATGG 1247  
|||||

Db 1239 gcaagcggagaacaactacaagaccagcctcccgtgctggactccagcggctcctctt 1298  
|||||

Qy 1248 GAGCGGAGAGAACTCAAGACACAGCGCTCCCGTGTGTGACTCCAGCGGCTCTCTT 1307  
|||||

Db 1299 cctctacagaagctcacggtggacaagcagcaggtggcagcaggggaacgtcttctcatg 1358  
|||||

Qy 1308 CTTCTACAGCAAGCTCACTGGTGAAGAGCAGGTGGCAGAGGGAAGGTCTTCTCATG 1367  
|||||

Db 1359 ctccgtgatgatgaggtctctgcacacccactacacgagaagagcctcctccgtctcc 1418  
|||||

Qy 1368 CTCGCTGATGCATGAGGCTCTGCACAAACCACTACACCCAGAGAGCGCTCTCCCTGTCTCC 1427  
|||||

Db 1419 gggtaaatga 1428  
|||||

Qy 1428 GGTAAATGA 1437

## RESULT 6

ID Q65629 standard; DNA; 9208 BP.  
AC Q65629;  
DT 01-FEB-1995 (first entry)  
DE Vector contg. TCAE 8 DNA.  
KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;  
KW cell lysis; ss.  
OS Synthetic.  
PN W09411026-A.  
PD 26-MAY-1994.  
PF 12-NOV-1993; U10953.  
PR 13-NOV-1992; US-978891.  
PR 03-NOV-1993; US-149099.  
PA (IDEC-) IDEC PHARM CORP.  
PI Anderson DR, Hama N, Leonard JE, Newman RA, Rastetter WH;  
PI Refine;  
DR WPI; 94-183162/22.  
PT Treating B cell lymphoma with chimeric antibody - against CD20,  
PT causing rapid depletion of peripheral B cells, also new  
PT antibodies and hybridomas  
PS Disclosure; Fig 3; 101pp; English.  
CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric  
CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8  
CC contains 4 transcriptional cassettes, human Ig light and heavy chain  
CC constant regions, dihydrofolate reductase, neomycin phosphotransferase  
CC and murine variable regions. The vector can be used to produce  
CC antibodies which cause depletion of peripheral blood B cells,  
CC including those associated with lymphoma. They mediate complement-  
CC dependent lysis and lyse target cells by antibody-dependent cellular  
CC cytotoxicity.  
CC See also Q65629-35.  
SQ Sequence 9208 BP; 2237 A; 2399 C; 2388 G; 2182 T;  
Query Match 70.4%; Score 1012; DB 11; Length 9208;  
Best Local Similarity 98.7%; Pred. No. 0.00e+00;  
Matches 1025; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 2775 taettcaatgtctggggcgagggagccaggtcacagctctctgcagctagcacaagggc 2834  
|||||

Qy 400 TACTTCGAATTTCTGGGGCCAGGGCCCTGGTGCACGCTCTCTCAGCTAGCAGCAGGGC 459  
|||||

Db 2835 ccacgtgcttccccctggcaccctcctccaagagcacctctggggcacagcgccctg 2894  
|||||

Qy 460 CCAFTGGGTCTTCCCTTGGCACCCCTCTCCAAAGAGACCTCTGGGGGGCAACAGGCGCTG 519  
|||||

Db 2895 ggcctgctgtgcaagactacttcccgaacccgtgacggtgctggaactcaagcgc 2954  
|||||

Qy 520 GCGTGCCTGGTCAAGGACTACTTCCCGAAACGGGTGACGCTGTCTGGAACCTAGGCGCC 579  
|||||

Db 2955 ctgaccagcggctgcacaccttcccggctgctcctacagtcctcaggactctactccctc 3014  
|||||

Qy 580 CTGACCAAGCGGGTGACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTC 639  
|||||

Db 3015 agcagcgtgtgacctgacctccctccagcagcttgggaacccagacacctacatctgaaactg 3074  
|||||

Qy 640 AGCAGCGTGGTGCCTGCGCTCCAGCAGCTTGGGGACCCAGCAGCTACATCTGCAAGCTG 699  
|||||

Db 3075 aatcacagcccgagcaaccaaaggtggacaagaagcagagcccaaatcttgtgacaaa 3134  
|||||

Qy 700 AATCACAGCCCCCAACCAACAGGTGGAGAAAGAACAGACGCCCAAAATCTTGTGACAAA 759  
|||||

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Db 3135 actcacacatgccacacgtgccacacacgtgaactcctctggggagccgtcagctctcttc 3194
Qy 760 ACTCACATGCCACACCTGCCGACACCTGAACCTCTGGGGGACCGTCAGTCTTCTC 819
Db 3195 ttcccccaaaacccaagagacacccctcatgatctccggagccctgaggtcacatgagtg 3254
Qy 820 TTCCCCCAAAACCCCAAGGACACCTCATGATCTCCGGACCCCTGAGGTACATGGCTG 879
Db 3255 gtggtggagctgagccaagaagacacctgaggtcaagtccaactggtagtggaagcgtg 3314
Qy 880 GTGGTGAGCTGAGGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAGCTGGACGGGCTG 939
Db 3315 gagggtgcataatgccaaagcaaacgcggggagagcagtcacacagcacgtaccgtgtg 3374
Qy 940 GAGGTGCATATGCCAAGACAAACCGCGGGAGGAGCATACACACGCTACCGCTGTG 999
Db 3375 gtccaggtcctcaccgtcctgcaccaggaactggctgaatggcaacaggtacaaagtcaag 3434
Qy 1000 GTCCAGGCTCTCACCGCTCTGTCACCAAGGACTGGCTGAATGGCAAGGACTCAAGTCCAAG 1059
Db 3435 gtctccacaagaagccctccagcccccatcgagaaaaccatctccaaagccaaagggcag 3494
Qy 1060 GTCTCCAAAGAGCGCTCCAGCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAG 1119
Db 3495 ccccgagaaccacaggtgtacacacctgcccccacccccgggagtgaggtgaccagaaccag 3554
Qy 1120 CCCCAGAGAACACAGGTGTACACCTGCCGCCCATCCGGGATGAGCTGACCAAGAACAG 1179
Db 3555 gtccagctgaacctgcctggctcaaaaggctctatccagcgacatcgcggtggagtggag 3614
Qy 1180 GTACGCTGACCTGCTGTGTAAGGCTTCTATCCAGGCGCATCGCGGTGAGTGGAG 1239
Db 3615 agcaatggcgagcggagaaacaactacaagaccagcgtcccggtgctggactccgaagcgc 3674
Qy 1240 AGCAATGGGCGAGCGGAGAACATACAAAGACACGCTCCCGGTGCTGGACTCCGACGGC 1299
Db 3675 tcctttctctctacagaagctaccgtggacaagagcaggtggcagcaggggaagctc 3734
Qy 1300 TCCTTCTCTCTACAGCAAGCTCACCTGGGCAAGAGCAGGCTGGCAGCGGCAAGCTC 1359
Db 3735 ttctcatgctccgtgatgatgaggtctgcacaaccactacacgagaagagcctctcc 3794
Qy 1360 TTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGCAAGAGGCTCTCC 1419
Db 3795 ctgtctccgggtaaatga 3812
Qy 1420 CTGTCTCCGGGTAATGA 1437
```

## RESULT 7

```
ID Q23570 standard; DNA; 1467 BP.
AC Q23570;
DT 20-OCT-1992 (first entry)
DE Reshaped CAMPATH-1 antibody heavy chain cDNA.
KW Antigen; CD8; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 36..1448
FT /*tag= a
FT misc feature 183..197
FT /*tag= b
FT /*note= *Complementarity determining region 1*
FT misc feature 240..296
```

```
FT /*tag= c
FT /*note= *Complementarity determining region 2*
FT misc feature 392..422
FT /*tag= f
FT /*note= *Complementarity determining region 3*
PN #09205274-A.
PD 02-APR-1992.
PF 16-SEP-1991; G01578.
PR 17-SEP-1990; GB-020282.
PA (GORM/) GORMAN S D.
PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.
DR WP1; 92-132139/15.
DR P-PDB; R22757.
PT Humanisation of antibodies binding to human CD4 antigen - by
PT mutation of framework-encoding regions of DNA encoding variable
PT domain of rat or mouse antibody chain
PS Disclosure; Fig 5; 74pp; English.
CC The sequence is that of the reshaped CAMPATH-1 heavy chain cDNA.
CC Reshaped CD4 antibody can be used to induce tolerance against an
CC antigen. It can also be used to alleviate autoimmune diseases such
CC as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC also be useful to alleviate allergies. Tolerance to allergens could
CC also be achieved. See also Q23566-Q23581.
SQ Sequence 1467 BP; 352 A; 467 C; 384 G; 264 T;

Query Match 70.1%; Score 1007; DB 4; Length 1467;
Best Local Similarity 98.6%; Pred. No. 0.00e+00;
Matches 1021; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Db 414 ttgattactgggtcaagcagacctcgtcacagttctctcagcctccaccaggggccca 473
Qy 403 TTCGAATTCCTGGGCCAGGGCGCTGGTCACGCTCTCTCAGCTAGCACCAAGGGCCCA 462
Db 474 tegtgttccccctggaccctcctccaagagcacctctgggggcacagggccctgggc 533
Qy 463 TCGGTCTTCCCTTGGCACCTCTCTCCAGAGCACCTCTTGGGGGCACAGGGCCCTGGGC 522
Db 534 tgcctgtcaaggaactacttccccgaaccggtgacggtgctggtgaactcaggccctcg 593
Qy 523 TGCCTGTGCAGGACTACTTCCCGCAACCGGTGACGGTGTGCTGGAACCTCAGGCCCTG 582
Db 594 accagcggcgtgcacaccttcccggtgtcctacagtcctcaggactctactccctcagc 653
Qy 583 ACCAGCGCGGTGCACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGC 642
Db 654 agcgtggtgacgtgacctcagcagcttggggaccaccagacctacatctgcaacgtgaat 713
Qy 643 AGCGTGTGACGCTGCCCTCCAGCAGCGTTGGGACCCAGACCTACATCTGCAACGCTGAAT 702
Db 714 cacaagcccaagcaacacgaagtggacaagaagtgtgacccaactcttgacaaaact 773
Qy 703 CACAGCCCAACACACGAGGTGGACAGAAAGACGACGCCCAATCTTCTGACAAACT 762
Db 774 cacacatgcccaaccgtgccacgacctgaactcctgggggacgctcagctcttctcttc 833
Qy 763 CACACATGCCACCGCTGCCCGAGCACCTGAACTCTCTGGGGGAGCCGTCAGTCTTCTCTTC 822
Db 834 cccccaaaacccaagggagacacctcatgatctccgggacctcaggtcacatgcgtggtg 893
Qy 823 CCCCCAAAACCAAGGACACCTCTCATGATCTCCCGGACCCCTCAGGTGACATCGGTG 882
Db 894 gtggagcgtgagccacgaagacctgaggtcaagttcaactggtacgtggagcgtggag 953
|||||
```

QY 883 GTGCAGGTGAGCCAGCAAGACCTGAGGTCAAGTTCAACTGTGTGACGTGACGGCGTGGAG 942

Db 954 gtgcataatgccaaagacaaacgcccgggagagcagtgacacacagcagtcacgtgtgttc 1013  
|||||

QY 943 GTGCATATGCCAGACAAACCGCGGGAGGAGCAGTACACACAGCTACCGTGTGCTC 1002  
|||||

Db 1014 agcgtcctcaccgtcctgcacacaggaactggctgaatggcaaggaggtacaaagtgcgaaggtc 1073  
|||||

QY 1003 AGCGTCTCACCCTCTCTGACACAGGACTGGCTGAATGGCAGAGGTACAAAGTCAAGGTC 1062  
|||||

Db 1074 tccaacaaagccctcccagcccccatcagaaaaccatctccaaagccaaagggcagccc 1133  
|||||

QY 1063 TCCAACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCC 1122  
|||||

Db 1134 cgagaacacacaggtgtacacccctgcccccatcccgggatgagctgaccaaagacccaggtc 1193  
|||||

QY 1123 CGAGAACACACAGGTGTACACCTGCCCTGCCCATCCGGGATGAGCTGACCAAGAACACAGGTC 1182  
|||||

Db 1194 agcctgacctgctgtgtcaaaaggcttctatcccagcgacatcgccgtggagtggagagc 1253  
|||||

QY 1183 AGCGTGAAGCTGCTGTCAAGAGCTTCTATCCAGCGACATGCCGTGAGCTGGGAGAGC 1242  
|||||

Db 1254 aatggcgagccggagaaacaactacaagaccacgctcccgtgtggactccgagcgctcc 1313  
|||||

QY 1243 AATGGGACGGCGGAGAAACATCAAGAACACCGCTCCGCTGCTGAGCTCCGAGCGCTCC 1302  
|||||

Db 1314 tcttctctacagaacgtcaccgtggaaagagcaggtgagcagaggaggaagctcttc 1373  
|||||

QY 1303 TTCTTCTCTACAGCAAGCTCACCCTGGACAAAGCAGGTGGCAGGGGCAAGCTGCTC 1362  
|||||

Db 1374 tcatgctccgtgatgatgaggtctgtgacaacccactacacgcaagagagcctctccctg 1433  
|||||

QY 1363 TCATGCTCCGTGATGATGAGGCTGTGCACAAACCACTACACGCAAGAGAGCTCTCCCTG 1422  
|||||

Db 1434 tctccgggtaaatga 1448  
|||||

QY 1423 TCTCCGGTAAATGA 1437  
|||||

RESULT 8

ID N90736 standard; DNA; 1135 BP.

AC N90736;

DT 06-JUN-1990 (first entry)

DE DNA encoding linked human IgG1 (gamma 1) chain fragment

KW Human IgG1; gamma 1; immunoglobulin; CD4; fusion protein.

OS Homo sapiens

FH Key Location/Qualifiers

FT CDS 8..1123

FT /\*tag= a

FT misc\_feature 133..134

FT /\*tag= b

FT /\*note="Insert site"

FT misc\_feature 439..440

FT /\*tag= c

FT /\*note="Insert site"

PN W08902922-A.

PD 06-APR-1989.

PF 03-OCT-1988; U03414.

PR 02-OCT-1987; US-104329.

PA (GETH) Genentech.

PI Capon DJ, Gregory TJ;

DR MPI; 89-114397/15.

DR P-PSDB; P93558.

PT New nucleic acid sequences encoding adhesion, esp. CD4, variants -

PT partic. with trans-membrane domain inactivated or fused to other

PS peptide, useful esp. for treating HIV infections

CC It is employed in the prepn. of CD4 fusions. The insert sites are

CC given in the Features Table. CD4 fusion proteins can have antiviral and

CC immunomodulatory activity and are esp. useful for treating HIV infections,

CC regardless of genetic variation within the virus. They and antibodies

CC raised against them can also be used diagnostically for assaying adhesions

CC and their ligands.

SQ Sequence 1135 BP; 255 A; 386 C; 302 G; 192 T;

Query Match 70.0%; Score 1006; DB 1; Length 1135;

Best Local Similarity 98.6%; Pred. No. 0.00e+00;

Matches 1020; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Db 90 tcgaccctggggcctgggaacctgtgcacgtctctcggcctccacaagggcccat 149  
|||||

QY 404 TCGAATTTGGGGCGAGGGCGCTGTGTCACTGCTCTCTCAGCTAGCACCAAGGGCCCAT 463  
|||||

Db 150 cggctcttcccctggcaacctctccaagagcacctctggggcgacagcgccctgggct 209  
|||||

QY 464 CGGTCTTCCCTTGGACCCCTCTCCAAAGACCTCTGGGGGCGACAGCGCTTGGGCT 523  
|||||

Db 210 gctcgtcaagagactctcccgaaacgggtgacgggtgtcgtggaactcaggcgccctga 269  
|||||

QY 524 GCCTGTCAAGGACTACTTCCCGCAACCGGTGACGGGTCTGTGGAACCTCAGCGCCCTGA 583  
|||||

Db 270 ccagcgcggtgcacacctcccggctgtcctacagtcctcaggactctactcctcagca 329  
|||||

QY 584 CCAGCGGGCTGCACACCTTCGCGGCTGTCTACAGTCTCAGGACTCTACTCGCTCAGCA 643  
|||||

Db 330 gctgtgacctgacctccagcagcttgggcacccagacctacatctgcaacgtgaac 389  
|||||

QY 644 CGGTGTGACGCTGCCCTCCAGCAGCTTGGGCGACCCAGACCTACATCTGCAACGTGAATC 703  
|||||

Db 390 acaagccagcaacacacaaaggtggacaagaagtggaccacaaatctgtgacaaaactc 449  
|||||

QY 704 ACAAGCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCCCAAAATCTTGTGACAAAAC 763  
|||||

Db 450 acacatgcccacagctgcccagacctgaaactcctggggggaccgtcagttcttctctcc 509  
|||||

QY 764 ACATATGCCACCTGCTCCAGCAGCTCAACTCTCTGGGGGACCGTCACTCTCTCTTCC 823  
|||||

Db 510 ccccaaaacccaaagacacctcatgatctcccggacccctgaggtcacatcggtggtg 569  
|||||

QY 824 CCGCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGTGG 883  
|||||

Db 570 tggactgagccacgaagacctgaggtcaagttcaactgggtacgtggagcggtggag 629  
|||||

QY 884 TGCAGCTGAGCCAGGAGACCCCTGAGGTCAAGTCAACTGTGCTGAGCGCGCTGGAGG 943  
|||||

Db 630 tgcaaatgccaagacaagcgggagagcagtgacacacagcacgtaccgggtgggtca 689  
|||||

QY 944 TGCATATGCCAAAGCAAAAGCCGCGGGAGGAGCAGTACAAACAGCAGCTGCTGTGTG 1003  
|||||

Db 690 gcgtcctcaccgtcctgcaccaggaactggctgaatggcaaggagtacaagtgaaggtct 749  
|||||

QY 1004 GCGTCTCAGCGCTCTCCACAGGACTGGCTGCAATGGCAAGGAGTACAAAGTCAAGGTCT 1063  
|||||

Db 750 ccaacaagacctcccagcccccatcgagaaacacatctccaaagccaaagggcagcccc 809  
|||||

QY 1064 CCAACAAGAGCCCTCCCAAGCCCCCATCGAGAAACCACTCTCCAAAGCCCAAGGGCAGCCCC 1123  
|||||

Db 810 gagaaccacaggtgtacacctgcccccattcccgggatgagctgaccaagaaccaggtca 869  
|||||

```
|||||
Qy 1124 GAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAGACAGGTCA 1183
Db 870 gcttgacctgctgtgctcaaggtcttatcccagagacatcccggtgagtgaggagagca 929
|||||
Qy 1184 GCTTGACCTGGCTGGTCAAGGCTTCTATCCAGCGACATCCGCGTGGAGTGGGAGACA 1243
Db 930 atgggcagccgagaaacaactacaagaccacccctcccggtgctggactccgagcgctcct 989
|||||
Qy 1244 ATGGCAGCGCGAGAACAACTACAAGACACACGCTCCCGTGTGGACTCCGACGGCTCT 1303
Db 990 tcttcctctacagaagctcaacctggacaagaagcaggtggcagcaggggaagcctctct 1049
|||||
Qy 1304 TCTTCTCTACAGCAAGCTCAGCTGGACAGAGCAGGTGGCAGGAGGAGCTCTCTCT 1363
Db 1050 catgtccgtgatgatgaggtctgcacaaccactacacgagagagcctctcctctgt 1109
|||||
Qy 1364 CATGCTCCGTGATGAGGCTCTGCACACCACTACAGCAGAGGCTCTCCCTGT 1423
Db 1110 ctccgggtaaatga 1123
Qy 1424 CTCGGGTAAATGA 1437
|||||

RESULT 9
ID N90779 standard; DNA; 1136 BP.
AC N90779;
DT 14-MAY-1990 (first entry)
DE Sequence of the linked immunoglobulin gamma chain fragment
KW Immunoglobulin gamma chain; IgG1 heavy chain constant region.
FH Key
FT CDS
FT /*tag= a
PN EP-314317-A.
PD 03-MAY-1989.
PF 03-OCT-1988; 309194.
PR 28-SEP-1988; US-250785, US-104329.
PA (GETH) Genentech Inc.
PI Capon DJ, Gregory TJ;
DR WPI; 89-131855.
DR P-PSDB; P91918.
PT Compns. contg. adhesion variants
PT - useful in therapy and diagnostics, eg CD4 variants
PT which are therapeutically useful for treating human
PT immuno-deficiency virus
PS Figure 4a-4b; 36pp; English.
CC The polypeptide id codes for may be fused to the first 180 N-terminal
CC residues of CD4 at the C-terminus. The fusion protein may be used for
CC antiviral of immunomodulatory therapy particularly in treatment of HIV
CC infection.
SQ Sequence 1136 BP; 256 A; 385 C; 303 G; 192 T;

Query Match 69.9%; Score 1005; DB 1; Length 1136;
Best Local Similarity 98.7%; Pred. No. 0.00e+00;
Matches 1018; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 90 tcgaccttggggctgggaaccttggtcacogtctcctcggctccaccaagggcccat 149
|||||
Qy 404 TCGAATTCGTGGGGCGAGGCGCCCTGTCACCGCTCTCTCAGCTAGCACCAAGGCGCCAT 463
Db 150 cgggtctccctcgtgcacctctcccaagacacctctgggggcacagcgccctgggct 209
|||||
Qy 464 CGGTCTTCCCTCGGACCCCTCTCTCCAGAGACACTCTCTGGGGGACAGCGGCGCTGGGCT 523
```

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Db 210 gcttggtcaagactacttcccgaaccggtgacggtgctggtggaactcaggccctga 269
|||||
Qy 524 GCCTGTGAAGACTACTTCTCCCGCAACCGGTGACGGTGTCTGTGAACCTCAGCGGCTGA 583
Db 270 ccaagcggtgcaacaccttcccggtgtcctacagtcctcaggaactctactccctcagca 329
|||||
Qy 584 CCAGCGGCTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCA 643
Db 330 ggttggtgacctgacctcagcaggttgggcccacagacctacatctgcaacgtgaatc 389
|||||
Qy 644 GCCTGTGACCGTGCCTCCAGAGCTTGGGCACCAGACTACATCTGCAAGCTGAATC 703
Db 390 acaagcccaagcaacccaaggtggacaagaagtggagcccaaatcttggacaaaactc 449
|||||
Qy 704 AGAAGCCGACGACACACAGGTGGACAGAAAGACAGAGCCCAAAATCTTGTGACAAACTC 763
Db 450 acacatgccacacctgccagcacctgaactcctgggggagcgtcagtcctctctcc 509
|||||
Qy 764 ACACATGCCACCGTGCACGACCTCAACTCTCTGGGGGACCGCTCAGTCTTCTCTTCC 823
Db 510 ccccaaaacccaaggaacacctcatgatctccgggacctcaggtcaeatggtggtgg 569
|||||
Qy 824 CCCCMAAACCAAGGACACCTCATCTCTCCGAGCCCTCGAGGTACATGCGTGGTGG 883
Db 570 tggagtgagccacyaagacctgaggtcaagtccaactggtacgtggacgggtggagg 629
|||||
Qy 884 TGGACGTGAGCCACGAAGACCTCTGAGGTCAAGTCAACTGTTAGCTGGAGCGGCTGGAGG 943
Db 630 tgcataatgccaaagacaaagccgggagagcagctacaacagcagctaccgggtggtca 689
|||||
Qy 944 TGCATATGCCAAGACAAAGCCGCGGAGGACGAGTACAAACAGCAGTACCGTGTGTGTC 1003
Db 690 gctgctcacogtctctgcacacagactggtgaatggcaagagatacaagtccaaggtct 749
|||||
Qy 1004 CGCTCTCACCGTCTCGACACGAGTGGCTGAATGGCAAGGAGTACAACTGCMAAGTCT 1063
Db 750 ccaacaaagccctcccagcccccatcgagaaaaacatctccaaagccaaagggagcccc 809
|||||
Qy 1064 CCAACAAAGCCCTCCAGGCCCATTCGAGAAAACCATCTCCAAGCCMAAGGGCAGCCCC 1123
Db 810 gagaacacaggtgtacacctgcccccatcccgggtgagctgacctgaccaagaccaggtca 869
|||||
Qy 1124 GAGAACCCACAGGTGTACACCTTCCCGCCATCCCGGATGAGCTGACCAAGACAGGTCA 1183
Db 870 gctgacctgctggtcaaggtcttctatcccagcgacatcccggtgagtgaggagagca 929
|||||
Qy 1184 GCCTGACCTGCTGGTCAAGGCTTCTATCCCGAGGACATCGCGCTGGAGTGGGAGAGCA 1243
Db 930 atgggcagccgagaaacaactacaagaccacacctcccggtgctggactccgagcgctcct 989
|||||
Qy 1244 ATGGGACGCGGAGAACAACTACAAGACACCGCTTCCCGTGTGGACTCCGACGGCTCT 1303
Db 990 tcttcctctacagaagctcaacctggacaagaagcaggtggcagcagggggaacgtctct 1049
|||||
Qy 1304 TCTTCTCTACAGCAAGCTCAGCGTGGACAGAGCAGGTGGCAGGAGGAGCTCTCTCT 1363
Db 1050 catgtccgtgatgatgaggtctgcacaaccactacacgagagagcctctcctctgt 1109
|||||
Qy 1364 CATGCTCCGTGATGAGGCTCTGCACACCACTACAGCAGAGGCTCTCCCTGT 1423
Db 1110 ctccgggtaa 1120
Qy 1424 CTCGGGTAAA 1434
|||||
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RESULT 10
ID Q23571 standard; DNA; 1458 BP.
AC Q23571;
DT 20-OCT-1992 (first entry)
DE Reshaped CD4 antibody heavy chain cDNA CDAVHNEM-Thr30
KW Antigen; CD4; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 36..1439
FT /*tag= a
FT misc feature 183..197
FT /*tag= b
FT /note= "Complementarity determining region 1"
FT misc feature 240..290
FT /*tag= c
FT /note= "Complementarity determining region 2"
FT misc feature 387..413
FT /*tag= d
FT /note= "Complementarity determining region 3"
PN W09205274-A.
PD 02-APR-1992.
PF 16-SEP-1991; G01578.
PR 17-SEP-1990; GB-020282.
PA (GORM/) GORMAN S D.
PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.
DR WPI; 92-132139/16.
DR P-PSDB; R22758.
PT Humanisation of antibodies binding to human CD4 antigen - by
PT mutation of framework-encoding regions of DNA encoding variable
PT domain of rat or mouse antibody chain
PS Disclosure; Fig 6; 74pp; English.
CC The sequence is that of the reshaped CD4 antibody heavy chain cDNA
CC CDAVHNEM-Thr30. Reshaped CD4 antibody can be used to induce tolerance
CC against an antigen. It can also be used to alleviate autoimmune diseases
CC such as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC also be useful to alleviate allergies. Tolerance to allergens could
CC also be achieved. See also Q23566-Q23581.
SQ Sequence 1458 BP; 345 A; 467 C; 385 G; 261 T;

Query Match 69.9%; Score 1005; DB 4; Length 1458;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 1016; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 413 ctgggtgcaaggcagctcgtoacagctctctcagcctccacaaaggcccatcgtctt 472
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 411 CTGGGGCCAGGGGGCCCTGCTCAGCGTCTCTCAGCTAGCACCAAGGGCCATCGGTCTT 470
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 473 cccctggcaccctctctccaaagacacctctggggcacagcgccctggctgctgggt 532
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 471 CCCCTGGGACCTCTCTCCAGACACCTCTCTGGGGGCACAGCGGCCCTGGGCTGCTGGT 530
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 533 caaggactacttcccgaaccggtgacggtgtcggtgaactcaggcgccctgaccagcg 592
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 531 CAGGACTACTTCCCGAACCAGGTCAGGTCGTGCGAAGTCTCAGCGCCCTGACCGCGG 590
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 593 cgtgcacacctctccggtgtctcactacagctcctcaggactctactcctcagcagcgtgg 652
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 591 CGTGCACACTCTCCGGGTCTCTACAGTCTCTACAGTCTCTACAGTCTCTACAGTCTCT 650
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 653 gaccgtgcctccagcajcttggggaccagacctacatctgcaacgtgaatcacaagcc 712
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 651 GACGCTGCCTCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAACGTGAATCACAAGCC 710
Db 713 caqcaacacaaaggtggacaagaattgagcccaaatcttctgacaaaactcacacatg 772
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 711 CAGCAACACCAAGGTGGACAGCAAGCAGAGCCCAATCTTGTGACAAAATCTCACATG 770
Db 773 cccacgtgtcccagcaccctgaactcctggggggaccgtcagttctctcttcccacaaa 832
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 771 CCCACCGTGCACGACCTGAACTCTCCGGGGGACCGTCAGTCTTCTTCTCCCCCAAA 830
Db 833 acccaagacacacctcatgatctccggagccctgaggtcacatcgctggtggtgagcgt 892
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 831 ACCCAAGGACACCTCATGATCTCCGGGACCCCTCAGGTCAATCGCTGGTGGAGCT 890
Db 893 gagccacgaagacctgaggtcaagttcaactggtacgtggagcggtggaggtgcataa 952
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 891 GAGCCAGCAAGACCTGAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGTGCATAA 950
Db 953 tgcacagacaaagccgaggagagcagtcacacagcagcagtcacctggtgagcgtcct 1012
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 951 TCCCAACACAAAGCGCGGAGGAGGAGTACAAAGCAGCAGTACCGTGTGTCAGGTCT 1010
Db 1013 caccgtctgcaccagcactgggtgaatggcgaaggtacaaagtgaaggtctccaacaa 1072
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1011 CACGCTCTGACAGCAGGACTGGCTGAATGGCAAGGAGTCAAGTCAAGGTCTCCAACAA 1070
Db 1073 agccctcccagcccccacatcgaaacacacatctccaaagccaaagggcagcccgagaacc 1132
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1071 AGCCCTCCGAGCCCATCGCAAAACCATCTCCAAGGCCAAAGGGCAGCCCGGAGAAC 1130
Db 1133 acaggtgtacacctgcccccatccccgggatgagctgaccaagaaccaggtcagcctgac 1192
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1131 ACAGGTGTACACCTCGCCCATCCCGGATGAGCTGACCAAGAACGAGTCAAGCTGAC 1190
Db 1193 ctgctcgtggtcaaaaggtcttctatcccagcagcagtcggtggagtgagagaatgggca 1252
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1191 CTGCTGTGTCAAAGGCTTCTATCCACCGACGATCGCGTGGAGTGGAGAGCAGTGGGCA 1250
Db 1253 gccgagaacactacaagaccagcctccgtgctgagctccagcagcctctcttctct 1312
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1251 GCGGAGAACTACTACAAGACCGCTCCGCTGGACTCCGAGCGGCTCTTCTTCTCT 1310
Db 1313 ctacagcaagctcacgtggacaagagcaggtggcagcaggggaaacgtcttctcatgctc 1372
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1311 CTACGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGGGAAACGCTTCTCATGCTC 1370
Db 1373 cgtgatgcattgaggtctctgcaacacactacacgagaagagcctctccctgtctccggg 1432
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1371 CGTGATGCAATGAGGCTCTGCACACCACTACAGCGCAGACAGCCTCTCCCTGCTCCGGG 1430
Db 1433 taatga 1439
|||||
Qy 1431 TAATGA 1437

RESULT 11
ID Q23581 standard; DNA; 1458 BP.
- AC Q23581;
DT 20-OCT-1992 (first entry)
DE Reshaped CD4 antibody heavy chain cDNA CDAVHNEM-Ser30
KW Antigen; CD4; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
```





PS Example 3; Page 42-48; 137pp; English.

CC A dicistronic vector (715932) comprises a regulatory region  
 CC derived from the SV40 virus early region, a selectable  
 CC dihydrofolate reductase (DHFR) gene positioned within an  
 CC intron having a 5' efficient splice donor site (GAC:GTAAGT), a  
 CC downstream sequence coding for anti-IgE heavy chain variable  
 CC region, and a poly-A sequence. Co-transfection of CHO cells with  
 CC this vector and another vector (715933) expressing the hygromycin  
 CC resistance gene and the antibody light chain (VL), with  
 CC subsequent DHFR and hygromycin B selections, yielded transfectants  
 CC capable of producing anti-IgE in yields of 41 mg/l.  
 SQ Sequence 6557 BP; 1618 A; 1764 C; 1606 G; 1569 T;

Query Match 69.7%; Score 1001; DB 18; Length 6557;  
 Best Local Similarity 98.3%; Pred. No. 0.00e+00;  
 Matches 1019; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 1682 atttcgctgtgggtcaagaacctgtcacctgtctcctcctcctccaccacgaagggcc 1741  
 QY 401 ACTTCGAATTCTGGGGCCAGGGCCCTGCTGTCACCGTCTCCTCAGCTAGCACCAGGGCC 460  
 Db 1742 catcggttctccctggcacctctccaagagcacctctgggggcacagcgccctgg 1801  
 QY 461 CATCGGTCTCCCGCTGGCAGCCCTCTCAAGAGCACCTCTGGGGGACAGCGGCGCTGG 520  
 Db 1802 gctgctgtcaaggactaetccccgaaccggtgacgtgtcgtggaactcagggccc 1861  
 QY 521 GCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGGTGTGGAACTCAGCGGCC 580  
 Db 1862 tgaccagcggtgacacctcccggtgtcctacagtcctcaggactctactccctca 1921  
 QY 581 TGACCAGCGGCTGCACACCTTCCGGGTGTCTTACAGTCTCAGGACTCTACTCCTCA 640  
 Db 1922 gaagcggtgactgtgcctctagacgttggggaaccacagactacatctgaacgtga 1981  
 QY 641 CGAGCGTGTGACCGTGGCCCTCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA 700  
 Db 1982 atcaaacgcccagcaacaccgaagtggacaagaagtggacccaactctgtgacaaaa 2041  
 QY 701 ATCACAGCCGACCAACCAAGGTGGACAGAAAGCAGAGCCCAATCTTGTGACAAAA 760  
 Db 2042 ctacacatgccacccgtgccagacacctgaactcctgggggaccgctcagctcttctct 2101  
 QY 761 CTCACATATGCCACCGTGGCCAGCACTGAACTCTGGGGGACCGTCACTCTTCTCT 820  
 Db 2102 tcccccaaaaacccaagcacacctcatgatctcccgagccctgaggtcacatgcgtgg 2161  
 QY 821 TCCCCCAAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACTGCGTGG 880  
 Db 2162 tgggtgaagtgagccacgaagacctgaggtcaagttcaactggctacgtgacggcgtgg 2221  
 QY 881 TGGTGGACGTGACCCACGACAGACCTGAGGTCAAGTTCACTGCTAGCTGGCAGCGGTGG 940  
 Db 2222 aggtgataatgccaaagaaacccggaggagcagttacaacagcagctacgtgtgg 2281  
 QY 941 AGGTGATAATGCCAAGAAAGCCCGGGAGGAGGAGCTTACAACAGCAGCTACCGTCTGG 1000  
 Db 2282 tcagcgctcctaccgtctcgcaccaggaactggctgaatggcaagagagtagcaagtgaagg 2341  
 QY 1001 TCAGCGCTCTCACCGTCTTCGACACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGG 1060  
 Db 2342 tctccaacaagacctctccagcccccatcgagaaaccatctccaagccaaagggcagc 2401  
 QY 1061 TCTCCAAGAGCCCTCTCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGC 1120

Db 2402 ccgagagaaccacaggtgtacacctgtcccccattccgggggaagagatgaccaagaaccagg 2461  
 QY 1121 CCCGAGAACACACAGGTGTACACCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1180  
 Db 2462 tcagctgacactgcctggtcaaggcttctatccacagcagacatgcgctggagtgaggaga 2521  
 QY 1181 TCAGGCTCAGCTGCCTGGTCAAGGGTCTTATCCAGGCACATCGCGCTGGAGTGGGAGA 1240  
 Db 2522 gcaatgggacggcggagaaacaactacaagaccagctcccggtgctggactccgacggct 2581  
 QY 1241 GCATGGCGACCGCGAGAACACTACAGACCGCGCTCCCGTCTGCTGACTCCGACCGCT 1300  
 Db 2582 ccttctctctacagcaagctcaecgtggacaagagcaggtggcagcaggggaacgtct 2641  
 QY 1301 CCTTCTCTCTTACAGCAAGCTCACCGTGGACAGAGAGGTGGCAGCGGGGAACGTCT 1360  
 Db 2642 tctcatgctcgtgatgcagtggaggtcttgcacaaccactacagcagaagagcctctccc 2701  
 QY 1361 TCTCATGCTCGGTGATGCATCAGGCTCTGCACAACCACTACAGCAGAGAGAGCCTCTCC 1420  
 Db 2702 tgtctccgggtaaatga 2718  
 QY 1421 TGTCTCCGGGTAAATGA 1437

## RESULT 13

ID Q54655 standard; cDNA; 1641 BP.  
 AC Q54655;  
 DT 24-JUN-1994 (first entry)  
 DE chiT84.12 H3 heavy chain.  
 KW Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant;  
 KW region; transform; myeloma cell; light chain; tumour; ss.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT CDS 52..1486  
 FT /\*tag= a  
 FT /product= chiT84.12 H3 heavy chain  
 PN W09325237-A.  
 PD 23-DEC-1993.  
 PF 15-JUN-1993; U05709.  
 PR 15-JUN-1992; US-904074.  
 PA (CITY ) CITY OF HOPE.  
 PA (YANG/) YANG Y.  
 PI Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;  
 PI Yang YH;  
 DR WPI; 94-007204/01.  
 DR P-PSDB; R47453.  
 PT New chimaeric T84.12 antibody active against carcinoembryonic  
 PT antigen - has murine variable and human constant regions, also  
 PT DNA encoding it and transformed myeloma cells  
 PS Claim 1; Page 22-23; 27pp; English.  
 CC The sequences (Q54651-52) show the light and heavy chain cDNAs  
 CC of murine T84.12. The T84.12 antibody is directed against the  
 CC tumour marker carcinoembryonic antigen, and is useful for  
 CC tumour imaging and immunotherapy.  
 SQ Sequence 1641 BP; 370 A; 516 C; 444 G; 311 T;  
 Query Match 69.6%; Score 1000; DB 9; Length 1641;  
 Best Local Similarity 97.9%; Pred. No. 0.00e+00;  
 Matches 1022; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
 Db 442 ggaagggttgattgttactggggcccaaggagactctggccactgtctcgtcagcctccacc 501  
 ||||| ||| | ||||| ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||



QY 394 GGAGGTTACTTCGAATTCTGGGGCAGGGCGCGCTGGTCAACGGTCTCCTCAGCTAGCAACC 453

Db 502 aaggccceatcggtcttccccctggcaccctctccaagagcacctctctggggcacagcg 561  
|||||

QY 454 AAGGGCCCTTGGGTCTTCCCGCTGGGACCGCTCTCCACAGACGCTCTGGGGGACAGGG 513  
|||||

Db 562 gccctgggctgacctggtcaaggaactactccccgaaccgggtgacggtgctgctggaactca 621  
|||||

QY 514 GCCCTGGGCTGGCTGGTCAAGGACTACTTCCCGAACCGGTGAGGGTGTCTGGAACCTCA 573  
|||||

Db 622 ggcgcctgacacaggggtgcacacctcccggtgctcctacagtcctcaggactctac 681  
|||||

QY 574 GGGCCCTGACACAGCGGGGTGCACACTTCCCGGGCTGTCTCAGACTCTCTCAGGACTCTAC 633  
|||||

Db 682 tccctcaagcagcgtggtgacctgacctccagcagcgttgggcaaccagacctacatctgc 741  
|||||

QY 634 TCCCTCAGAGCCTGTGACCGGTGCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 693  
|||||

Db 742 aacgtgaatcacagccacgacacccaaggtggacaagaagtggagcccaaatcttgt 801  
|||||

QY 694 AAGTGAATCACAAAGCCAGACACCAAGGTGGACAAAGCAAGGCCCAATCTTGT 753  
|||||

Db 802 gacaaactcacatgcccacgctgccacgacctgaactcctggggagaccgtcagtc 861  
|||||

QY 754 GACAAACTCACACATGCCACCGCTGCCACGACCTGAACTCTTGGGGGACCGTCAGTC 813  
|||||

Db 862 ttcccttccccccaaaacccaagagacacctcatgatctccgggacctgaggtcaaa 921  
|||||

QY 814 TTCTCTTCCCGCCAAAACCCAAAGACACCTCATGATCTCCGGACCCCTCAGGTCA 873  
|||||

Db 922 tgcgtggtggtgacgcgagccagacccctgaggtcaagttcaactggtacgtggac 981  
|||||

QY 874 TGGCTGCTGGTGGACGCTGAGCCGACGAACCCCTGAGGTCAAGTTCACCTGCTAGCTGGAC 933  
|||||

Db 982 ggcgtggaggtgcaataatgccaaagacgacgacgggagagagcagtcacacagacagtc 1041  
|||||

QY 934 GGGCTGAGGTGCAATAATGCCACAGCAAGCCGGGGAGGAGCAGTACACAGCAGCTAC 993  
|||||

Db 1042 cgtggtgacgctcctcaccgctcctgaccagcagcagcagcagcagcagcagcagcagc 1101  
|||||

QY 994 CGTGTGGTGAAGCTCTCAGCGCTCTGCACCAAGGACTTGGCTGAATGGCAAGGACTCAAG 1053  
|||||

Db 1102 tgaaggtctccaaaagacccctcccagcccccatcgagaaaaccatctccaaagccaaa 1161  
|||||

QY 1054 TGCAGGCTTCCAAACAAAGCCCTCCAGCGCCCATCGAAGAACATCTCCAAAGCCAAA 1113  
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Db 1162 gggcagccccgagaaccacaggtgtacacctgcccccatcccggtgatgagctgaccaag 1221  
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Db 1222 aaccaggtgacgctgacctgctggtcaaaagcttctatccccagcgacatcgccgtggag 1281  
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QY 1174 AACAGGTGAGCCTGACCTGCTGTTCAAGGCTTCTATCCACCGACATCGCCGTGGAG 1233  
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QY 1234 TGGGAGCAATGGCGACCGGAGAACACTACAAAGACCGCTCCCGTGGACTCC 1293  
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Db 1342 gacgctctcttctctctacacgaagctcacgctggacaagacaggtggcagcagggg 1401  
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QY 1294 GAGGGCTCTTCTCTTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGAGGGG 1353  
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Db 1402 aacgtcttctatgctcgtgatgatgaggtctctgcacaaccactacacgagaagagc 1461  
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QY 1414 CTCTCGCTGTCTCCGGGTAAATGA 1437

RESULT 14

ID Q25692 standard; cDNA; 1412 BP.

AC Q25692;

DT 28-DEC-1992 (first entry)

DE Sequence of the chimeric H chain cDNA contained in pTB1373

KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;

KW antithrombotic agent; myocardial infarction therapy; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT sig\_peptide 13..69

FT /\*tag= a

FT /product= Leader

FT CDS 70..414

FT /\*tag= .b

FT /product= VH

FT CDS 415..708

FT /\*tag= c

FT /product= CH1

FT CDS 709..753

FT /\*tag= d

FT /product= hinge

FT CDS 754..1083

FT /\*tag= e

FT /product= CH2

FT CDS 1084..1407

FT /\*tag= f

FT /product= CH3

PN EP-491351-A.

PD 24-JUN-1992.

PF 17-DEC-1991; 121591.

PR 18-DEC-1990; JP-413829.

PR 11-NOV-1991; JP-294464.

PA (TAKE ) TAKEDA CHEM IND LTD.

PI Iwasa S, Taka H, Watanabe T, Tada H;

DR WPI; 92-209528/26.

DR P-PSDB; R24812.

PT Chimeric monoclonal antibodies - contain anti-human fibrin

PT antibody light and heavy chain variable and constant for treating

PT thrombotic conditions e.g. myocardial infarction

PS Example; Figure 11; 87pp; English.

CC Plasmid pTB1373 contains the whole length of a mouse-human

CC chimeric anti-human fibrin heavy chain cDNA open reading

CC frame. It was prepd. using Poly(A) + RNA from the anti-fibrin

CC chimeric Ab-producing transformant FIB1-H01/X63 as a template

CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as

CC a primer for first strand cDNA synthesis and the 5'CZH and 3'EH

CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain

CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader

CC peptide cDNA were amplified using the primers 3'EH, 3'CZH and 3'CLH

CC respectively as a primer for first strand cDNA synthesis and the

CC primer combination of 5'CLH and 3'CZH, of 5' LH and 3'CLH and of

CC 5' SH and 3' LH respectively as primers for PCR. The amplified gene

CC products were isolated and used to produce plasmids. After

CC confirmation of the cDNA sequence of each plasmid, the cDNA

CC encoding LH, VH, CH1 and CH2CH3 were joined together to give

CC plasmid pTB1373 contg. the whole length chimeric H chain



Db 2332 ggaactctactccctcagcagcgtggtgacogtgcctccagcagcttcggaacccagacc 2391  
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Qy 865 GAGGTCAATGCGTGGTGGACGTGAGCCAGCAGACCCCTGAGGTCAAGTTCAACTGG 924  
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Qy 925 TAGCTGACGGCGTGCAGTGCATTAATGCCAAGCAAAAGCCGGGAGGAGCAGCTACAAC 984  
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Qy 1045 GAGTACAGTGCAGGTCTCCACAAAGCCCTCCAGCGCCCATCGAANAACCATCTCC 1104  
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Query Match          74.3%; Score 528; DB 51; Length 827;
Best Local Similarity 91.7%; Pred. No. 0.00e+00;
Matches 597; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

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Qy 62 AGTCTGTCTGTACACAGCGCGCCTCAGTGTCTGGGGCCCGACGAGAGGTCAACATCT 121
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Db 137 cttgtctggagcaggttccaaatcctggggcaggttcattcattgtgcatgtaccagaag 196
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Qy 122 CGTGCACTGGGACACCTCCAACTGG---AGTTATGATCTACATTGCTACACAGCAGC 178
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Db 197 ttccaggacagcccccacaaactctcatctatgtgacaaacatcgccctcagggtcc 256
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Qy 179 TCCAGGAGCGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGCCCTCAGGAATTT 238
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Db 257 ctgaccgaatctctggtccaagtggcgacttcagctccctggccatcactgggtcc 316
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Qy 239 CTGACCGATTCTCTGGCTCCAGTCTGTGTACCGCGCCTCCCTGGCATCACTGGGCTCC 298
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Db 317 gggctgaagtggctgattactgacctgagtcctttgacagcagcctgagtggtggg 376
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Qy 299 AGACTGAGGATGAGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTGATGCTCAGG 358
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Db 377 ttttcggggagcgacccaactgacctgctcggtcagcccaaggctgccccctcggtca 436
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Qy 359 TATTCCGAGAGGGACCGCGCTGACGCTCTAGTTCAGCCGACGAGGCTGCCCTCGGTCA 418
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Db 437 ctctgttccacactctctctgagaggtctcaagccaacaaagccactggtgtctca 496
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Qy 419 CTCCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCA 478
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Db 497 taagtgaactctaccggggagcgtgacagtggtcctggaaggcagatagagcccgctca 556
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Qy 479 TAACTGACTTCTACCGGAGCGGTGACAGTGGCTTGAAGGCAGATAGCAGCCCGCTCA 538
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Db 557 cggcgaggatggagaccaccacacctccacaacaaagcaacaagtacgcggcgagca 616
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Qy 539 AGGGGGAGTGGAGACACACACACCTCTCAACAAAGCAACACAGTACCGGGCCAGCA 598
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Db 617 gtaacctgagctgagcgtgagcagtggaagtcccccaaaaagctacagctgccaggtca 676
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Db 677 cgcataaggagaccgtggagaagacagtggtccctacagaattgtcat 727
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Qy 659 CGCATGAAGGAGCACCCTGGAGAGACAGTGGCCCTCAGAGAATGTTCTAT 709
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RESULT 5
LOCUS H5IGVL032 802 bp RNA PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57822
NID 937423
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Carnivora; Homiinae; Homo.
REFERENCE 1 (bases 1 to 802)
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AUTHORS Klobeck, H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
REFERENCE 2 (bases 342 to 388)
AUTHORS Combriato, G. and Klobeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

FEATURES
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Best Local Similarity 90.3%; Pred. No. 0.00e+00;
Matches 585; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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Qy 62 AGTCTGTCTGTACACAGCGCCCTCAGTGTCTGGGGCCCGACGAGGAGGTCAACATCT 121
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Db 117 cttgttctggaagcactccaacatcggaagtaactgtgaaactgtgaccagaactcc 176
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Qy 122 CGTCACTGGAGACCTCCACATTGGAGGTTATGATCTACATTGGTACGACGCTCC 181

Db 177 caggaaagcccccagaagctctcatctataataatgagcgccctcaagggtccctg 236  
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Qy 182 CAGGAACGGCCCCAACTCTCATCTATGACATTAAACAGCGACCTCAGGAATTTCTG 241

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Qy 242 ACCGATTCTTGGCTCCAACTCTGTAGCGGCTCTCTGGCCATCACTGGGCTCCAGA 301

Db 297 ctgacgatgaggtgattattactgtgcagcatgggatgacagctctgaatgcgcgcttt 356  
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Qy 302 CTGAGGATGAGGCTGATTATTACTGCCAGTCTTATGACAGCACCTGGAATGCTCAGGTAT 361

Db 357 tggcgaggaggacaagtgtgacgtctcagtcagcccaaggctgccccctcgctcactc 416  
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Qy 362 TCGAGGAGGACCGCGCTGACCGCTTAGGTCAGCCCAAGGCTGCCCTCGGTCACTC 421

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Qy 422 TGTTCGGCGCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGGTGTCTCATAA 481

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Qy 482 GTGACTTCTACCGGGAGCGGTGACAGTGGCTTGGAGGAGATAGAGCGCCGCTCAGG 541

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Qy 662 ATGAAGGAGCACCTGGAGACAGCTGGCCCTACAGAACTGTCAT 709

RESULT 6

LOCUS H5IGVL025 810 bp RNA PRI 04-NOV-1994

DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.

ACCESSION X57815

NID g33729

KEYWORDS Ig lambda light chain; immunoglobulin.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 810)

AUTHORS Klobeck, H.G.

TITLE Direct Submission

JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany

REFERENCE 2 (bases 349 to 395)

AUTHORS Combiato, G. and Klobeck, H.G.

TITLE V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism

JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)

MEDLINE 91257162

COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33729

FEATURES

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/note="variable region; V(lambda)I"

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/note="J-segment"

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/gene="immunoglobulin lambda light chain"

/note="constant region"

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Best Local Similarity 90.1%; Pred. No. 0.00e+00;

Matches 584; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Qy 122 CGTGCACTGGGAGCACCTCCACATTGGAGGTTATGATCTACATTGGTACGACGCTCC 181

Db 184 caggaaagcccccagaagctctcatctataggaataatcagcgccctcaggggtccctg 243  
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Qy 182 CAGGAACGGCCCCAACTCTCATCTATGACATTAAACAGCGACCTCAGGAATTTCTG 241

Db 244 accgattctctggtccaaagtctggctcctcagctccctggccatcagtggtgctcagt 303

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QY 362 TCGGAGGAGGAGCCGGCTGACCGTCTTAGGTGACGCCAAGGCTGCCCTCGGTCACTC 421
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RESULT 7
LOCUS H5IGVL009 915 bp RNA PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57809
NID g33714
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominiidae; Homo.
1 (bases 1 to 915)
REFERENCE
AUTHORS Klobbeck,H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobbeck, Inst fuer Physiologische Chemie, Physiologische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
2 (bases 452 to 498)
REFERENCE
AUTHORS Combratio,G. and Klobbeck,H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.
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## FEATURES

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Qy 659 CGCATGAGGAGGACACCTGGAGAGACAGTGGCCCTACAGATGTTTCAT 709

RESULT 9 S42404 642 bp mRNA PRI 15-NOV-1992  
LOCUS Ig lambda chain=anti-Rh(D) antibody [human, mRNA Partial, 642 nt].  
DEFINITION S42404  
ACCESSION S42404  
NID 9253701

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 642)

AUTHORS Chouchane, L., Van Sprosen, A., Breyer, J., Guglielmi, P. and

Stroberg, A.D.

TITLE Molecular characterization of a human anti-Rh(D) antibody with a DH

segment encoded by a germ-line sequence

JOURNAL Eur. J. Biochem. 207 (3), 1115-1121 (1992)

MEDLINE 92362614

REMARK GenBank staff at the National Library of Medicine created this

entry [NCBI glibsq 111063] from the original journal article.

COMMENT This sequence comes from Fig. 4.

NCBI gi: 253701

FEATURES

location/Qualifiers

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/partial

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Author-given protein sequence is in conflict with the

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ORIGIN

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Matches 551; Conservative 0; Mismatches 35; Indels 6; Gaps 3;

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Qy 178 CTCCCAGGACGGCCCCCAAACTCTCTATGACATTAACAAGCGACCTCAGGAATT 237

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Qy 238 TCTGACCATTTCTTGGTCCAAAGTCTGGTACCGGGGCTCTCTTGGCCATCACTGGGCTC 297

Db 181 caagctgagagatgaaggtgattattactgccagacgatatgacatcagcctgaactg-t--g 237

Qy 298 CAGACTGAGGATGAGCGTGATTACTGCCAGCTCTATGACAGCAGAGCTGAATGCTCAG 357

Db 238 gtattcggcgaggagaccaagctgaccctcctgggtcagcccaaggctgccccctcggtc 297

Qy 358 GTATTCCGAGGAGGAGCCGGCTGACCGTCTAGTGTGAGCCCAAGGCTGCCCTCGGTC 417

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Qy 478 ATNAGTGACTTCTACCCGGGAGCGGTGACATGGCTGGAGGCATAGCAGCCCGTC 537

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Qy 598 AGTACTGTAGCCTGACGCGCTGAGCAGTGGAGTCCACAGAGCTTACAGTCCAGGTC 657

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Qy 658 ACCGATGAAGGAGCACCGTGGAGAGACAGCTGGCCCTACAGANTGTTTCAT 709

RESULT 10

LOCUS HSU07991 663 bp mRNA PRI 06-APR-1994

DEFINITION Human lymphoma immunoglobulin lambda light chain mRNA, partial cds.

ACCESSION U07991

NID 9468246

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eucaryote; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 663)

AUTHORS Watkins, B.A., Davis, A.E. and Reitz, M.S.

TITLE Complex secondary structure of immunoglobulin VH region mRNAs:

Potential problems to representation in repertoire libraries

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 663)

AUTHORS Watkins, B.A.

TITLE Direct Submission

JOURNAL Submitted (24-MAR-1994) Brynmor A. Watkins, LTCB, National Cancer

Institute, NIH, Building 37/6C09, 9000 Rockville Pike, Bethesda, MD

20892, USA

NCBI gi: 468246

FEATURES

Location/Qualifiers

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BASE COUNT 151 a 204 c 175 g 133 t  
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Best Local Similarity 87.5%; Pred. No. 0.00e+00;  
Matches 566; Conservative 0; Mismatches 78; Indels 3; Gaps 2;

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RESULT 11

ID HS07991 standard; RNA; PRI; 663 BP.

AC U07991;

DT 07-APR-1994 (Rel. 39, Created)

DT 18-FEB-1996 (Rel. 46, Last updated, Version 2)

DE Human lymphoma immunoglobulin lambda light chain mRNA, partial cde.

KW

OS Homo sapiens (human)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea;  
RN [1]  
RP 1-663  
RA Watkins B.A., Davis A.E., Fiorentini S., Reitz M.S.;  
RT "V-region and class specific RT-PCR amplification of human  
immunoglobulin heavy and light chain genes from B-cell lines";  
RL Scand. J. Immunol. 42:442-448(1995).  
RN [2]  
RP 1-663  
RA Watkins B.A.;  
RT /  
RL Submitted (24-MAR-1994) to the EMBL/GenBank/DBJ databases.  
RL Bynnmor A. Watkins, LTCB, National Cancer Institute, NIH, Building  
RL 37/6C09, 9000 Rockville Pike, Bethesda, MD 20892, USA  
CC NCBI gi: 468246  
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SQ Sequence 663 BP; 151 A; 204 C; 175 G; 133 T; 0 other;

Query Match 66.1%; Score 470; DB 9; Length 663;  
Best Local Similarity 87.5%; Pred. No. 0.00e+00;  
Matches 566; Conservative 0; Mismatches 78; Indels 3; Gaps 2;

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176 a 253 c 202 g 152 t
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Best Local Similarity 86.54; Pred. No. 0.00e+00;
Matches 566; Conservative 0; Mismatches 82; Indels 6; Gaps 3;

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RESULT 15
LOCUS HSIGVL034 756 bp RNA PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57824
NID 933747
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS Klobeck,H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
REFERENCE 2 (bases 344 to 390)
AUTHORS Combratio,G. and Klobeck,H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33747
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/isolate="individual S"
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/note="NCBI gi: 33748"
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Dec 17 22:36

US-08-487-550-9.rge

27

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ORIGIN
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Best Local Similarity 86.6%; Pred. No. 0.00e+00;  
Matches 564; Conservative 0; Mismatches 81; Indels 6; Gaps 5;

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Db 416 ctctgtcccgccctcctctgaggagcttcaagccaagaaggccacactggtgtctca 475
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Db 536 gggcggaggtggagaccacacacctccaaacaagcaacaacaagtaacgcgccagca 595
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Db 596 gctatctgagcctgacg-cctgagcagtggaagtcacacagaagctacagctgccaggtca 655
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Dec 17 22:36

US-08-487-550-9.rge

28

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Search completed: Tue Dec 17 22:50:47 1996
Job time : 444 secs.
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\*\*\*\*\*  
 (TM)  
 \*\*\*\*\*

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 Distribution rights by IntelliGenetics, Inc.

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 22:51:06 1996; MacPar time 62.24 Seconds  
 890.366 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-550-9  
 Description: (1-711) from US08487550.seq  
 Perfect Score: 711  
 N.A. Sequence: 1 ATGAGGTCGCCGCTCAGCT.....CCCTACAGATGTTTCATCA 711  
 Comp: TACTCCAGGGGGAGTCA.....GGGATGTTTACAGTACT

Scoring table: TABLE default

Gap 6

Mismatch STD : Dbase 0; Query 0

Searched: 102519 seqs, 38967980 bases x 2

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: n-geneseq21  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
 14:part14 15:part15 16:part16 17:part17 18:part18  
 19:part19

Statistics: Mean 8.765; Variance 5.477; scale 1.600

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	DB	ID	Description	Pred. No.
1	546	76.8	884	1	Q03609 Sequence encoding 4G1	0.00e+00
2	520	73.1	654	8	Q49835 Anti-HIV-1 recombinan	0.00e+00
3	459	64.6	902	6	Q35100 Antibody D lambda lig	7.11e-287
4	430	60.5	872	1	N81655 VDJC regions of human	4.33e-267
5	318	44.7	8387	3	Q22489 Human U266 lambda gen	5.82e-191
6	318	44.7	9071	3	Q23370 U266-Lambda gene and	5.82e-191
7	318	44.7	9071	3	Q22491 Human U266 lambda gen	5.82e-191
8	232	32.6	330	1	Q03607 Sequence encoding 4G1	5.62e-133

9	224	31.5	318	2	Q11187	Immunoglobulin lambda	1.29e-127
10	218	30.7	333	2	Q11945	Anti-human Rhd FOG-B	1.34e-123
11	214	30.1	333	19	T10940	Vllambda coding seque	6.36e-121
12	209	29.4	816	17	Q98724	Anti-HIV-1 MAb 447 ei	1.39e-117
13	205	28.8	318	2	Q10674	Feline immunoglobulin	6.54e-115
14	205	28.8	318	11	Q64170	Sequence of feline he	6.54e-115
15	201	28.3	330	16	Q98903	Human tumor-associate	3.05e-112
16	181	25.5	701	1	N80473	Inseert of clone p2183	6.19e-99
17	181	25.5	870	1	N80471	Sequence specifically	6.19e-99
18	165	23.2	2192	1	N80474	Genomic form of lambd	2.45e-88
19	160	22.5	312	17	T04634	Human derived light c	4.90e-85
20	154	21.7	628	6	Q36134	MR4H7 MAB light chain	4.41e-81
21	154	21.7	1044	2	Q12840	Variable region of la	4.41e-81
22	151	21.2	333	19	T10327	Human anti-pseudomona	4.16e-79
23	131	18.4	333	9	Q55659	Monoclonal antibody G	5.22e-66
24	130	18.3	650	6	Q36132	IN2A8 MAB light chain	2.34e-65
25	119	16.7	863	1	N81656	LVJ regions of human	3.28e-58
26	115	16.2	324	10	Q64054	Sequence of the VL re	1.27e-55
27	113	15.9	309	17	T04638	Human derived light c	2.48e-54
28	109	15.3	387	6	Q35904	Anti-CD4 V-lambda cod	9.37e-52
29	98	13.8	324	5	Q33036	MAB 1-3-1 variable re	1.04e-44
30	90	12.7	318	10	Q64057	Sequence of the VL re	1.26e-39
31	86	12.1	333	2	Q11946	Anti-human Rhd PAG-1	4.21e-37
32	82	11.5	201	17	T04636	Human derived light c	1.37e-34
33	73	10.3	336	12	Q70086	DNA encoding MAB ligh	5.48e-29
34	67	9.4	360	1	N80175	Light chain variable	2.68e-25
35	67	9.4	1047	2	Q10572	Human Natriuretic Pep	2.68e-25
36	66	9.3	435	3	Q15163	V186 region of lambda	1.09e-24
37	64	9.0	747	1	N80179	Binding site.	1.81e-23
38	63	8.9	397	1	Q04041	Anti-Leu 3a light cha	7.30e-23
39	62	8.7	8540	11	Q65628	Vector contg. TCAC 8	2.94e-22
40	58	8.2	1047	2	Q10572	Human Natriuretic Pep	7.51e-20
41	57	8.0	330	8	Q49505	Aglycosylated antibod	2.97e-19
42	57	8.0	330	4	Q24515	Recombinant light cha	2.97e-19
43	57	8.0	462	5	Q28740	cDNA of VLA25 antibod	2.97e-19
44	57	8.0	1701	5	Q30919	pMDR1006 insert.	2.97e-19
45	57	8.0	1701	5	Q30920	Vector pMDR1007.	2.97e-19

## ALIGNMENTS

RESULT	ID	Q03609 standard; cDNA; 884 BP.
1	DT	06-AUG-1989 (first entry)
AC	Q03609;	
DE	Sequence encoding 4G12 monoclonal antibody (MAB) L chain .	
KW	4G12 MAb; human lung cancer; oesophageal carcinoma; ss.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
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FT	polyA_signal 835..840	
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Qy 539 AGCGGGAGTGGAGCCACACACCTCCCAACAAGCAACAAGTACGGCGCGCAGCA 598  
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Qy 599 CTTACTGAGCTGAGCGCTGAGAGTGGAGTCCACAGAGCTACAGCTCCAGGTCA 658  
Db 687 cgcataagggagcagcctggagaagacagtgccctacagaatgtcat 737  
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Qy 659 CGCATCAAGGGAGCAGCCGTGGAGAGACAGTGGCGCCCTACAGATGTTCAT 709

## RESULT 4

ID N81655 standard; DNA; 872 BP.

AC N81655;

DT 09-NOV-1990 (first entry)

DE VDJC regions of human sperm-immobilising monoclonal antibody.

KW Anti-human sperm-immobilising monoclonal antibody; leader region;

KW variable region; joining region; constant region; sterility;

KW vaccine; contraceptive; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 40..729

FT /\*tag= a

FT /product=VJC region

FT misc feature 91..375

FT /\*tag= b

FT /label=V region

FT misc feature 376..412

FT /\*tag= c

FT /label=J region

FT misc feature 413..729

FT /\*tag= d

FT /label=C region

PN J63126482-A.

PD 30-MAY-1988.

PF 15-NOV-1986; 272412.

PR 15-NOV-1986; JP-272412.

PA (TOFU) TOA NENRYO KOGYO KK.

DR WPI; 88-187839/27.

DR P-PSDB; P81260.

PT Cell strain producing human sperm-immobilising monoclonal antibody -

PT has at least V-gene in H chain coding genetic family and V gene in L

PT chain of DNA originating from antibody of sterile woman.

PS Disclosure; 14pp; Japanese.

CC A VDJC segment is inserted into pSC41ambda5 together with a

CC leader region. A cell strain, pref. a myeloma cell, can

CC produce the Ab with immobilising value (SI50) of at least 5000,

CC sperm agglutination value at least 1:1600 dilution, specifically

CC reacting against human ejaculated sperm. The product can be used

CC as a vaccine and contraceptive.

CC See also N81654-N81656.

SQ Sequence 872 BP; 211 A; 269 C; 220 G; 172 T;

## Query Match

Best Local Similarity 60.5%; Score 430; DB 1; Length 872;

Matches 487; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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Db 247 ccctcagggatccagacagccgattctctggctccacctcaagaaacacagcttctctgacc 306  
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Qy 226 CCCTCAGGAATTTCTGACCGGATTTCTGGCTCCAACTCTGGTACCGGGCTCCCTGGCC 285  
Db 307 atcactggggctcaggcggaagatgaggctgactattactgtaactccccgggacagcagt 366  
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Qy 346 CTGATGCTCAGCTATTCGAGGAGGAGCGGCTGACCGTCTAGGTGAGGCGCCNAGGCT 405  
Db 427 gccctcgggtcaactctgtcccgccctctctgagagcttcaagccaacaagccaca 486  
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Qy 406 GCGCCCTGGGTCACTCTGTCCCGCCCTCTCTCAGAGCTTCAAGCCAACAGGCCACA 465  
Db 487 ctggtgtgtctcataagtgaacttctaccggggagccgtgacagtgccctggaaggagat 546  
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Qy 466 CTGGTGTCTCATTAAGTGACTTCTACCGGGAGCCGTGACAGTGGCTGGAAGGCAGAT 525  
Db 547 agcagccccgtcaaggcgggagtgagaccaccacacctccaacaagaagcaacaag 606  
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Qy 526 AGCAGCGCCGTCAAGCGGGAGTGGAGACCAACACACCCCTCCAAACAAGCAACAACAG 585  
Db 607 tacgcgccagcagctatctgagcctgacgctgagcagtggaagtgccacagaagctac 666  
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Qy 586 TAGCGCGCCAGCAGCTACCTGAGCCTGACGCTGAGAGTGGAGTGGAGTCCCAAGAGGTAC 645  
Db 667 agtgcagggtcacgcatgaaggagcagcgtggagaagacagtgggccctcacagaagt 726  
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Qy 646 AGTGCCAGGTCAAGGCAAGCGGTGAGAGACAGACAGTGGCCCTTACAGAATGT 705  
Db 727 tcatt 730  
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Qy 706 TCAT 709

## RESULT 5

ID Q22489 standard; DNA; 8387 BP.

AC Q22489;

DT 31-JUL-1992 (first entry)

DE Human U266 lambda gene.

KW Human myeloma U266 cell line; rearranged lambda gene; Ig;

KW immunoglobulin light chain; humoral immunity; ds.

OS Homo sapiens.

PN W09204440-A.

PD 19-MAR-1992.

PF 27-AUG-1991; 106124.

PR 29-AUG-1990; US-575005.

PA (HARD ) HARVARD COLLEGE.

PI Vasicek TJ, Leder P;

DR WPI; 92-114348/14.

PT B cell deficient transgenic non-human animals - comprise DNA

PT encoding the U266 immunoglobulin light chain and an enhancer

PT region used as models of B cell deficiency

PS Disclosure; Fig 2; 41pp; English.

CC This sequence is the EcoRI/HindIII fragment of the rearranged lambda

CC gene isolated from human myeloma U266 cell line. The coding sequence

CC is placed under the control of the mouse heavy chain enhancer. The

CC resulting transgene was used in the production of transgenic mice in



CC which the proportion of spleen cells which are mature B cells is not  
CC more than a quarter of that in wild-type animals. The animals are more  
CC susceptible to infectious diseases than the wild-type and are  
CC models for severe B cell deficiency. See also Q22491 for the  
CC transgene sequence.  
SQ Sequence 8387 BP; 1957 A; 2348 C; 2109 G; 1973 T;

Query Match 44.7%; Score 318; DB 3; Length 8387;  
Best Local Similarity 99.7%; Pred. No. 5.82e-191;  
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7062 aggtcagcccaaggtgccccctcgtgtaactctgttcccgccctctctgaagagttca 7121  
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Qy 390 AGGTGAGCCCAAGGTCGCCCTCGGTGCTCTGTCGCGCCCTCTCTGAGGAGCTTCA 449  
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Db 7122 agccacaagggccacactggtgtgtctcataagtgactttaccggggagcggtgacagt 7181  
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Qy 450 AGCCACAAAGGCCACACACTGGTGTCTCTCATTAAGTGACTTCTACCGGGGAGCGGTGACAGT 509  
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Db 7182 ggcctggaagcgatagcagcccgctcaaggcggtgagagcaccacaccctccaa 7241  
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Qy 510 GGCTTGAAGGCGAGTAGCAGCCCGCTCAAGCGCGGAGTGGAGACCAACACCCCTCCAA 569  
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Db 7242 acaagcaacaacaagtacggcgccagcagctatctgagcctgagcctgagcagtgaa 7301  
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Qy 570 ACAAGCAACAACAAGTACGGCGCCAGCAGCTTACCTGAGCCTGACGCTGACGAGTGAA 629  
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Db 7302 gtccacagaagctacagctgccaggtcacgcatgaaggagcaccgctggagaagacagt 7361  
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Qy 630 GTCCCAAGAAGCTACAGCTGCCAGGTACGATGAAGGGAGCACCGCTGGAGAAGACAGT 689  
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Db 7362 ggcctcacagaatgttcat 7380  
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Qy 690 GGCCCTACAGATGTTTCA 709  
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## RESULT 6

ID Q23370 standard; DNA; 9071 BP.  
AC Q23370;  
DT 14-AUG-1992 (first entry)  
DE U266-lambda gene and downstream murine Ig Heavy chain enhancer.  
KW Lambda-E-mu; rearranged; immunoglobulin; light chain; transgene;  
KW B cell deficiency; common variable immunodeficiency; CVID;  
KW ATCC # 72003; ds.  
OS Chimeric Mus.  
PN WO9204443-A.  
PD 19-MAR-1992.  
PF 27-AUG-1991; U06106.  
PR 29-AUG-1990; US-575006.  
PA (HARD ) HARVARD COLLEGE.  
PI Vasicek TJ, Leder P;  
DR WPI; 92-114351/14.  
PT B cell deficient transgenic FVB/N mice - comprise DNA encoding  
PT the lambda light chain of a non-human animal for modelling of B  
PT cell deficiency  
PS Disclosure; Fig 7; 41pp; English.  
CC DNA from the IgE-lambda human myeloma U266 cell line was digested  
CC with EcoRI and used to prepare a phage library. The clone  
CC containing the active lambda gene was identified by probing the  
CC library with a radiolabelled BamHI fragment of the human lambda 2  
CC gene. (The complete sequence of U266-lambda gene has EMBL Acc.#  
CC X51754). The lambda-E-mu construct was prepared by cutting the  
CC lambda construct at the HindIII site 0.9kb downstream of

CC C(Lambda)2. The fragment was blunt-ended and ligated to a 995bp  
CC XbaI fragment of pTAR-7 containing the mouse Ig heavy chain  
CC enhancer. The transgene construct was used to transfect mouse  
CC cells for the production of B cell deficient transgenic mice. The  
CC mice can be used to study e.g. X-linked agammaglobulinemia.  
SQ Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T;

Query Match 44.7%; Score 318; DB 3; Length 9071;  
Best Local Similarity 99.7%; Pred. No. 5.82e-191;  
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 7121 agccacaagggccacactggtgtgtctcataagtgactttaccggggagcggtgacagt 7180  
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Qy 450 AGCCACAAAGGCCACACACTGGTGTCTCTCATTAAGTGACTTCTACCGGGGAGCGGTGACAGT 509  
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Db 7181 ggcctggaagcgatagcagcccgctcaaggcggtgagagcaccacaccctccaa 7240  
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Db 7241 acaagcaacaacaagtacggcgccagcagctatctgagcctgagcctgagcagtgaa 7300  
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Qy 570 ACAAGCAACAACAAGTACGGCGCCAGCAGCTTACCTGAGCCTGACGCTGACGAGTGAA 629  
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Db 7301 gtccacagaagctacagctgccaggtcacgcatgaaggagcaccgctggagaagacagt 7360  
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Qy 630 GTCCCAAGAAGCTACAGCTGCCAGGTACGATGAAGGGAGCACCGCTGGAGAAGACAGT 689  
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Db 7361 ggcctcacagaatgttcat 7380  
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Qy 690 GGCCCTACAGATGTTTCA 709  
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## RESULT 7

ID Q22491 standard; DNA; 9071 BP.  
AC Q22491;  
DT 31-JUL-1992 (first entry)  
DE Human U266 lambda gene.  
KW Human myeloma U266 cell line; rearranged lambda gene; Ig;  
KW immunoglobulin light chain; pTAR-7; heavy chain enhancer;  
KW humoral immunity; transgenic mouse; ATCC No. 72003; ds.  
OS Chimeric Homo sapiens.  
FH Key Location/Qualifiers  
FT misc\_feature 1..8385  
FT /\*tag= a  
FT /note= "U266-lambda gene"  
FT misc\_feature 8386..9071  
FT /\*tag= b  
FT /note= "portion of 995bp XbaI-EcoRI fragment of  
FT pTAR-7 contg. mouse H chain enhancer"  
PN WO9204440-A.  
PD 19-MAR-1992.  
PF 27-AUG-1991; 106124.  
PR 29-AUG-1990; US-575005.  
PA (HARD ) HARVARD COLLEGE.  
PI Vasicek TJ, Leder P;  
DR WPI; 92-114348/14.  
PT B cell deficient transgenic non-human animals - comprise DNA  
PT encoding the U266 immunoglobulin light chain and an enhancer  
PT region used as models of B cell deficiency

PS Disclosure; Fig 7; 41pp; English.

CC This sequence is the EcoRI/HindIII fragment of the rearranged lambda  
CC gene isolated from human myeloma U266 cell line ligated to the mouse  
CC heavy chain enhancer. The resulting transgene was used in the  
CC production of transgenic mice in which the proportion of spleen cells  
CC which are mature B cells is not more than a quarter of that in  
CC wild-type animals. The animals are more susceptible to infectious  
CC diseases than the wild-type and are models for severe B cell  
CC deficiency. See also 022489 for the transgene sequence.  
SQ Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T;

Query Match 44.7%; Score 318; DB 3; Length 9071;  
Best Local Similarity 99.7%; Pred. No. 5.82e-191;  
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7061 aggtcagcccaaggtgccccctcggtcactctgttcccgccctctctgagagcttca 7120  
|||||  
Qy 390 AGTGAAGCCCAAGGCTGCCCGCTCGTCACTCTCTTCCGCGCTTCTCTGAGAGCTTCA 449  
|||||  
Db 7121 agccacaagccacactggtgtgtctcataagtgaactctaccggagccgtgacagt 7180  
|||||  
Qy 450 AGCCACAAGCCACACTGGTGTCTCTATAAGTCACTTCTACCCGGAGCGGTGACAGT 509  
|||||  
Db 7181 ggcctggaagcagatagcagcccgctcaaggcggagtgagacacacacccctccaa 7240  
|||||  
Qy 510 GGCCTGAAGCAGATAGCAGCCCGCTCAAGCGGAGTGGAGACACCAACCCCTCAA 569  
|||||  
Db 7241 acaagcaacaagaatcagcggcagcagctatctgagcctgagcctgagcagtgaa 7300  
|||||  
Qy 570 ACAAGCAACACATAGTCGGCGCGCAGCAGCTACTGACCTGACGCTGACGACTGAA 629  
|||||  
Db 7301 gtccacagaagctcacagctcaggtcagcagcatgaaggagcagcgtggaagacagt 7360  
|||||  
Qy 630 GTCCACAGAAGCTCAGCTGCCAGTGCACGATGAAGGAGCAGCGGTGGAAGACAGT 689  
|||||  
Db 7361 ggcctcacaagatgttcat 7380  
|||||  
Qy 690 GGGCCCTACAGATGTTTAT 709  
|||||

## RESULT 8

ID Q03607 standard; DNA; 330 BP.  
AC Q03607;  
DE Sequence encoding 4G12 monoclonal antibody (MAb) L chain V region.  
KW 4G12 MAb; human lung cancer; oesophageal carcinoma; ss.  
OS Synthetic.  
PN J02046289-A.  
PD 15-FEB-1990.  
PF 05-AUG-1988; 196647.  
PR 05-AUG-1988; JP-196647.  
PA (YOSH) Yoshitomi Pharm. Ind. KK.  
DR WPI; 90-094983/13.  
PT DNA base sequence coding for 4G12 monoclonal antibody - which reacts  
PT specifically with human lung cancer and oesophageal carcinoma.  
PS Claim 1; Page 545; 9pp; Japanese.  
CC The sequence (subclass Lambda) is determined by cloning  
CC cDNA of 4G12 MAb L chain using  
CC synthetic DNA/RNA of human Ab L chain C region as probe.  
CC See also Q03608-Q03610.  
SQ Sequence 330 BP; 75 A; 99 C; 88 G; 68 T;

Query Match 32.6%; Score 232; DB 1; Length 330;  
Best Local Similarity 85.2%; Pred. No. 5.62e-133;

Matches 281; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Db 1 tctgtgtgacgagcgcctcagtgctgcccagcagagaggtcaccatctcc 60  
|||||  
Qy 64 TCTGTCTGACACAGCGGCTCAGTCTCTGGGCGCGGAGGAGGTCCATCTCG 123  
|||||  
Db 61 tgcctggaagcagctccacattgggaataattatgtatcctgtaccagcagctccca 120  
|||||  
Qy 124 TGCACCTGGGAGCAGCTCCAACTTGGAGGTTATGATCTACATTGGTACCAGCAGCTCCA 183  
|||||  
Db 121 ggaacagcccaaaactcctcatttatgacaataataagcagccctcaggatctccgac 180  
|||||  
Qy 184 GGAACGGCGCCCAACTCTCATCTATGACATTAAACAGCGACGCTCAGGAATTTCTCAC 243  
|||||  
Db 181 cgattctctggtccaaagtctggcagcctcagccaccctgggcatcaccgagctccagact 240  
|||||  
Qy 244 CGATTCTCTGGCTCCAAAGTCTGGTACCGCGGCGCTCCCTGGCCATCCTGGGCTCCAGACT 303  
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Db 241 ggggagcagggccgattattactcgggaacatgggagcagcctgagctggtgggtattc 300  
|||||  
Qy 304 GAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTGAATGCTCAGGTATTC 363  
|||||  
Db 301 ggcgagggagcacaagctgacgctcctaggt 330  
|||||  
Qy 364 GGAGGAGGAGCGCGCTGACGCTCTTAGGT 393  
|||||

## RESULT 9

ID Q11187 standard; cDNA to mRNA; 318 BP.  
AC Q11187;  
DT 31-MAY-1991 (first entry)  
DE Immunoglobulin lambda chain constant region.  
KW Antibody; canine distemper virus; parvovirus; hepatitis; ss.  
OS Canis familiaris.  
PN EP-419858-A.  
PD 03-APR-1991.  
PF 24-AUG-1990; 116258.  
PR 25-AUG-1989; JP-219889.  
PR 30-SEP-1989; JP-255425.  
PR 07-JUN-1990; JP-150673.  
PA (KAGA) CHEMO-SERO-THERAP.  
PI Maeda H, Eda Y, Kimachi K, Ono Y, Tokiyoshi S;  
DR WPI; 91-095353/14.  
DR P-PSDB; R11366.  
PT Gene fragments coding for constant region of canine  
PT immunoglobulin(s) - used to produce mouse-dog antibodies for  
PT diagnosis, treatment and prevention of canine.  
PS Claim 6; Page 15; 49pp; English.  
CC The DNA encodes the constant region of canine Ig lambda chain. It can  
CC be used to produce mouse-dog chimeric antibodies for the diagnosis,  
CC treatment and prevention of canine diseases caused by e.g. canine  
CC distemper virus, canine parvovirus and canine hepatitis virus.  
CC See also Q11188-91.  
SQ Sequence 318 BP; 69 A; 115 C; 91 G; 43 T;

Query Match 31.5%; Score 224; DB 2; Length 318;  
Best Local Similarity 85.7%; Pred. No. 1.29e-127;  
Matches 269; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 1 cagcccaagcctccccctcggtcacactctcccgccctctctgagagcctcgcgcc 60  
|||||  
Qy 394 CAGCCCAAGGCTGCCCGCTCAGTCTGTCTCCCGCCCTCTCTGAGGAGCTTCAAGCC 453  
|||||  
Db 61 aacaagccaccctggtgtgctcctcagcagcttctaccacagcggtgacggtggcc 120



Query Match 29.4%; Score 209; DB 17; Length 816;  
Best Local Similarity 82.2%; Pred. No. 1.3e-117;  
Matches 286; Conservative 0; Mismatches 59; Indels 3; Gaps

[illegible]

Db	61	aacagggccacctgggtgtctctgcagtgactctatccccagcggtgtgcaggtggcc	120
Qy	454	AACAAGGCCACACTGCTGTGTCTCATAAGCTGACTTCTACCGGGAGCGGTGACAGTGGCC	513
Db	121	tggaaaggaagatggcaccgcccatcaaccaagggcctggagaccaccagccctccagacag	180
Qy	514	TGCAAGGCAGATAGCAGCCCGCTCAAGCGGGGAGTGGAGCCACCACACCTCCAAACAA	573
Db	181	agcaacaacaagtaacgcyggccagcagctacctgagcctgtcacccgaacagtggaatct	240
Qy	574	AGCAACAACAGTAGTCGGGCCAGCAGCTAGCTGAGGCTGACGCTGAGCAGTGGAGTCC	633
Db	241	cacagcagatcacctgccaggtcacgcacagggaggacactgtggagaagagtgtggct	300
Qy	634	CACAGAAGCTACAGCTGCCAGTTCACGGTACAGGGAGCACCGTGAGGAGACAGTGGCC	693
Db	301	ctctgcagagtgc	311
Qy	694	CCTACAGAATG	704

RESULT	14	
ID	Q64170 standard; cDNA to mRNA; 318 BP.	
AC	Q64170;	
DT	29-DEC-1994 (first entry)	
DE	Sequence of feline herpes virus (FHV-1) cDNA.	
KW	Feline herpes virus; FHV-1; monoclonal antibody; ss.	
OS	Felis catus.	
EH	Key	Location/Qualifiers
FT	CDS	1..318
ET	/*tag= a	
PN	W09412661-A.	
PD	09-JUN-1994.	
PE	25-NOV-1993; J01724.	
PF	28-NOV-1992; JP-341255.	
PP	(KAGA ) CHEMO SERO THERAPEUTIC RES INST.	
PA	Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;	
PI	WPI; 94-200288/24.	
DR	P-PSDB; R54096.	
DD	P-PSDB; R54096.	
PT	Feline monoclonal antibody and recombinant antibodies specific	
PT	for FHV-1 - for detection, treatment and prevention of FHV-1	
PT	infection.	
PP	Claim 20; Page 23-24; 53pp; Japanese.	
CC	The inventors claim a monoclonal antibody against feline herpes	
CC	virus (FHV-1), the sequence of which is given in Q64188, Q64169	
CC	and Q64170. They also claim a recombinant antibody against FHV-1	
CC	and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are	
CC	used in the detection, treatment and prevention of FHV-1. The	
CC	sequences of the CDRs in the VH of the recombinant anti-FHV-1	
CC	antibody are given in R54092. The sequences of the CDRs in the VL of	
CC	the recombinant anti-FHV-1 antibody are given in R54093. These CDR	
CC	sequences are claimed.	
SQ	Sequence 318 BP:	77 A; 106 G; 88 G; 47 T;

	Query Match	28.8%;	Score 205;	DB 11;	Length 318;
	Best Local Similarity	83.0%;	Pred. No. 6,54e-115;		
	Matches 258;	Conservative	0;	Mismatches 53;	Indels 0;
	Gaps	0;			
Db	1	cagcccaagtcggcccttcggtcacactttccacccctccagtcgagagctcagcgca	60		
Qy	394	CAGCCCAAGGTCGCCCTCGGTCATCTGTTCCCGCCCTCCCTCTGAGAGCTTCAAGCC	453		
Db	61	aaacaggccacctggtgtgtctgttcgttcgacttaccacccagcggtctgacggtggcc	120		

QY	454	AACAAGGCCACACTGGTGTGTCTCATNAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCC	513
Db	121	tggaaaggaagatggcaccoccccatcaccaaggggcgtggagaccaccaaagccctccagaag	180
QY	514	TGGAGGGCAGATACAGACGCCCGCTCAAGGGCGGAGTGGAGACCAACACCCCTCCAACAA	573
Db	181	agcaacaacaagtacgcygcagcagctacctgagccgtgtcaccgaagagatggaaatct	240
QY	574	AGCAACAACAGTACCCGGCCAGCAGCTACTCTGAGCTCAGCGCTTGACGAGTGGAAATCC	633
Db	241	cacagcagatataacctgccaggtccacgcagagggagcactgtggagaagatgtgtctc	300
QY	634	CACAGAGCTACAGTGCAGGCTCAGCATCAAGGGGACCCGTGGAGAGACAGCAGTGGCC	693
Db	301	cctgcagagtg	311
QY	694	CCTCAGAATG	704

RESULT	15	ID	Q98903 standard; cDNA; 330 BP.
AC	Q98903;	DT	11-FEB-1996 (first entry)
DE	Human tumor-associated Mab 123AV16 IgA-lambda 2 variable light region.	KE	Tumor-associated antigen; tumor therapy; bowel cancer therapy;
KW	monoclonal antibody; IgA; immunoglobulin; variable light chain;	KW	CDR; complementarity determining region; da.
KW	Homo sapiens.	OS	Homo sapiens.
FH	Key	Location/Qualifiers	
FT	CDS	1..330	
FT	/tag= a		
FT	misc_binding	67..106	
FT	/tag= b		
FT	/note= "complementarity determining region-1"		
FT	misc_binding	152..173	
FT	/tag= c		
FT	/note= "complementarity determining region-2"		
FT	misc_binding	270..303	
FT	/tag= d		
FT	/note= "complementarity determining region-3"		
FT	misc_binding	304..330	
PN	W09522613-Al.	PD	24-AUG-1995.
PF	16-FEB-1995; E00581.	PP	22-FEB-1994; US-199911.
PR	(ALKU ) AKZO NOBEL NV.	PA	Haspel MW, Kobrin BJ;
PI	WPI; 95-302719/39.	PI	P-PSDB; R80621.
DR	Antibody variable regions specific for human colon tumour antigen -	PT	useful in prepn. of immunoconjugates to target drugs and
PT	radio-metals for therapy and diagnostic imaging of tumours	PT	Claim 1; Page 32-33; 42pp; English.
PS	This cDNA encodes the variable light chain region of human	CC	monoclonal antibody 123AV16 IgA-lambda2 which is specific for a
CC	human colon tumor antigen. This sequence contains 3 CDRs (CDR1, CDR2	CC	and CDR3). The specificity of the CDRs may be useful in the
CC	preparation of immunoconjugates for the detection, diagnosis and	CC	treatment of human colon tumors. Also, the CDR sequences provide
CC	information for manufacturing chimeric and multifunctional	CC	antibodies. The MAb is produced from peripheral blood B-lymphocytes
CC	of cancer patients actively immunized with autologous colon tumor	CC	antigen. The B-cells were transformed by Epstein-Barr virus.
CC	Sequence 330 BP; 75 A; 103 C; 84 G; 68 T;	SQ	

Sequence	330 BP;	75 A;	103 C;	84 G;	68 T;
SQ					

Dec 17 22:38

US-08-487-550-9.rng

19

Query Match 28.3%; Score 201; DB 16; Length 330;  
Best Local Similarity 80.5%; Pred. No. 3.05e-112;  
Matches 265; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Db 2 agtctcggttgacgcagccgcctcagtatctcgcgcccccagagacagaaggtcaaccatct 61
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Qy 62 AGTCTCTCTGCACACAGCGCGCCCTCAGTCTGTGGGGCCCGCAGGTCAGAGGTCACCATCT 121

Db 62 cctgctctggaaaccagctccaaacattgggaataattttgtatctctgtaccacaattcc 121
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Qy 122 CGTGCACTGGGAGCACCCTCCACACTTGGAGGTTATGATCTACATTGGTACCAGAGCTCC 181

Db 122 caggagacagcccccacaaactcctctattatgacaataataagcaccctcaggggttctctg 181
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Qy 182 CAGGACGCGCCCGCAACTCTCTCATATGACATTAACAGCGACCCCTCAGGAATTCTTG 241

Db 182 accgattctctgggtccaaagtctggcagctcagccaccctgggcatcacgggactccaga 241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 242 ACCGATTCTCTGGCTCCAAAGTCTGGTACCGCGGCGCTCCCTGGCCATCAGTGGGCTCCAGA 301

Db 242 ctgggagcagagccgattattactcggggaacatgggataccaagactgcgcgctgggtgt 301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 302 CTCAGGATCAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCCTGAATGCTCAGGTAT 361

Db 302 tcggcgaggaggaaccaagctgaccgtccta 330
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Qy 362 TCGGAGGAGGACCGCGGCTGACCGCTCCTTA 390
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Search completed: Tue Dec 17 22:52:14 1996  
Job time : 68 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 22:52:36 1996; MasPar time 273.63 Seconds  
934.180 Million cell updates/sec

Title: >US-08-487-550-9

Description: (1-711) from US08487550.seq

Perfect Score: 711  
N.A. Sequence: 1 ATAGGGTCCCCGCTCACT.....CCCCACAGAAATTTCATGA 711  
Comp: TACTCCACGGGGCAGTCA.....GGGGATCTTACAAAGTACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 514334 seqs. 179763086 bases x 2

Post-processing: Minimum Match 0%

### Listing first 45 summaries

Database: EST-SMS

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Database:
EST-ST5
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST23 24:EST24 25:EST25 26:EST26
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Database:

CMU-SLS-LS3

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103:EST96 104:EST97 105:EST98 106:EST99 107:EST100

108:EST101 109:gnEST1 110:gnEST2 111:gnEST3 112:gnEST4

113:gnEST5 114:gnEST6 115:gnEST7 116:gnEST8 117:gnEST9

118:gnEST10 119:gnEST11 120:gnEST12 121:gnEST13

122:gnEST14 123:gnEST15 124:gnSTS1 125:gnSTS2 126:enEST

127:enEST2 128:enEST3 129:enEST4 130:enEST5 131:enEST6

Statistics: Mean 10.505; Variance 2.161; scale 4.860

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			ID	Description	Pred. No.
		Match	Length	DB			
c 1	330	46.4	570	136	HS777270	yy91f04.s1 Homo sapie	0.00e+00
c 2	330	46.4	570	116	N32777	yy91f04.s1 Homo sapie	0.00e+00
c 3	299	42.1	469	66	R73382	yj92all.s1 Homo sapie	0.00e+00
c 4	297	41.8	471	67	R73492	yj93d09.s1 Homo sapie	0.00e+00
c 5	296	41.6	376	12	H26070	y152h11.r1 Homo sapie	0.00e+00
c 6	296	41.6	463	11	H25405	y146h10.s1 Homo sapie	0.00e+00
c 7	290	40.8	436	61	R55314	yj77h05.s1 Homo sapie	0.00e+00
c 8	285	40.1	425	59	R48172	yj66g10.r1 Homo sapie	0.00e+00
c 9	282	39.7	491	69	R83196	yp87h10.s1 Homo sapie	0.00e+00
c 10	279	39.2	297	124	G13531	human STS SHGC-11074.	0.00e+00
c 11	277	39.0	329	22	H60966	yr22c08.r1 Homo sapie	0.00e+00
c 12	277	39.0	435	71	R88208	yp08b06.s1 Homo sapie	0.00e+00
c 13	275	38.7	443	137	HS851303	za22c10.s1 Homo sapie	0.00e+00
c 14	273	38.4	487	69	R83348	yp06b01.r1 Homo sapie	0.00e+00
c 15	272	38.3	356	24	H67544	yv68e12.r1 Homo sapie	0.00e+00
c 16	272	38.3	431	11	H26023	y152h11.s1 Homo sapie	0.00e+00
c 17	270	38.0	428	11	H25133	y143e10.r1 Homo sapie	0.00e+00
c 18	270	38.0	470	8	H15922	y127e07.s1 Homo sapie	0.00e+00
c 19	268	37.7	325	60	R49901	yj58a10.r1 Homo sapie	0.00e+00
c 20	267	37.6	428	17	H45690	yp23e04.s1 Homo sapie	0.00e+00
c 21	267	37.6	445	99	T67053	yv52e05.s1 Homo sapie	0.00e+00
c 22	267	37.6	509	17	H45859	yp22e04.r1 Homo sapie	0.00e+00
c 23	266	37.4	446	13	H30137	yv59f07.r1 Homo sapie	0.00e+00
c 24	266	37.4	512	88	T50252	yv78b01.s1 Homo sapie	0.00e+00
c 25	264	37.1	410	66	R72739	yj91a09.s1 Homo sapie	0.00e+00
c 26	264	37.1	516	90	T57780	ycl4a06.s1 Homo sapie	0.00e+00
c 27	261	36.7	387	19	H53265	yp07g04.s1 Homo sapie	0.00e+00
c 28	261	36.7	451	11	H23960	y130a03.s1 Homo sapie	0.00e+00
c 29	258	36.3	365	11	H25486	y147f08.r1 Homo sapie	0.00e+00
c 30	254	35.7	350	12	H26065	y152g09.r1 Homo sapie	0.00e+00
c 31	253	35.6	434	10	H21406	y132h05.s1 Homo sapie	0.00e+00
c 32	251	35.3	428	101	T41479	yv53f06.r1 Homo sapie	0.00e+00
c 33	250	35.2	277	85	T39258	ya02f12.r2 Homo sapie	0.00e+00
c 34	249	35.0	436	107	T94334	ye31e10.s1 Homo sapie	0.00e+00
c 35	249	35.0	480	100	T70889	y142h08.s1 Homo sapie	0.00e+00
c 36	247	34.7	379	11	H24839	y146b06.s1 Homo sapie	0.00e+00
c 37	247	34.7	381	17	H43633	yp24a07.s1 Homo sapie	0.00e+00
c 38	246	34.6	346	11	H25740	y153h11.r1 Homo sapie	0.00e+00
c 39	245	34.5	419	10	T21654	y134c12.r1 Homo sapie	0.00e+00
c 40	245	34.5	422	12	H28778	yp03e07.s1 Homo sapie	0.00e+00
c 41	245	34.5	436	64	R64294	y121h08.r1 Homo sapie	0.00e+00
c 42	243	34.2	397	106	T92408	y119g05.r1 Homo sapie	0.00e+00
c 43	243	34.2	405	8	H14996	y126a12.s1 Homo sapie	0.00e+00
c 44	241	33.9	374	11	H25441	y147f08.s1 Homo sapie	0.00e+00
c 45	241	33.9	406	17	H43557	ye64f09.s1 Homo sapie	0.00e+00

## ALIGNMENTS

## RESULT



Query Match	46.4%	Score 330;	DB 136;	Length 570;
Best Local Similarity	91.7%;	Pred. No. 0.00e+00;		
Matches 399;	Conservative 0;	Mismatches 29;	Indels 7;	Gaps 7;

Cp	351	ATTACGCTGCTCATAGCACTGGCAGTAATAATACGCTCATCTCATCTGTGGAGCC	292
Ds	556	agaatggtcaggga 570	
Cp	291	ACTGATGCCAGGGA 277	
RESULTS	2		
LOCUS	N32777	570 bp mRNA	EST
DEFINITION	Y9104.s1 Homo sapiens cDNA clone 259615 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);		
ACCESSION	N32777		
NTD	g1153176		
KEYWORDS	EST.		
SOURCE	human clone=259615 primer=ml3 -40 forward library=Soares placenta 8to9weeks 2N6H98to9W vector=PT3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsetel=Not I Rset2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - oligo (dT) primer [5'-TGTTACCAATCTCAAGTCAGGCGCGCGCATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Ronaldo.		
ORGANISM	Homo sapiens		
	Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 570)		
AUTHORS	Hillier, L., Clark, N., Duboue, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.		
TITLE	The WashU-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu High quality sequence stops: 356 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.		
FEATURES	NCBI gi: 1153176		
source	Location/Qualifiers		
	1..570		
	/organism="Homo sapiens"		
	/clone="259615"		
	/note="human"		
	<1..>570		
BASE COUNT	103 a 140 c 180 g 145 t		2 others
ORIGIN			
Query Match	46.4%;	Score 330;	DB 116; Length 570;
Best Local Similarity	91.7%;	Pred. No. 0.00e+000;	
Matches	399; Conservative	0; Mismatches	29; Indels 7; Gaps 7;





Db 71 gnaactctgttccgcctcctctgaggagcttcaaggccaacaaaggccacactggtgtg 130  
|||||  
Qy 416 -TCACTCTGTTCCGGCCCTCTCTGAGGAGCTTCAAGCCAAGCCACACTGTGTGT 474  
|||||  
Db 131 ctcataagtgactctaccggagagcgtgacagtggcctgggaagcagcatagtcagc 190  
|||||  
Qy 475 CTATAAGTGACTTCTACCCGGAGCGGTGACAGTGGCCCTGG-AAGGCAG-ATAG-CAGC 531  
|||||  
Db 191 ccngtcaagntcggagtagngagaccacacacccctccaaacaaagcaacaagaagtcagc 250  
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Qy 532 CCGCTCAAGG-CGGGAGTGGAGACACACACACCCCTCCAAACAAAGCAACAACAGTACGC 590  
|||||  
Db 251 gggcagcagctatctgagcctgacgctgagcagtggaagtccacagaagctnccagctg 310  
|||||  
Qy 591 GGGCAGCAGCTACCTGAGCCTGAGCCTGAGCAGTGGAGTCCCAAGAGCTACAGCTG 650  
|||||  
Db 311 ccaggtacgcatgagggagcaccgtggaagacattngccctncagaatnt 366  
|||||  
Qy 651 CCAGGTACCGATGAAGGAGACCCGTGGAGACAGAGTGGCCCTTACAGAAATGTT 706  
|||||

RESULT 6 H25405 463 bp mRNA EST 10-JUL-1995  
LOCUS y146h10.e1 Homo sapiens cDNA clone 161347 3' similar to gb:X57809  
DEFINITION IG LAMBDA CHAIN C REGIONS (HUMAN);  
ACCESSION H25405  
NID g894528  
KEYWORDS EST.  
SOURCE human clone=161347 library=Soares breast 3NbHBst vector=pT73D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=Promega -21ml3 Reitel=Not I Rsite2=Eco RI Adult  
human. 1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5' TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pT73 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 20. Library constructed by Bento Soares  
and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 463)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

The WashU-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 313  
Source: IMAGE Consortium, L1NL  
This clone is available royalty-free through L1NL; contact the  
IMAGE Consortium (info@image.l1nl.gov) for further information.

FEATURES source  
NCBI gi: 894528 Location/Qualifiers  
1..463  
/organism="Homo sapiens"  
/clone="161347"  
/note="human"  
BASE COUNT 77 a 111 c 141 g 122 t 12 others  
ORIGIN

Query Match 41.6%; Score 296; DB 11; Length 463;  
Best Local Similarity 94.4%; Pred. No. 0.00e+00;  
Matches 306; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 140 atgaacattctnaggggccactntcttccacaggtgctcccttcacgtgacctggc 199  
|||||  
Cp 709 ATGACATTTCTGTAGGGGCCACTGCTCTCCAGCGGTGCTCCCTTCATGCGTACCTGGC 650  
|||||  
Db 200 agctgtagctctctgggaacttccactgctcagcgctcaggtcagatagctggtggcg 259  
|||||  
Cp 649 AGCTGTAGCTTCTGTGGCACTTCCACTGCTCAGGCGTCAAGGCTCAGGTAGCTGCTGGCGC 590  
|||||

Db 260 cgtactgttctgttctgttggagggtntggtgctccactcccgcttgacggggc 319  
|||||  
Cp 589 CGTACTGTGTTGCTTCTTTGGAGGGGTGCTGCTCCACTCCCGGCTTACGGGGC 530  
|||||

Db 320 tgtatctgcttccagggcactnccaggtcccgggtagagtcacttatgacacaca 379  
|||||  
Cp 529 TCGTATCTGCTTCCAGGCCACTCTCAGCGCTCCGGGTGAGAACTTATGACACACA 470  
|||||

Db 380 ccagtttngccttttggcctnaagctccccagaggaggcggaacagagttaccagg 439  
|||||

Cp 469 CCAGTGTGGCCTTCTTGGCTTGAAGCTCTCAGAGGAGGAGGGGGGACAGAGTACCCGAGG 410  
|||||

Db 440 ggcagccttnggttaacnaggga 463  
|||||

Cp 409 GGCAGCCTTGGCGTCACTAGGA 386  
|||||

## RESULT 7

LOCUS R55314 436 bp mRNA EST 22-MAY-1995  
DEFINITION y77h05.e1 Homo sapiens cDNA clone 154809 3' similar to gb:X57809  
IG LAMBDA CHAIN C REGIONS (HUMAN);  
ACCESSION R55314  
NID 9824609  
KEYWORDS EST.

## SOURCE

human clones=154809 library=Soares breast 2NbHBst vector=pT73D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=Promega -21ml3 Reitel=Not I Rsite2=Eco RI Adult  
female. 1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5' TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pT73 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 230. Library constructed by Bento  
Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 436)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence steps: 361  
Source: IMAGE Consortium, LINL  
This clone is available royalty-free through LINL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 824609  
FEATURES  
source  
Location/Qualifiers  
1..436  
/organism="Homo sapiens"  
/clone="154809"  
/note="human"  
BASE COUNT 74 a 101 c 142 g 111 t 8 others  
ORIGIN

Query Match 40.8%; Score 290; DB 61; Length 436;  
Best Local Similarity 97.0%; Pred. No. 0.00e+00;  
Matches 292; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 136 atgaacattgttagggccaactgtcttcacaggtgtctccttcattcgtagctggc 195  
|||||  
Cp 709 ATGACATTCTGTAGGGCCACTGTCTTCTCCACGGTGTCCCTTCATCGTAGCTGCG 650  
Db 196 agctgtagctttgtgggaactccaactgtcaggcgtcaggctcaggtagctgtgccc 255  
|||||  
Cp 649 AGCTGTAGCTTCTGTGGGACTTCCACTGCTCAGCGGTCAAGGCTCAGGTAGCTGTGCGG 590  
Db 256 cgtactgttctgttctgttggagggtgtggtgtccantcccgcttgacggggc 315  
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Cp 589 CGTACTGTGTGCTTGTGTTGGAGGGTGTGGTGTCTCCACTCCGGCTTGACGGGGC 530  
Db 316 tgctatctgcttccaggncactntcacgntccgggtagaagtcacttatgagacaca 375  
|||||  
Cp 529 TGTATCTGCTTCCAGGCCACTGTCCAGGGTCCCGGGTAGAAGTCACTTATGAGACACA 470  
Db 376 ccagtgctgcttctgttgcctgaagctcctcagagganggtnggaacagatnacagagg 435  
|||||  
Cp 469 CCAGTGTGCTTGTGCTTGAAGCTCTCAGAGGGGGGGGAAACAGATGACCGAGG 410  
Db 436 g 436  
Cp 409 C 409  
RESULT 8  
LOCUS R48172 425 bp mRNA EST 18-MAY-1995  
DEFINITION yj66g10.r1 Homo sapiens cDNA clone 153762 5' similar to gb:K57809  
IG LAMBDA CHAIN C REGIONS (HUMAN);  
ACCESSION R48172  
NID g810198  
KEYWORDS NID  
SOURCE human clone=153762 library=Soares breast 2NblBst vector=pT7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer=M13Rp1 Reitel=Not I Reite?=Eco RI Adult female.  
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGGCCCTTTTITTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pT7T3 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 230. Library constructed by Bento  
Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 425)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence steps: 263  
Source: IMAGE Consortium, LINL  
This clone is available royalty-free through LINL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 810198  
FEATURES  
source  
Location/Qualifiers  
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/organism="Homo sapiens"  
/clone="153762"  
/note="human"  
BASE COUNT 98 a 122 c 121 g 78 t 6 others  
ORIGIN

Query Match 40.1%; Score 285; DB 59; Length 425;  
Best Local Similarity 92.4%; Pred. No. 0.00e+00;  
Matches 352; Conservative 0; Mismatches 21; Indels 8; Gaps 8;

Db 3 gatagcagctgacttctgggtattcggcgaggaccacaaactgccgtctcaggctcag 62  
|||||

Qy 337 CACAGCAGCCTGATCTCAGGTATTCCGAGGAGGAGCCCGCTGACCGTCTCAGTCTCAG 396  
|||||

Db 63 cccaaggctgccctccggtcactctgttcccgcctctctgaggagcttcaagccaac 122  
|||||

Qy 397 CCAAGGCTGCCCGCTCGCTCCTCTGTTCCCGCTCTCTGTGAGGAGCTTCAAGCCAAC 456  
|||||

Db 123 aagggcacactggtgtgtctcataagtgaacttaccgggagcggtgacagtgccgtgg 182  
|||||

Qy 457 AAGGCCACACTGCTGTCTCATTAAGTCACTTCTACCGGGAGCGCTGACAGTGCCTCG 516  
|||||

Db 183 gaaggagatagcagcccgctcaaggggggagtgagaccaccacacccctcccaacaaag 242  
|||||

Qy 517 -AAGGCAGATAGCAGCGCCGCTCAAGCGGGAGTGGAGACACACACCCCTCCCAACAAAG 575  
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Db 243 caacaagaatcagcgccagcagctatctgagcctgagcctgagcagtgagtggaagtc 302  
|||||

Qy 576 CAACAACAGTACCGCGCAGCAGCTACCTGAGCGCTGAGCAGCT-GGAGTCCC 634  
 Db 303 acagaaggttacaggtccaggttcacgttgcaaggggagcaccgtgggagagacagct 362  
 Qy 635 ACAGAGCT-ACAGCTGCCAGG-TCACGATGAGAGG-AGCACCGTGG-AGAG-ACAGT 689  
 Db 363 nggccttacagatttttnt 383  
 Qy 690 -GGCCCTACAGAAATGTTTAT 709

RESULT 9  
 LOCUS R83196 491 bp mRNA EST 04-AUG-1995  
 DEFINITION yp87h10.s1 Homo sapiens cDNA clone 194467 3' similar to gb:X57809  
 1G LAMBDA CHAIN C REGIONS (HUMAN);  
 ACCESSION R83196  
 NID 928073  
 KEYWORDS EST.  
 SOURCE human clone=194467 library=Soares fetal liver spleen INFLS  
 vector=p7n3D (Pharmacia) with a modified polylinker host=DH10B  
 (ampicillin resistant) primer=Promega -21ml3 Reitel=Pac I  
 Reitel=Eco RI Liver and spleen from a 20 week-post conception male  
 fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer  
 [5' ACTGGAGAAATTAATGAATCTTTTTTTTTTTTTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
 digested with Pac I and cloned into the Pac I and Eco RI sites of  
 the modified p7T3 vector. Library went through one round of  
 normalization. Library constructed by Bento Soares and M.Fatima  
 Bonaldo.

## ORGANISM

Homo sapiens  
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.

## REFERENCE

1 (bases 1 to 491)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawking, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

## TITLE

The WashU-Merck EST Project

## COMMENT

Unpublished (1995)

Contact: Wilton RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

High quality sequence scope: 229

Source: IMAGE Consortium, LBNL

This clone is available royalty-free through LBNL; contact the  
 IMAGE Consortium (info@image.lbnl.gov) for further information.

## FEATURES

## source

NCBI gi: 928073  
 Location/Qualifiers  
 1..491  
 /organism="Homo sapiens"  
 /clone="194467"  
 /note="human"

## BASE COUNT

82 a 118 c 147 g 132 t 12 others

## ORIGIN

Query Match 39.7%; Score 282; DB 69; Length 491;  
 Best Local Similarity 92.2%; Pred. No. 0.00e+00;  
 Matches 319; Conservative 0; Mismatches 23; Indels 4; Gaps 4;  
 Db 147 atgaacattctgtaggcccaactgtcttctccacaggtgtctccctcatcgtagctggc 206  
 Cp 709 ATGAACATTCTGTAGGGCCACTGTCTTCTCCACGGTGTCCCTTCATGCGTGACCTGGC 650  
 Db 207 agctntagcttctgtgggaattccactgtctcaggtcaggtcaggttagctgtgctggc 266  
 Cp 649 AGCTGTAGCTTCTGTGGCACTTCCACTGCTCAGGCTCAGGCTCAGTGTGCTGGCG 590  
 Db 267 cgtactgt 326  
 Cp 589 CGTACTGT 530  
 Db 327 tgcctatgccttccaggggaactttcacggctccnggtagaagtcacttntgagacaca 386  
 Cp 529 TCGTATCTGCTTCCAGGCCACTGTCCAGGCTCCCGGCTAGAGTCACTTATGACACACA 470  
 Db 387 ccagntgtgctgt 445  
 Cp 469 CCAGTGTGCGCTTGT 411  
 Db 446 ggggcagc-ttnggttancatgaagaccgtcagttng-tcctctctc 489  
 Cp 410 GGGCAGCGCTTGGGCTGACCTAGACCGTCCGCGGTCCCTCCTC 365

## RESULT 10

LOCUS G13531 297 bp DNA STS 04-JAN-1996  
 DEFINITION human STS SHGC-11074.  
 ACCESSION G13531  
 NID g1129270  
 KEYWORDS STS sequence; primer; sequence tagged site.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
 Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 297)  
 AUTHORS Myers, R.M.  
 JOURNAL Unpublished (1995)  
 COMMENT

Contact: Richard M. Myers  
 Stanford Human Genome Center (SHGC)  
 Stanford University School of Medicine  
 Department of Genetics, M-344, Stanford, CA 94305, USA  
 Tel: 4157259687  
 Fax: 4157259689  
 Email: myers@shgc.stanford.edu

Primer A: TAGTCAGCCCAAGGCTG

Primer B: TCGCACTTCCACTGCTCAG

STS size: 247

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30





Db 242 tgagccgcagcagctggaagctccacagaagctacagctgccagctcacgcctgaagta 301  
Qy 611 TGAGCCTTGACGACTGGAAGTCCACAGAAGCTACAGTCCAGGTACGCATGAAGGA 670  
Db 302 gcacgctggagaagacagt 320  
Qy 671 GCACCTGGAGAAGACAGT 689

RESULT	12
LOCUS	R88208 435 bp mRNA 16-AUG-1995
DEFINITION	yp08b06.s1 Homo sapiens cDNA clone 186803 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);.
ACCESSION	R88208
NID	9947021
KEYWORDS	EST.
SOURCE	human clone=186803 library=Soares breast 3NbHBst vector=p7T73D (Pharmacia) with a modified polylinker host=DHI08 (ampicillin resistant) primer=Promega -21ml3 Reitel=Not I Rsite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACAACTGAGTCGGAGCGCCGCTTTTTTTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of modified p7T73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcoteriyii; Chonata; Tetrapoda; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 435)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

**TITLE**

JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 241  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact  
IMAGE Consortium (info@image.llnl.gov) for further info

## FEATURES

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/cloned="186803"
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Cp 709 ATGAACATTTCTGAGGGCCACTGTCTTCTCCAGGTGCTCCCTTCATCGTGACCTGC 650  
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Cp 589 CGTACTTGTGTGCTTGTCTTGAGA GGGTGTGTGTGCTCTCACTCCCGCCTTGACGGGGC 530  
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RESULT 13

ID HS951303 standard; RNA; EST; 443 BP.  
AC N64851;  
DT 02-MAR-1996 (Rel. 47, Created)  
DT 02-MAR-1996 (Rel. 47, Last updated, Version 1)  
DE za22c10.s1 Homo sapiens cDNA clone 295298 3' similar to gb:X57809  
DE IG LAMBDA CHINA C REGIONS (HUMAN);

OS Homo sapiens (human)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.  
ESL.

RN	[1]
RP	I-443
RA	Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
RA	Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA	Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
RA	Trevasakis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;
RT	"The WashU-Merck EST Project";
RL	Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University  
CC School of Medicine 4444 Forest Park Parkway, Box 501, St. Louis,  
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:  
CC est@wustl.edu High quality sequence stops: 318 Source: IMAGE  
CC Consortium, LLNL This clone is available royalty-free through LLNL  
CC ; contact the IMAGE Consortium (info@image.llnl.gov) for further  
CC information. NCBI gi: 1212680

EH	Key	Location/Qualifiers
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Best Local Similarity 95.4%; Pred. No. 0.00e+00;  
Matches 288; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.

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Cp 649 AGCTGTAGCTTCTGTGGGACTTCCACTGCTCAGGCCGTCAGGTAGCTGGCCG 590

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Cp 589 CGTACTTGTTGCTTGTGAGGGTGGTGGTCTCCACTCCCGCCCTGACGGGC 530

Db 296 tactatctgccttccaggccactatcacqqgqctcccqqqtacaaqtacacttatqagcac 355

Cp 529 TGCTATCTGCCTTCCAGGCCACTGTCAAGG-CTCCCGGGTAGAAGTCACTTATGAGACAC 471

Db 356 accagtgtngqccctgttgggttgaagctccccagaggagggcnggaacaaagtaaccn 415

Cp 470 ACCAGTGT-GGCCTTGTGGCTTGAAGCTCCTCAGAGGA-GGGCGGGAACAGAGTGACCG 413

Db 416 aggggggcanccttgggqtna 436

Cp 412 AGGGG-CAGCCTTGGGCTGA 393

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	H67544	yu6e12.r1 Homo sapiens cDNA clone 238990 5' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN) ;.				

**NID**  
**KEYWORDS**  
**SOURCE**  
q1026284  
EST.  
human clone=238990 primer=M13Rp1 library=Weizmann Olfactory  
Epithelium vector=pBluescript SK- host=501R cells (kanamycin  
resistant) Rsite=EcoRI Rsite2=XhoI from 35 year old female. The  
cDNA was oligo (dT) primed with an XhoI restriction enzyme  
recognition site and an 18 base poly dT sequence. For the 5' end  
the synthesized cDNA termini were treated with T4 DNA polymerase  
and EcoRI adaptors were ligated to the blunt ends.

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chondata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 356)

REFERENCE  
HILLIER, L., CLARK, N., DUBUQUE, T., ELLISTON, K., HAWKINS, M.,

**AUTHORS** Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Cp 709 ATGAACATTCTGTAGGGGCCACTCTCTTCCACGGTGCTCCCTTCATCGCTGACCTGGC 650

Cp 649 AGCTGTAGTTCCTGTGGACTTCCACTGCTCAGGGCGTCAGGCTCAGGTAGCTGCTGGCG 590

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529 TGGTATCTGCTTCCAGSSCCACTCTCACGGCTCCGGGTAGAGTCACTTATAGACACA 470

469 CCAGTGTGGCCTGTGTGGCTTCAAGSCTCCTCAGAGGAGGGGGGGAACAGACTGACCGAGG 410

DD 440 99 441  
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Cp 409 GG 408

RESULT	14	p83348	187 bp	rDNA	EST	04-MTC-1005
LOCUS						

IG LAMBDA CHAIN C REGIONS (HUMAN);

NID 9978725  
KEYWORDS EST.  
SOURCE human clone=186601 library=Soares breast 3NbHBst vector=pT7T3D

human. Left strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCGATGGAGGCGGCCCTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of modified pR73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fátima Bonaldo.

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

**AUTHORS**  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Willson, R.

**JOURNAL Unpublished (1995)**

WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
WashU-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 255  
Source: IMAGE Consortium, L1NL  
This clone is available royalty-free through L1NL ; contact the  
IMAGE Consortium (info@image.l1nl.gov) for further information.

NCBI gi: 1026284  
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BASE COUNT 88 a 108 c 95 g 63 t 2 others  
ORIGIN

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Qy 379 CTGACCGCTCTAGGTGAGCCCAAGGTCGCCCTCGGTCTCTCTCTCTCTCTCT 438  
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Qy 499 GCCCTGACAGTGGCCTGGAGGCGAGATAGCAGCCCGCTCAAGGCGGAGCTG 558  
Db 180 acacctccaaacaagaacaaagaacaaagaacaaagaacaaagaacaaagaac 239  
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Search completed: Tue Dec 17 22:57:19 1996  
Job time : 283 secs.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**KEYWORDS** complementarity-determining region; constant region; immunoglobulin gamma-chain; immunoglobulin heavy chain;

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QY	496	GGGGCGCACAGGGCCCTGGGCTGCTGTCAAGGCACTACTTCCCGACCGGTGACGGTG	555
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## RESULT 2

LOCUS A21385 1549 bp RNA PAT 19-DEC-1994

DEFINITION Plasmid DNA with human cDNA insert.

ACCESSION A21385

NID g583507

KEYWORDS .

SOURCE .

ORGANISM .

REFERENCE 1 (bases 1 to 1549)

AUTHORS .

TITLE RECOMBINANT PROTEIN WHICH BINDS TO A COMPLEX VIRAL ANTIGEN OF HIV-1

JOURNAL Patent: WO 9118983-A 1 12-DEC-1991;

COMMENT NCBI gi: 583507

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BASE COUNT 362 a 463 c 417 g 307 t

## ORIGIN

Query Match 73.3%; Score 1049; DB 36; Length 1549;  
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Matches 1235; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

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Db 903 tcttctctctcccccaaaaacccaagacacacctcatgatctcccgacacctcaggttca 962  
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RESULT 3 LOCUS 109303 1135 bp PAT 14-NOV-1994

DEFINITION Sequence 5 from patent WO 8902922.

ACCESSION 109303

NTD 9587989

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1135)

AUTHORS Capon,D.J. and Gregory,T.J.

TITLE ADHESION VARIANTS

JOURNAL Patent: WO 8902922-A 5 06-APR-1989;

COMMENT NCBI gi: 587989

FEATURES

source Location/Qualifiers

1..1135

BASE COUNT 255 a 385 c 303 g 192 t

ORIGIN

Query Match

Best Local Similarity 71.6%; Score 1024; DB 37; Length 1135;

Matches 1079; Conservative 0; Mismatches 43; Indels 2; Gaps 2;

Db 1 gaattctgtcaetgccgggacagccgtatattactgtgcgagagc-caccttttgc 59  
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QY 548 TGACGCTGTCTGGAACCTCAGCGCCCTGACACAGCGCGGTGCACACTTCCCGGCTGTCC 607  
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QY 608 TAGCTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCAGCTGG 667  
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**TITLE** Humanized monoclonal antibody CAMPATH-1H: myeloma cell expression of genomic constructs, nucleotide sequence of cDNA constructs and comparison of effector mechanisms of myeloma and Chinese hamster ovary cell-derived material

**JOURNAL** Clin. Exp. Immunol. 87 (1), 105-110 (1992)

**MEDLINE** 92127884

**REMARK** GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 79307] from the original journal article. This sequence comes from Figure 2.a.

NCBI gi: 243865

Location/Qualifiers

source

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/organism="Homo sapiens"

/note="human"

36..1448

/gene="Ig gamma&gt;"

/note="This sequence comes from Figure 2.a. NCBI gi:

243866"

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BASE COUNT 352 a 466 c 383 g 264 t

ORIGIN

Query Match

Best Local Similarity 70.1%; Score 1003; DB 59; Length 1465;

Matches 1019; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 414 ttgtattatgggtgaaggagcctctcacagtctctcagctcctcaccacgaagggcca 473

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Qy 517 TCCTGTGTAAGACTACTTCCCGGACCGGTGACGGTGTGTTGGAACTCAGGCGCCCTG 576

Db 594 accagggcgtcacacttcccggtgctctacagctcctcaggactactcctcagc 653

Qy 577 ACCAGGGCGTGCACACTTCCGGCTGCTCTACAGTCTCTCAGGACTCTACTCCCTCAGC 636

Db 654 agcgtggtgacgtgacctcagcagcttgggacccagacctacatctgcaacgtgaat 713

Qy 637 AGCGTGTGACGTGCTCTCAGAGCTTGGGACCCAGACCTACATCTGCAACGTGAAT 696

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Qy 697 CACAGCCAGCAACACAGGTGACAGAGGAGGAGCCCAATCTTGTGACAAACT 756

Db 774 cacatgcccacgtgcccagcaactgaaactctggggggagccgtcagttctcttc 833

Qy 757 CACATGCCCCACCGTGCACAGCACTGAACTCTCTGGGGGACCGGTCTTCTCTTC 816

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Qy 817 CCCCCAAAACCAAGACACCCCTCATGATCTCCCGAGCCCTGAGTCACATGCGTGGTG 876

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Qy 997 AGCGTCTCAGCGCTCTGCACAGGACTGGCTCAATGGCAAGGAGTACAAGTGCAGAGTC 1056

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Qy 1417 TCTCCGGGTAAATGA 1431

RESULT 6

LOCUS A07562 1341 bp DNA PAT 28-JUN-1993

DEFINITION DNA sequence of chimeric monoclonal TSH antibody, gamma chain.

ACCESSION A07562

NID 9413075

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 1341)

AUTHORS Kalura, B. and Lenz, H.

TITLE Diagnostic method using chimeric antibodies

JOURNAL Patent: EP 0378175-A 13 18-JUL-1990;

COMMENT BOEHRINGER MANNHEIM GMBH

NCBI gi: 413075

FEATURES Location/Qualifiers

source 1..1341

/organism="Artificial sequences"





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REFERENCE 1 (bases 1 to 768)
AUTHORS
  Filpula,D.
TITLE
  H. sapiens mRNA for immunoglobulin G1, Fc fragment
JOURNAL
  Unpublished
REFERENCE 2 (bases 1 to 768)
AUTHORS
  Filpula,D.R.
TITLE
  Direct Submission
JOURNAL
  Submitted (10-FEB-1993) to the EMBL/GenBank/DBJ databases. D.R.
  Filpula, Enzon Labs, 16020 Industrial Drive, Gaithersburg, Maryland
  20877, USA
COMMENT
  NCBI gi: 33068
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ACCESSION  X81695
NID         9940515
KEYWORDS   constant region; immunoglobulin heavy chain; variable region.
SOURCE     human.
ORGANISM   Homo sapiens
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REFERENCE  1 (bases 1 to 1163)
AUTHORS    Khamlichi,A.A., Aoucuturier,P., Preud'homme,J.L. and Cogne,M.
TITLE      Structure of abnormal heavy chains in human heavy-chain-deposition
            disease
JOURNAL    Eur. J. Biochem. 229 (1), 54-60 (1995)
MEDLINE    95262687
REFERENCE  2 (bases 1 to 1163)
AUTHORS    Khamlichi,A.A.
TITLE      Direct Submission
JOURNAL    Submitted (14-SEP-1994) to the EMBL/GenBank/DBJ databases. A.A.
            Khamlichi, CNRS URA 1172, LAB-IMMUN AND GENETICS, IBMTG FACULTY OF
            SCIENCES, F-86022 POITIERS CEDEX, FRANCE
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Query Match      36.6%; Score 524; DB 34; Length 1547;
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Db 138 gtccqccaagctccaaggaagggtcgagctgggtcgatggatggattgatggaggt 197
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Qy 289 AACCAGTTCTCGCTGAAGCTGAACCTATATGACCGCGCGGACACGCGGCTGTTACTGT 348
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Qy 349 GTGAGATCGCTCTTTTTCAGTTGTTGGATGCTTTACAAACATGTTGTTGATGCTGG 408
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Db 378 ggccaggggacctcgctcacctgtcctcagcttcaccacgccccaccatcggttttccca 437
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Qy 409 GGCOCGGGATGCTCCTGGTACCGGTCTCTCAGCTAGCACCAAGGGGCCATCGGTCTTCGCC 468
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Db 438 ctggcccccagctggggggccaccaccacacagtggtccctggcctggcctgggtgtcc 497
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Qy 469 CTGGCACCCTCTCCAAAGACACCTCTGGGGGCACAGCGGCCCTGGGCTGGCTGGTCAAG 528
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Db 498 ggtcattccctgagctgtcactgtctcctggaactccggctccttgaccagcggtgtg 557
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Qy 529 GACTACTTCCCGAACCAGCGGTGACGGTGTCTGTGGAACCTCAGGCGCCTGACCAAGCGGTG 588
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Qy 589 CACACCTTCCCGGCTGCTCTACAGTCTCTAGAGCTCTACTCCCTCAGCAGCGGTGGTACC 648
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Db 618 gtgcctccagcaggtggcccaagacaccttcatctgcacctggcccaccacagcagct 677
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Qy 649 GTGCCCTCCAGCAGGTTGGGCACCCAGACCTTACTCTGCACGCTGATCATCAAGCCCAAGC 708
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Db 678 aacaccaggtggacaagagagtgcccccaggaataattcctccgccatgcacatgtccc 737
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Qy 769 CCGTCCCGCAGACCTGAACCTCTCTGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAAGCC 828
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Db 798 agggacacctctccatttccgaacccccggaggtcacatgcattggtggtggacctg--- 854
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Qy 949 AAGACAAAGCCCGGAGGAGCAGTACAAAGCAGCGTACCCTGTGTGTGTCAGGCTCTCACC 1008
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Db 1092 gtgtatgtctctgcccctcatcccggagcagctgagcaagacacaggggtcagtgacctgc 1151
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Qy 1129 GTGTACACCTCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGCTCAGCCTGACTGC 1188
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Db 1332 gcggtgctgcataagcgctcacacaccacacacagcagagaccatctcccagctctccg 1391
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Db 1392 gqtaaatga 1400
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Qy 1423 GGTAAATGA 1431

RESULT 14
LOCUS PIGIGHGA 1551 bp mRNA MAM 29-OCT-1994
DEFINITION S.domesticus immunoglobulin rearranged gamma chain mRNA, VJC
region, complete cds.
ACCESSION M81769
NID g164502
KEYWORDS C-region; D-region; J-region; V-region;
immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.
SOURCE Sus scrofa (individual isolate 5063-3, strain Minnesota miniature
swine, sub_species domesticus) adult spleen cDNA to mRNA.
ORGANISM Sus scrofa
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Artiodactyla; Suiformes; Suidae.
REFERENCE 1 (bases 1 to 1551)
AUTHORS Bosch,B.L., Beaman,K.D. and Kim,Y.B.
JOURNAL Unpublished (1991)
COMMENT NCBI gi: 164502
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/organism="Sus scrofa"
/isolate="5063-3"
/strain="Minnesota miniature swine"
/sub_species="domesticus"
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SRDTSGNVALGCLASYPFPPVTVTWSGALSSGVHTFSPVLQPSGLYSLSSWTVP
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471..1457
CDS
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translation of the corresponding C_region. Presently
translation qualifiers on C_region features are illegal."
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KQOTREPOVTVLPPHAELELSRSKVSITCLVIGFPPDIDVEMORNGOPELEGNYRTTP
PQDDVDGTYFLYSKFSVDKASWGGGIFQCAVWHEALHNHYTKSISLTPCK"
BASE COUNT 345 a 489 c 432 g 285 t
ORIGIN
Query Match 34.6%; Score 495; DB 34; Length 1551;
Best Local Similarity 73.3%; Pred. No. 0.00e+00;
Matches 1015; Conservative 0; Mismatches 340; Indels 30; Gaps 17;
Db 91 aggagaagctgggtgagctctggaggagcctggcgagcctgggggggtctctgagactc 150
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Qy 59 AGGTGCAGCTGCAGAGTTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCCTCA 118
Db 151 cctgtgttgctctggattcaccttcag---tacttatgaatacagctgggtccgcagg 207
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Qy 119 CTTGGCGTGTCTCTGTGGTCCATCAGCGGTGGTTATGCTGGGGTGGATCGGCAGC 178
Db 208 ctccaggaaagggccagagtggtcggcaggcattggttggtgtattatagtgtagca 267
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Qy 179 CCCAGGGAAGGGCTGGAGTGGATTG--GGAGTTTCTA--TAGT-AGTA--GTGGGAACA 232
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Db 328 cggcctatctgcaaatgaacagcctgagaccgaagatacggccgcgtattattgtgca 387
Qy 293 AGTTCTCCCTGAAGCTGAACCTCTATGACCCGCCGCCGACACGGCCGTTACTGTGTGA 352
Db 388 tagattcccttaagttggtgggtgcg-gttaacgtaagtgcagta--atctctggggcc 444
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Qy 413 CGGAGTCTCTGGTACCGCTCTCTCAGCTAGCACCAAGGCCCATCGGTCCTCCCTCGG 472
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Qy 473 CACCTCTCTCAAGAGACACCTCTGGGGGCACACGGCCCTCGGCTCCCTGGTCAAGACT 532
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Qy 713 CCNAGGTGCACAGAAACAGACGCCCAANTCTTGTGCACAAACTCAGACATGCCCAACGT 772
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Db 796 gccagctgtgaa-tcaccaggge--cc-tcgggtttctatcttccctccaaaccccaagg 852
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Qy 893 AAGACCTTGAGGTCAAGTTCAACTGTGACGTGGACGGCGTGAGGTGCATAATGCCAAGA 952
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Qy 1427 AATGA 1431
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RESULT 15
LOCUS RABIGHAD 1235 bp mRNA MAM 23-MAR-1995
DEFINITION Rabbit Ig active gamma H-chain (allotype Vha2 de12,14) mRNA.
ACCESSION K00752 M12187 M24226
NID g165127
KEYWORDS C-region; D-region; J-region; V-region;
heavy chain allotype Vha2; heavy chain allotype de12,14;
immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.
SOURCE Rabbit (haplotype F-1; Vha2 de12,14 allotype) spleen, cDNA to mRNA,
clone p-gamma-B1-12,14.
ORGANISM Oryctolagus cuniculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Lagomorpha; Leporidae.
REFERENCE 1 (bases 1 to 1235)
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AUTHORS Bernstein,K.E., Alexander,C.B. and Mage,R.G.
TITLE Nucleotide sequence of a rabbit IgG heavy chain from the
recombinant F-1 haplotype
JOURNAL Immunogenetics 18 (4), 387-397 (1983)
MEDLINE 84030930
COMMENT Original entry prepared by Dr. Rose Mage. The V-region is compared
[1] with the Vha2 allotype p-mu-3 and the human genomic VH2
sequence. The two rabbit V-regions are 89.5% homologous, and this
sequence is 77% homologous with the human segment. This sequence,
as well as the p-mu-3 sequence, shows remarkable homology with the
human CDR2 and D minigenes. The C-region is compared [1] with two
rabbit C-regions, one of del1,15 allotype and the other of e15 and
unknown d allotype.

NCBI gi: 165127 Location/Qualifiers
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<1..1209
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misc_recomb /organism="Oryctolagus cuniculus"
BASE COUNT 278 a 423 c 341 g 193 t
ORIGIN 9 bp upstream of AvalI site.

Query Match 34.0%; Score 487; DB 34; Length 1235;
Best Local Similarity 78.8%; Pred. No. 0.00e+00;
Matches 810; Conservative 0; Mismatches 197; Indels 21; Gaps 9;

Db 203 tctggggccaggcaccctggtcacgtctcctcaggcaacctaaaggctccatcagctc 262
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Qy 464 TCCCTCTGGCACCCCTCTCCACAGACACCTCTGGGGGACAGCGGCCCTGGGCTGGCTGG 523
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Db 494 ccacacacacaaagtggacaaagaccttgacccc---tc-----gacatg---cag-aa 542
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(TM)

Result No.	Query			ID	Description	Pred. No.
	Score	Match	Length			
1	1228	85.8	1431	T18059	Monoclonal antibody D	0.00e+00
2	1047	73.2	1549	Q20066	Encodes heavy chain o	0.00e+00
3	1048	73.2	1617	Q35099	Antibody D heavy chai	0.00e+00
4	1022	71.4	1135	I N90736	DNA encoding linker	0.00e+00
5	1021	71.3	1136	I N90779	Sequence of the linke	0.00e+00
6	1013	70.8	9208	11 Q65629	Vector contg. TCAE 8	0.00e+00
7	1008	70.4	1576	8 Q49944	Human anti-HBs heavy	0.00e+00
8	1003	70.1	1467	4 Q23570	Reshaped CAMPATH-1a	0.00e+00

PD - 13-FEB-1986.  
PF 20-FEB-1985; 030742.  
PR 18-FEB-1984; JP-021628.  
PA (NISN ) NISSHINBO IND INC.  
PA (TANA/) TANAKA H.



DR	WPI; 96-154852/16.	
DR	P-PSDB; R93553.	
PT	Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -	
PT	produced by primer amplification, used in the diagnosis of hCMV	
PT	infection	
PS	Claim 6; Page 16-18; 22pp; Japanese.	
CC	The sequences given in T18059-60 encode the heavy and light chains	
CC	respectively of a monoclonal antibody against a 65 kD antigen of human	
CC	cytomegalovirus (hCMV). These sequences were amplified using the	
CC	sequences given in T18040-58. The monoclonal antibody may be used	
CC	in the diagnosis of hCMV.	
SQ	Sequence 1431 BP; 314 A; 475 C; 379 G; 263 T;	
	Query Match 85.8%; Score 1228; DB 19; Length 1431;	
	Best Local Similarity 94.7%; Pred. No. 0.00e+00;	
	Matches 1359; Conservative 0; Mismatches 65; Indels 11; Gaps 8	
Db	1 atgaacatctgtggtttctctctgtgtggtggtccccagatcggtcgtcgtccccag 60	
Qy	1 ATGAACACCTGTGGTTCCTCTCTCTGGTGGCAGCTCCAGATGGGTCTGTCCGAC 60	
Db	61 ctgcagctgcaggagtcggggcccgagactggtgaagcctctggagaccctgtccctcc 120	
Qy	61 GTGACGTGCGAGGATCGGGCCCCAGAGACTGGTCAAGCCCTCGGAGACCCCTGTCCCTCAC 120	
Db	121 tgcactgtctctgtgtgactccatcagcaggagtactactcctggggtgcatccgcag 180	
Qy	121 TGGCGCTGTCTGTGGTCCATCAGC--G-GTGGTTATGGCTGGGGCTGGATCCGCCAG 177	
Db	181 cccccggggaagcctcgtgagtgagtgagactatctat--ta-tagtggagacactac 237	
Qy	178 CCCCCAGGCAAGGGCTGGAGTGGATTGGCAGTTTCTATAGTAGTAGTGGGACACCTAC 237	
Db	238 tacaacccgtccctcaagtgctgagtgccacatcctcgtagcgcgtccacaacacagttc 297	
Qy	238 TACAACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACAGCTGCCAAGACAGTTT 297	
Db	298 tccctgaagctgagctctgtgacgcgcgcgcgcgcgcgcgtgtgtattctgtgcgaga-ac 356	
Qy	298 TCCCTGAAGCTGAAGTCTATGACCCCGCCGACACGGCCGTGTATTACTGTGTGAGAT 357	
Db	357 c--tgcgcg--cagftattacgactcttttgactggttccttccctcactactcagcggcaggg 413	
Qy	358 CGTCTTTTTTCAGTGTGTGGATGGTTTACACAACATCGTTGCATGT-CTGGGGCGCGGG 416	
Db	414 aacctgggtcacgtctctcagcctccaccaaggcccatcggtcttccccctggcacc 473	
Qy	417 AGTCTGTGTCAACCGTCTCTCAGCTAGCACAAGGGCCCATCGGTCTTCCCTGTGCACC 476	
Db	474 ctctccaagagcaactctctgggggcacagcgccctggggtgctgtgtaaggactactt 533	
Qy	477 CTCTCCAAGAGCACCTCTGGGGGCACAGGGGCCCTGGGCTGGCTGGTGGTCAAGAGTACTT 536	
Db	534 ccccgaaacggtgacggtgtcgtggaaactcaggcgccctgaccagcggcgtgcacacctt 593	
Qy	537 CCCCGAACCGGTGAGGGTGTCTGGAAGTCAAGGGCCCTGACACAGCGGGGTGCACACCTT 596	
Db	594 cccggctgtcctacagtctcaggactctactccctcagcagcgtggtgacgcgtgcctc 653	
Qy	597 CCGGGGTGTCTTACAGTCTCAGAGACTCTACTCCCTCAGACAGCGTGGTGAACCGTGCCTC 656	
Db	654 cagcagcttgggcaccacagacctacatctgcaactgaatcacagccacgacaacacaa 713	
Qy	657 CACAGCTTTGGGACCCACACACCTAGTCTGCAAGCTGAATCAAGCCGACGACACCAA 716	

Db	714	ggtggacaagaagtgtgagcccaaatctcttgacaaaactcaacatgccaccgtgcc	713
Qy	717	GGTGACAAGAAAGACGAGCCAAATCTTGTGACAAACTTCACACATGCCACCGTGCC	716
Db	774	agcaactgaactcctggggggaccgtcagctcttcctctccccccaaaacccaagcac	833
Qy	777	AGCACTGAACTCCTGGGGGACCGTCAGTTCCTCTTCCCCCCAAACCCAGGACAC	836
Db	834	cctcatgatctcccggaacctgaggtgcacatcgtggtggagcgtgagccacgaaga	893
Qy	837	CCTCATGATCTCCGGACCCCTGAGTGCATCGGTGCTGGAGCTGACCCACCAAGA	896
Db	894	ccctgaggtcaagttcaactggtacgtggacggcgtggagtgcatatgccaagacaaa	953
Qy	897	CCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGCATTAATGCCAAGACAA	956
Db	954	gcccgggaggagcagtcacaacgacgtacctgtggtcagcgtcctcaccgtctgca	1013
Qy	957	GCCCGGGAGGACGAGTACACACGACACGTACCGTGTGCTCAGCGTCTCACCGTCTGCA	1016
Db	1014	ccaggaactgctgaatgcaagagtgatcaacagtgcaagtgctccaacaagaacctccccgc	1073
Qy	1017	CCAGGACTGGCTGAATGGCAAGGAGTACAGTGCMAAGGTCTCCAAACAAAGCCCTCCACG	1076
Db	1074	ccccatcgagaaaaccatctccaaagccaaaggcgagcccccggagaaccacacaggtgtacac	1133
Qy	1077	CCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTACAC	1136
Db	1134	cctgccccctcccgggatgagctgaccaagaaccaggtcgagctgacctgacctgcctggtcaa	1193
Qy	1137	CTGCGCCCATCCCGGATGAGTGCACAGACACAGGTGAGCTGACCTGCTGCTGCTGCTCA	1196
Db	1194	aggcttctatcccagcgacatcgccgtggagtgggagagcaatggcgagccggagacaaa	1253
Qy	1197	AGGCTTCTATCCCGGACATCCCGCTGGAGTGGGAGAGCATGGGCGACGGGAGAACAA	1256
Db	1254	ctacaagaccacgctcccgctgctgagctccgagcgctctctctctacagcaagt	1313
Qy	1257	CTAAGACACACGCTCCCGCTGCACTCCGACGCGCTCTTCTCCTCTACAGCAAGCT	1316
Db	1314	caccgtggacaagagcaggtggcagcaggggaacgtctctcagctccgtgatgcata	1373
Qy	1317	CACCGTGGCAAGACGAGGTGGCAGCGGGGAAACGTCTTCTCATGCTCCGCTGATGATCA	1376
Db	1374	ggctctgcaaaccaactacaacgacgaagacctctccctgctccgggtaaatga	1428
Qy	1377	GGCTCTGCACAACCATACAGCAGAGAGCGCTTCCCTGTCTCCGGGTAATGA	1431
RESULT 2			
ID	Q20066 standard; DNA; 1549 BP.		
AC	Q20066;		
DE	25-MAR-1992 (first entry)		
DT	Encodes heavy chain of 3D6 antibody.		
KW	Plasmid pUC36HC; human immunodeficiency virus; AIDS; as.		
OS	Homo sapiens.		
FX	Key	Location/Qualifiers	
FT	sig_peptide	101..157	
FT	/*tag= a		
FT	mat_peptide	158..1528	
FT	/*tag= b		
FT	5'UTR	1..100	
FT	/*tag= c		

RESULT	2	
ID	Q20066	standard; DNA; 1549 BP.
AC	Q20066;	
DT	25-MAR-1992	(first entry)
DE	Encodes heavy chain of 3D6 antibody.	
KW	Plasmid pUC3D6HC; human immunodeficiency virus; AIDS; ss.	
OS	Homo sapiens.	
Key	Location/Qualifiers	
FT	sig_peptide	101..157
FT	/*tag= a	
FT	mat_peptide	158..1528
FT	/*tag= b	
FT	5'UTR	1..100
FT	/*tag= c	



QY 1106 AGGGCAGCCCGAGNACACAGGTGTACACCTGCCCTCCCGATGAGTGACCA 1165  
 Db 1263 agaaccaggtcagcctgacctgcttcaagggtttctatcccagcgacatcccgctgg 1322  
 QY 1166 AGAACAGGTGACCTGACCTGCTGGTCAAGGCTTCTATCCACGGCATCGCGGTGG 1225  
 Db 1323 agtggagagaactggcagcgagagaaactacaagacagcctccgtgctgact 1382  
 QY 1226 AGTGGGAGCAATGGCAGCGGAGAACAACTACAAGACACGCTCCCGTGTGGACT 1285  
 Db 1383 ccgaagctcttctctctacagcaagctccacgtggacaagagcaggtggcagcagg 1442  
 QY 1286 CCGAGCGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAGACGAGTGGCAGCAGG 1345  
 Db 1443 ggaacgtcttctcatgctccgtgatgcatgaggtctgtcacaaccactacacagaaga 1502  
 QY 1346 GGAAGCTTCTCATGCTCTCGCTGATGCATGAGGCTCTGCACACCACTACACGAGA 1405  
 Db 1503 gctctccctgtctcgggtaaatga 1528  
 QY 1406 GCCTCTCCCTGTCTCCGGTAATGA 1431

## RESULT 3

ID Q35099 standard; DNA; 1617 BP.  
 AC Q35099;  
 DT 19-MAY-1993 (first entry)  
 DE Antibody D heavy chain.  
 KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;  
 KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;  
 KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H; ss.  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT CDS 35..1465

FT /\*tag= a 35..91  
 FT sig\_peptide  
 FT /\*tag= b 92..181  
 FT misc\_RNA  
 FT /\*tag= c 182..196  
 FT /\*tag= d 197..238  
 FT /\*tag= e 239..239  
 FT /\*tag= f 290..385  
 FT /\*tag= g 386..439  
 FT /\*tag= h 440..472  
 FT /\*tag= i 473..763  
 FT /\*tag= j 764..811  
 FT /\*tag= k

FT /label= HINGE 812..1141  
 FT misc\_RNA  
 FT /\*tag= l 1142..1462  
 FT /label= CH2  
 FT misc\_RNA  
 FT /\*tag= m 1566..1571  
 FT /label= CH3  
 FT TATA\_signal  
 FT /\*tag= n  
 PN EP-523949-A.  
 PD 20-JAN-1993.  
 PF 14-JUL-1992; 306420.  
 PR 15-JUL-1991; GB-015284.  
 PR 01-AUG-1991; GB-016594.  
 PR 23-MAR-1992; GB-006284.  
 PA (WELL ) WELLCOME FOUND LTD.  
 PI Crowe JS, Lewis AP;  
 DR WPI; 93-019951/03.  
 DR P-PSDB; R31024.  
 PT Prodn. of recombinant primate antibodies - useful for treating  
 PT infections caused by hepatitis A, B and C, herpes,  
 PT cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,  
 PT arthritis etc.  
 PS Disclosure; Fig 2; 35pp; English.  
 CC The sequences given in Q35099-100 encode the heavy and light chains  
 CC of Antibody D respectively. Antibody D is a monoclonal antibody which  
 CC was derived from peripheral blood lymphocytes from a hepatitis A virus  
 CC (HAV) sero positive patient. Antibody D is closely related in nature  
 CC to murine antibody B5B3. Total RNA was isolated from antibody D  
 CC expressing cells and polyadenylated RNA was extracted. These polyA  
 CC RNA's were used to prepare a cDNA library which was screened for human  
 CC kappa light (L) chains and two positive clones were detected.  
 CC Further heavy (H) chain clones were also isolated.  
 SQ Sequence 1617 BP; 375 A; 526 C; 441 G; 275 T;

Query Match 73.2%; Score 1048; DB 6; Length 1617;  
 Best Local Similarity 88.1%; Pred. No. 0.00e+00;  
 Matches 1247; Conservative 0; Mismatches 163; Indels 6; Gaps 4;  
 Db 53 ttcccttctgtgtggcagcagctacaggtgtccagtcacagatgcaggtgtgagcagct 112  
 QY 19 TTCTCTCTCTGCTGGCAGCTCCACAGTGGCTCTCTCCAGTGGCAGCTCAGGAGTGG 78  
 Db 113 ggggtctgaagtaagcctgggtcctcggtgacgtctctctgcaaggcatctggagcc 172  
 QY 79 GGGCCAGGACCTGGTGAAGCCTTCGGAGACCCCTGCTCCCTCACCCTGGCTCTCTGTGGTGGC 138  
 Db 173 accttcagcaaac---tatgtctatcagctgggtgcagcagggccctggacaaggcttgag 229  
 QY 139 TCCATCACCGGTGGTTATGGCTGGGGCTGGATCGCCACAGCCCCCGGAGAGGGGCTGGAG 198  
 Db 230 tggatgggagggatcatccctcttttgggtacacacaaactactacagaaacttccagggc 289  
 QY 199 TGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTACAACCCCTCCCTCAAGAT 258  
 Db 290 agagtcaagattaccgcgagcaaaatccaccagcaagcccacatggagctgactagcctg 349  
 QY 259 CAAGTCACCATTTCAACAGACAGCTCCAAGAACCCAGTTCTCTCCCTGAAGCTGAAGCTATG 318  
 Db 350 agatctcaggacagggcggtgtattctgtgcacagatcgtctacagggcaggaatttt 409  
 QY 319 ACCGCGCGGACACGGCGCTATTACTGTGTGAGAGATCG-T-CTTTTTT-CAGTTGTT 375  
 Db 410 gaccgggcccgggttggtctgacctctgggcccagggcaccctggtcaccgtctccc 469

376 GGAATGGTTTACAA CAATGGTTTCATGTCTGGGGCCGGAGTCTGGTCAACGCTCTCC 435  
470 tgaagctcccaagggccactcggtcttcccccctggacccctctcccaagagacacctt 529  
436 TGAAGTACACACNAGGGCCATCGGTCTCCCTGGACACCTCTCCCAAGACGACCTCT 495  
530 gggggcacacggccctgggtgctgctcaaggactacttccccgaaccggtgacgggtg 589  
496 GGGGACACAGCGCCCTGGGTCTGGTCAAGGACTATTCCTCCCGAAGCGGTGACGGTG 555  
590 tgaagctcccaagggccactgacccagcggtgcaacaccttcccggtgctccacagtc 649  
556 TCGTGAAGTACAGGGCCCTGACACGCGGCTGCACACCTTCCTCCGCGTCTCTACAGTCC 615  
650 tgaagctcccaagggccactgacccagcggtgacccgtgcccctccagcagcttgggcaaccag 709  
616 TGAAGTCTACTCTCTGACGCGGTGACCGTCCCTGACGCGCTCCACGAGCTTGGGACCCAG 675  
710 acctacatctgaacgtgaatcacaagccagcaacacaaaggtggacaagaagttag 769  
676 ACTTACTCTGCAAGCGTGAATCAAGGCCAGCAACCAAGGTGGACAAGAACGACAG 735  
770 cccaaatcttgacaaaactcaacatgcccacagcggtcccagcactgaactcctcgggg 829  
736 CCCAAATCTTGTGACAAAATCTACATGCCACCGTCCCGACGACCTGAACCTCTCGGG 795  
830 ggaagctcccaagggccactgacccagcggtgcaacaccttcccggtgctccacagtc 889  
796 GGAGCGTCACTCTCTCTTCCTCCCGCAAAACCCAGGACACCTCATGATCTCCCGGACC 855  
890 cctgagctccatcggtggtgagctgagccacgaagcctcgaggtcaagtcaac 949  
856 CTGAGGTACATGCGTGGTGGACGTGAGCGCAGGACCTGAGGTCAAGTTCAC 915  
950 tggtagctggaagcggtgaggtgacatgaatgccaagacgaagcggtgagagcaagtcac 1009  
916 TGTAGCTGAGCGGTGAGGTGACATGATGCAAGAACGCGCGGAGGAGGACGATC 975  
1010 aacagcagctacgtggtgagcgtcctcagcgtcctgacagagcgtgctgaatggc 1069  
976 AACAGCAGCTACCGTGTGTCAGCGTCTCAGCGTCTGACGAGGACTGGCTGAATGCC 1035  
1070 aaggagtcgaagtgaaggtctcccaagagccttccagcccccatcgagaaaccatc 1129  
1036 AAGGAGTACAGTGCAGGCTTCAACAAAGCCCTCCAGCGCCCATGAGAAAACATC 1095  
1130 tccaaagcgaagggcagccccgagaacacaggtgtacacccctgcccccatccccggat 1189  
1096 TCCAAAGCAGGAGGACGCCCCGAGACGACAGGTGTACACCTGCCCGCATCCCGGAT 1155  
1190 gagctgaccaagaacacaggtcagcctgacgtgctcgttcaaggcttctatccagcagac 1249  
1156 GAGCTGACCAAGAACAGGTCAGCTGACCTGGCTGGTCAAGGCTTCTATCCAGCGAC 1215  
1250 atcgccgtgagtggaagacaaatgggagcgggagaaacactacaagacacagcctccc 1309  
1216 ATCGCGGTGAGTGGAGAGCAATGGGACGCGGAGAACTACAAAGACACGCGCTCCC 1275  
1310 gtcgtgactccagcgggtcctctctctctcagcaagctcaccgtggacaagagcagg 1369  
1276 GTGCTGGACTCCGACGGTTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAGCAGG 1335  
1370 tggcagcaggggaacgtcttctctcgtgatgatgatgaggtctgcaaacactac 1429

1336 TGGCAGAGGGGAAGCTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACACCACTAC 1395  
1430 acqacagaagcctctccctgctccgggtaaatga 1465  
1396 ACGCAAGAGGCTCTCCCTGCTCCGGGTAAATGA 1431  
RESULT 4  
ID N90736 standard; DNA; 1135 BP.  
AC N90736;  
DT 06-JUN-1990 (first entry)  
DE DNA encoding linked human IgG1 (gamma 1) chain fragment  
KW Human IgG1; gamma 1; immunoglobulin; CD4; fusion protein.  
OS Homo sapiens  
FH Key Location/Qualifiers  
FT CDS 8..1123  
FT /tag= a  
FT misc feature 133..134  
FT /tag= b  
FT /note= "Insert site"  
FT misc feature 439..440  
FT /tag= c  
FT /note= "Insert site"  
PN W08902922-A.  
PD 06-APR-1989.  
PF 03-OCT-1988; U03414.  
PR 02-OCT-1987; US-104329.  
PA (GETH) Genentech.  
PI Capon DJ, Gregory TJ;  
DR WPI; 89-114397/15.  
DR P-PSDB; P93558.  
PT New nucleic acid sequences encoding adhesion, esp. CD4, variants -  
PT partic. with trans-membrane domain inactivated or fused to other  
PT peptide, useful esp. for treating HIV infections  
PS Figure 4A-4B; pp. 10/13-12/13; 78pp; English.  
CC It is employed in the prepn. of CD4 fusions. The insert sites are  
CC given in the Features Table. CD4 fusion proteins can have antiviral and  
CC immunomodulatory activity and are esp. useful for treating HIV infections,  
CC regardless of genetic variation within the virus. They and antibodies  
CC raised against them can also be used diagnostically for assaying adheons  
CC and their ligands.  
SQ Sequence 1135 BP; 255 A; 386 C; 302 G; 192 T;  
Query Match 71.4%; Score 1022; DB 1; Length 1135;  
Best Local Similarity 95.9%; Pred. No. 0.00e+00;  
Matches 1078; Conservative 0; Mismatches 44; Indels 2; Gaps 2;  
Db 1 gaatctgtcaactgcgcgaacacggcggtatattactgtgcgaagc-caccttttgc 59  
309 GAATCTATATCGCGCGGACACGCGCGGTATTACTGTGAGAGATCGCTTTTTC 368  
60 tatgttaacagggagcgtccccccttggatcgaccccctggggcctgggaacccctggta 119  
369 AGTTGTGGAATGTTTACAACT-GTTTCGATGCTGTGGGCGGGAGTCTGTGTC 427  
120 cagctctcggctccaccaagcccccatcggtttctcccccctggcaccctctccaaga 179  
428 CCGTCTCTCAGGTAGCACCAAGGCGCCATCGGTCTTCCCTCCGACCCCTCTCCACA 487  
180 gcaactctggggcacagcgccctgggctgcctggtcaaggactacttccccgaacgg 239  
488 GCACTCTGGGGGCGACACGCGCCCTGGGCTGCTGTGTCAGGACTACTTCCCGAACCG 547



540	Db	ccccgaccctcgaggtccacatgcggtgggtggagctgagccacgaagaccctgaggtca	599
848	Qy	ccccgacccctgaggttcacatgcctgctggtggagctgagccacgaagaccctgaggtca	907
600	Db	agttcaactggtacgtgagcggcggtggaggtgcataatgccaaagacaaagccggcgagg	659
908	Qy	agttcaactggtacgtgagcggcggtggaggtgcataatgccaaagacaaagccggcgagg	967
660	Db	agcagtacaacagcagctaccgggtggtcagcgtcctcacgctcgaccagagactggc	719
968	Qy	agcagtacaacagcagctaccgggtggtcagcgtcctcacgctcgaccagagactggc	1027
720	Db	tgaatggccaaggagtacagtgcaaggtctccaacaagaagccctcccagcccccacgaga	779
1028	Qy	tgaatggccaaggagtacagtgcaaggtctccaacaagaagccctcccagcccccacgaga	1087
780	Db	aaaccatctccaaagccaaagggcagcccgagaaacacagtgtagacacctgcccccat	839
1088	Qy	aaaccatctccaaagccaaagggcagcccgagaaacacagtgtagacacctgcccccat	1147
840	Db	cccgggatgagctgaccaaagcaacaggctcagcctgacctgctcgtggtcaaaaggtctatc	899
1148	Qy	cccgggatgagctgaccaaagcaacaggctcagcctgacctgctcgtggtcaaaaggtctatc	1207
900	Db	ccagcgacatcgccctggaatggagagcaaatggcagccggagaaacaactacaagacca	959
1208	Qy	ccagcgacatcgccctggaatggagagcaaatggcagccggagaaacaactacaagacca	1267
960	Db	cgcctcccggtgctggaattccagcggctccttctcctacagaagctccagtgagaca	1019
1268	Qy	cgcctcccggtgctggaattccagcggctccttctcctacagaagctccagtgagaca	1327
1020	Db	agagcagggtggcagcaggggaacgctctctcatgctccggtgatgcattgaggtctcgaca	1079
1328	Qy	agagcagggtggcagcaggggaacgctctctcatgctccggtgatgcattgaggtctcgaca	1387
1080	Db	accactacaagcaggaagagcctctcctgtctccgggtaaa	1120
1388	Qy	accactacaagcaggaagagcctctcctgtctccgggtaaa	1428

## RESULT

ID	Q65629 standard; DNA; 9208 BP.
AC	Q65629;
DT	01-FEB-1995 (first entry)
DE	Vector contg. TCAE 8 DNA.
KW	B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
KM	cell lysis; ss.
OS	Synthetic.
PN	W09411026-A.
PD	26-MAY-1994.
PF	12-NOV-1993; U10953.
PR	13-NOV-1992; US-978891.
PR	03-NOV-1993; US-149099.
PA	(IDEC-) IDEC PHARM CORP.
PI	Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;
PI	Refme;
DR	WPI; 94-183162/22.
PT	Treating B cell lymphoma with chimeric antibody - against CD20,
PT	causing rapid depletion of peripheral B cells, also new
PT	antibodies and hybridomas
PS	Disclosure; Fig 3; 101pp; English.
CC	The sequence shows a vector contg. TCAE8, a gene encoding a chimeric



QY 1117 CGAGAACCAAGGTGTACACCCCTGCCCCCATCCCGGGATGAGCTGACCAAGACCCAGGTC 1176  
|||||  
Db 3558 agcctgacctgacctggtcaaaagcttctatcccagagacatcccggtggagtggagagac 3617  
|||||  
QY 1177 AGCTTGACCTGCTGGTCAAGGCTCTATCCACGGACATCCGCCGTGAGCTGGAGAGC 1236  
|||||  
Db 3618 aatggcagccagagaaactacaagaccacgctcccgctgctgactccgacgctcc 3677  
|||||  
QY 1237 AATGGCAGCCGGAGAACTACAAGACACACGCTCCCGCTGCTGACTCCGACGGCTCC 1296  
|||||  
Db 3678 ticttctctacagcaggtcaacctggacaagagcaggtggcagcaggaggaactcttc 3737  
|||||  
QY 1297 TTCTTCTCTACAGCAAGCTCACCGTGGCAAGACAGCAGGTGGCAGCGGCAAGCTCTC 1356  
|||||  
Db 3738 tcatgctccgtgatgatgaggtctctgcacacccactacagcaggaagagctctccctg 3797  
|||||  
QY 1357 TCATCTCCTGATCATGAGGCTCTGCACACCACTACAGCAGAGAGGCTCTCCCTG 1416  
|||||  
Db 3798 tctccgggttaata 3812  
|||||  
QY 1417 TCTCCGGTAAATGA 1431  
|||||

## RESULT 7

ID Q49944 standard; cDNA; 1576 BP.  
AC Q49944;  
DT 29-APR-1994 (first entry)  
DE Human anti-HBs heavy chain.  
KW Antibody; Ab; light; heavy; chain; hepatitis B;  
KW HB; surface antigen; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 15..1394  
FT /\*tag= a 15..41  
FT sig\_peptide  
FT /\*tag= b  
FT mat\_peptide 42..1391  
FT /\*tag= c  
FT /note= "claim 2, page 27"  
PN W09320205-A.  
PD 14-OCT-1993.  
PF 30-MAR-1993; J00396.  
PR 30-MAR-1992; JP-074678.  
PA (SUNR ) SUNTORY LTD.  
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;  
DR WP1; 93-336913/42.  
DR P-PSDB; R42066.  
PT Human anti-hepatitis B surface antigen antibody gene - can be  
PT used to produce L and H chains of the antibody in large quantity  
PS Disclosure; Fig 6-8; 46pp; Japanese.  
CC Polynucleotides encoding the L and H chains of human anti-HBs  
CC Ab are given in Q49943-Q49944. The Ab can be easily produced in  
CC large quantities for therapeutic use.  
SQ Sequence 1576 BP; 394 A; 483 C; 425 G; 273 T;

Query Match 70.48; Score 1008; DB 8; Length 1576;  
Best Local Similarity 98.5%; Pred. No. 0.00e+00;  
Matches 1024; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 355 acagattgactcctggggccagggaacacctggtcacgctctctcagcctccaccaagg 414  
|||||  
QY 392 ACTGGTTCGATCTCTGGGGCGGGAGTCTCTGTCACCGCTCTCTCAGCTAGCACCAAGG 451  
|||||

Db 415 gccatcggtttccccctggcaacctctctccaaggaacctctcggggacacagcgccc 474  
|||||  
QY 452 GCCATCGGCTTCCCCCTTGGCACCCCTCCAAAGAGCACCTTGGGGGCACACGCGGCC 511  
|||||  
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Qy 1424 GTAAATGA 1431

RESULT 10  
ID Q23571 standard; DNA; 1458 BP.  
AC Q23571;  
DT 20-OCT-1992 (first entry)  
DE Reshaped CD4 antibody heavy chain cDNA CD4VHNEW-Thr30  
KW Antigen; CDR; complementarity determining region; graft rejection;  
KW autoimmune diseases; rheumatoid arthritis; allergy; as.  
OS Rattus rattus.  
FH Key Location/Qualifiers  
FT CDS 36..1439  
FT /tag= a  
FT misc\_feature 183..197  
FT /tag= b  
FT /note= "Complementarity determining region 1"  
FT misc\_feature 240..290  
FT /tag= c  
FT /note= "Complementarity determining region 2"  
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FT /note= "Complementarity determining region 3"  
PN W09205274-A.  
PD 02-APR-1992.  
PF 16-SEP-1991; G01578.  
PR 17-SEP-1990; GB-020282.  
PA (GORM/) GORMAN S D.  
PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.  
DR WP1; 92-132139/16.  
DR P-PSDB; R22758.  
PT Humanisation of antibodies binding to human CD4 antigen - by  
PT mutation of framework-encoding regions of DNA encoding variable  
PT domain of rat or mouse antibody chain  
PS Disclosure; Fig 6; 74pp; English.  
CC The sequence is that of the reshaped CD4 antibody heavy chain cDNA  
CC CD4VHNEW-Thr30. Reshaped CD4 antibody can be used to induce tolerance  
CC against an antigen. It can also be used to alleviate autoimmune diseases  
CC such as rheumatoid arthritis, and to prevent graft rejection. Tolerance  
CC to a graft, e.g. an organ graft or a bone marrow transplantation can  
CC also be useful to alleviate allergies. Tolerance to allergens could  
CC also be achieved. See also Q23566-Q23581.  
SQ Sequence 1458 BP; 345 A; 467 C; 385 G; 261 T;

Query Match 70.0%; Score 1001; DB 4; Length 1458;  
Best Local Similarity 98.7%; Pred. No. 0.00e+00;  
Matches 1014; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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## RESULT 15

ID Q25692 standard; cDNA; 1412 BP.  
AC Q25692;  
DT 28-DEC-1992 (first entry)  
DE Sequence of the chimeric H chain cDNA contained in pBI373  
KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;  
KW antithrombotic agent; myocardial infarction therapy; ss.  
OS Synthetic.

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FH Key Location/Qualifiers
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FT /product= Leader
FT CDS 70..414
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PN EF-491351-A.
PD 24-JUN-1992.
PF 17-DEC-1991; 121591.
PR 18-DEC-1990; JP-413829.
PR 11-NOV-1991; JP-294464.
PI (TAKE ) TAKEDA CHEM IND LTD.
PI Iwasa S, Taka H, Watanabe T, Tada H;
DR WPI; 92-209528/26.
DR P-PSDB; R24812.
PT Chimeric monoclonal antibodies - contain anti-human fibrin
PT antibody light and heavy chain variable and constant for treating
PT thrombotic conditions e.g. myocardial infarction
PS Example; Figure 11; 8/pp; English.
CC Plasmid pBI373 contains the whole length of a mouse-human
CC chimeric anti-human fibrin heavy chain cDNA open reading
CC frame. It was prep'd. using Poly(A)+ RNA from the anti-fibrin
CC chimeric Ab-producing transformant FIB1-H01/X63 as a template
CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
CC a primer for first strand cDNA synthesis and the 5'CZH and 3'EH
CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
CC peptide cDNA were amplified using the primers 3'EH, 3'CZH and 3'CIH
CC respectively as a primer for first strand cDNA synthesis and the
CC primer combination of 5'CIH and 3'CZH, of 5'LIH and 3'CIH and of
CC 5'SH and 3'LIH respectively as primers for PCR. The amplified gene
CC products were isolated and used to produce plasmids. After
CC confirmation of the cDNA sequence of each plasmid, the cDNA
CC encoding LH, VH, CH1 and CH2CH3 were joined together to give
CC plasmid pBI373 contg. the whole length chimeric H chain
CC (LH, VH, CH1, CH2CH3), also abbreviated as Igh-FIB,
SQ Sequence 1412 BP; 325 A; 433 C; 381 G; 273 T;
Query Match 68.7%; Score 983; DB 4; Length 1412;
Best Local Similarity 97.9%; Pred. No. 0.00e+00;
Matches 1005; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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Db 441 cccctggcaccctcctccaagagcacctctgggggacagcgccctgggctgcctggt 500

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397:EST398 398:EST399 399:EST400 400:EST401 401:EST402  
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417:EST418 418:EST419 419:EST420 420:EST421 421:EST422  
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522:EST523 523:EST524 524:EST525 525:EST526 526:EST527  
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537:EST538 538:EST539 539:EST540 540:EST541 541:EST542  
542:EST543 543:EST544 54

## RESULT 1



IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 922191  
Location/Qualifiers  
source 1..384  
/organism="Homo sapiens"  
/clone="235928"  
<1..>384

BASE COUNT 98 a 113 c 104 g 64 t 5 others

ORIGIN

Query Match 23.3%; Score 334; DB 20; Length 384;  
Best Local Similarity 96.1%; Pred. No. 0.00e+00;  
Matches 369; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

Db 1 gtgaatcaagccagcaacacagagtgagacagagtgagcccaaatcttggac 60  
|||||  
Qy 691 GTGAATCAAGCCAGCAACCAAGGTGGACAAGAAAGCAGAGCCCAATCTTTGTGAC 750  
|||||

Db 61 aaactcacatgccaccgtgccagaccctgaactcctgggggaccgtcagttctc 120  
|||||  
Qy 751 AAATCTACACATGCCACCTGCCAGCAGCTGAATCTCTGGGGGACCGTCACTCTTC 810  
|||||

Db 121 ctcttcccccaaaacccaagacacccctcatgatctcccggaccctcctgaggtcacatgc 180  
|||||  
Qy 811 CTCTTCCCCCAAAACCAAGACACCCCTCATGTCTCCCGGACCCCTGAGTCACATGC 870  
|||||

Db 181 gtggtgtggagctgagccaggaagaccctgaggtcaagtcaactgtgtaagtggagcgc 240  
|||||  
Qy 871 GTGCTGTGGACCTGAGCCAGCAGACCCCTGAGTCAAGTTCAGTCTGTTAGTGGCGC 930  
|||||

Db 241 gtgaggtgcaataatgccaaagcaaacgcgggagmgcagtcagtcacagcacgtacct 300  
|||||  
Qy 931 GTGGAGTGCATATGCCAAGACAAAGCCGGGAGGAGCAGTACAAACAGCAGCTACCGT 990  
|||||

Db 301 gtgttcagctcctcaccgtcctggcaccaggantggctganttggcaagngtacaag 360  
|||||  
Qy 991 GTGCT-CAGGCTCCTCAGCTCTGTG-CAGCAGAGCTGGCTGAAT-GCAGAGAGTACAG 1047  
|||||

Db 361 tgcaaggttttccaanaaagccc 384  
|||||  
Qy 1048 TGC-AAGGTCT-CCAAAGAGCCC 1069  
|||||

RESULT 3  
LOCUS T93165 415 bp mRNA EST 22-MAR-1995  
DEFINITION ye24c07.r1 Homo sapiens cDNA clone 118668 5' similar to gb:M87789  
IG GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION T93165  
NID 9725078  
KEYWORDS EST.

SOURCE human clone=118668 library=Stratagene lung (#937210)  
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)  
primer=M13RP1 Reite1=EcORI Reite2=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTCGGCAGGAG-3'; 3' adaptor sequence:  
5'-CTCAGATTTTTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 415)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskie, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
WashU-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 299  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 725078  
Location/Qualifiers  
source 1..415  
/organism="Homo sapiens"  
/clone="118668"  
/note="human"

BASE COUNT 104 a 134 c 103 g 71 t 3 others

ORIGIN

Query Match 22.1%; Score 316; DB 107; Length 415;  
Best Local Similarity 96.9%; Pred. No. 0.00e+00;  
Matches 378; Conservative 0; Mismatches 2; Indels 10; Gaps 9;

Db 1 acaaaactcacatgcccacngtgcacacacatgaactcctctggggggaccctcagtc 60  
|||||  
Qy 749 ACAAAACTCACATGCCACC-GTCCACGACCTGAATCTCTGGGGGACCGTCAGTC 807  
|||||

Db 61 ttcttctcccccaaaacccaagaccctcatgatctcccgaccctcagggtcaca 120  
|||||  
Qy 808 TTCTCTTTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCTGAGTCA 867  
|||||

Db 121 tgcgtgtggtggagctgagccagacccctgaggtcgaagtccaacttggtacgtggac 180  
|||||  
Qy 868 TGCCTGTGTGTGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGTGTGAG 927  
|||||

Db 181 ggcgtggaggtgcataatgccaaagcaagccgggagagcagtcacacagcacgtac 240  
|||||  
Qy 928 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGTACACAGCAGCTAC 987  
|||||

Db 241 cgtgtgttcagctcctcaccgtcctgcaccaggagactgcttgatgagcaagagatc 300  
|||||  
Qy 988 CGTGTGTGAGCGTCTCAACCGTCTGCACGAG-ACT-GGCT-GAATGGCAAGAGTAC 1044  
|||||

Db 301 aagttgcaaggtttccacaagaagccctccagcccttcgaggaagaaaccattctcca 360  
|||||

Qy 1045 AAGT-CCAGGTCT-CCACAAAGAGCCCTCCAGCCGCCCATCGA--GAAACCATCT-CCA 1099  
|||||

Db 361 aagcacaagggcagcccgaggaaccacag 390  
|||||

Qy 1100 AAGCCAAAGGCGACCCCGCAG-AACCACAG 1128  
|||||

RESULT 4  
LOCUS R82750 484 bp mRNA EST 14-JUN-1995  
DEFINITION yj25c07.r1 Homo sapiens cDNA clone 149772 5' similar to gb:M87789  
IG GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION R82750

NID 9862141  
 KEYWORDS EST.  
 SOURCE human clone=149772 library=Soares placenta Nb2HP vector=pf7T3D (Pharmacia) with a host=modified polylinker host=DHI0B (ampicillin resistant) primer=M13RPI Rsite1=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo (dT) primer [5'  
 AACTGCAGAAATTCGGCGCCGACGAAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pf7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 484)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT

Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 290  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 862141  
 Location/Qualifiers  
 1..484  
 /organism="Homo sapiens"  
 /clone="149772"  
 /note="human"  
 BASE COUNT 122 a 143 c 129 g 88 t 2 others  
 ORIGIN  
 Query Match 21.7%; Score 310; DB 69; Length 484;  
 Best Local Similarity 91.9%; Pred. No. 0.00e+00;  
 Matches 442; Conservative 0; Mismatches 20; Indels 19; Gaps 19;  
 Db 1 cacaagcccaacacacacaggtggacagagattggacccaaatctgtgacaaaact 60  
 Qy 697 CACAGCCGACGACACACAGGTGGACAGACAGAGCCCAATCTGTGACAAACT 756  
 Db 61 cacacatgccaccgtgcccagcacctgactctgggggacccgtcagctctctcttc 120  
 Qy 757 CACATGCCACCGCTGCCAGCACCTGAATCTCTGGGGGACCGTCATCTTCCTTC 816  
 Db 121 ccccaaaac 180  
 Qy 817 CCCCCAAACCAAGGACACCCCTCATCTCTCCCGGACCCCTGAGGTGCATCGGTG 876  
 Db 181 gtggacgtgagccacgaagacccctgaggtcaagttcaactggtacgtggcgggtgag 240

Qy 877 GTGAGCTGAGCCACGACGACCTGAGGTCAAGTTCAGTGTGACGCGCGTGGAG 936  
 Db 241 gtccataatgccaaagacaaacccgaggagagcagtcacacacacagcagtcagtggtt 300  
 Qy 937 GTCATAATGCCAAGACAAAGCCGCGGAGCAGCAGTACACACGACGACCTGCGTGGT- 995  
 Db 301 cagcgttccacgttccctcctggcaccagagattgggtgaatgggcaaggaggttacaagt 360  
 Qy 996 CAGCGT-CCTACCGT-CCTG-CACGAGGACTGGCT-GAATCG-CAAGG-AGT-ACAAGT 1048  
 Db 361 tgaaggtnttccaaacaaagccttccagggcccttttttaggaaacaccttttccaaa 420  
 Qy 1049 -GCAAGGCT-CCAAAGACGCT-CCAG-CCCCATCG-AG-AAACCATCT-CCAAA 1101  
 Db 421 gccaaagggcagcccgaggagacacacagtcgttacaacttggcccttccccggaggga 480  
 Qy 1102 GCCAAGGG-CAG-CCCCGAG-NACCACAGGTGTACACCTGCCCCCAT-CCCCGGATGA 1157  
 Db 481 g 481  
 Qy 1158 G 1158

RESULT 5  
 LOCUS H67250 364 bp mRNA EST 27-OCT-1995  
 DEFINITION yu65h03.r1 Homo sapiens cDNA clone 238709 5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION H67250  
 NID g1025990  
 KEYWORDS EST.  
 SOURCE human clone=238709 primer=M13RPI library=Weizmann Olfactory Epithelium vector=pBluescript SK- host=SOLR cells (kanamycin resistant) Rsite1=EcoRI Rsite2=XhoI From 35 year old female. The cDNA was oligo (dT) primed with an XhoI restriction enzyme recognition site and an 18 base poly dt sequence. For the 5' end, the synthesized cDNA termini were treated with T4 DNA polymerase and EcoRI adaptors were ligated to the blunt ends.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 364)  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 TITLE WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT

Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 241  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 1025990

## FEATURES

Location/Qualifiers

## source

1..364

/organism="Homo sapiens"

/clone="238709"

/note="human"

&lt;1..&gt;364

BASE COUNT 79 a 117 c 101 g 65 t 2 others

## ORIGIN

Query Match 21.2%; Score 304; DB 24; Length 364;

Best Local Similarity 98.4%; Pred. No. 0.00e+00;

Matches 312; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 1 ccgaagaacacagctgtatataccctgcccccatcccgagatgagctgaccaagaaccaggt 60

|||||

Qy 1116 CCGAGACACAGGTGTACACCTGCCCCCATCCGGGATGACGTGACCAAGACAGGT 1175

|||||

Db 61 cagctgacctgctggtcaaaaggttctatccagcagacatcgccgtggagtggaag 120

|||||

Qy 1176 CAGCCTGACCTGCTGGTCAAAAGGCTTCTATCCACGCGACATCGCGTGGAGTGGCAGAG 1235

|||||

Db 121 caatggcagccggagaaactacaagacagcctccctgctggaactccgagcgtc 180

|||||

Qy 1236 CAATGGCAGCGGAGAACTACAGACCCAGCGCTCCGCTGGACTCCGACGGCTC 1295

|||||

Db 181 cttctctctacagaagctaccgtggacaagagcaggtngcagcggggaactctt 240

|||||

Qy 1296 CTTCTCTCTACAGCAAGCTACCGTGGACAGACGAGTGGCAGCGGGAACGTCTT 1355

|||||

Db 241 ctcatgctcgtgatgctgagctctgcacaaacactacacgagagagcmtctccct 300

|||||

Qy 1356 CTCATGCTCGGTGATGATGAGGCTCTGCACAACTACAGCAGAGAGCTCTCCCT 1415

|||||

Db 301 gtttccgggtaaatga 317

|||||

Qy 1416 GTCT-CCGGGTAAATCA 1431

|||||

## RESULT

## LOCUS

T59711

474 bp mRNA

EST

09-FEB-1995

yell3h10.s1 Homo sapiens cDNA clone 80611 3' similar to gb:M87789 IG

GAMMA-1 CHAIN C REGION (HUMAN);

## ACCESSION

T59711

## NID

g661548

## KEYWORDS

EST.

## SOURCE

human clone=80611 library=Stratagene lung (#937210)

vector=pBlueScript SK- host=SOLR cells (kanamycin resistant)

primer=-21ml3 Reitel-EcoRI Reite2=XhoI Normal lung tissue from a 72

year old male. Cloned unidirectionally. Primer: Oligo dt. Average

insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:

5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:

5'-CTCAGATTCTTTTTTTTTTTT-3'.

## ORGANISM

Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 474)

## AUTHORS

Hillier, L., Clark, N., Duboue, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevas, E.,

Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

## WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 353

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

source

NCBI gi: 661548

Location/Qualifiers

1..474

/organism="Homo sapiens"

/clone="80611"

/note="human"

BASE COUNT 74 a 125 c 145 g 117 t 13 others

## ORIGIN

Query Match 21.0%; Score 300; DB 98; Length 474;

Best Local Similarity 93.7%; Pred. No. 0.00e+00;

Matches 341; Conservative 0; Mismatches 17; Indels 6; Gaps 6;

Db 110 tcattaccggagacaggagagcgtctctgctntagtggtntgagagcctcatg 169

|||||

Cp 1431 TCATTTATCCCGAGACAGGAGAGGCTCTCTGCGTGTAGTGTGTGAGAGCCTCATG 1372

|||||

Db 170 catcacggagcatgagaagcgttccctgctgccaactgctcttntccacggttagctt 229

|||||

Cp 1371 CATCAGGAGCATGAGAGAGCTTCCCTGCTGCCACCTGCTTCTCCAGGCTGAGCTT 1312

|||||

Db 230 gctntagaggaagaaggagcctcgantccagcagggagcgtggtctgttagttgt 289

|||||

Cp 1311 GCTGTAGAGGAGACAGAGGAGCGCTCGGAGGTCCAGCAGGGAGCGGCTGTGTAGTTGTT 1252

|||||

Db 290 ctccggctgccatgctctccactccagcgagctgctggggatagagccttta 349

|||||

Cp 1251 CTCGGGCTGCCCATTTGCTCTCCACCTCCACGCGGATGCTGCTGGG-ATAGAAGCCTTGA 1193

|||||

Db 350 ccagggcaggtcaggtcnaactgggtcttcttgctcagctcatcccgagatggggcaggg 409

|||||

Cp 1192 CCAGG-CAGGTCAGGCTGACCTGG-TTCTT-GGTCAAGTCTATCCGGATGGGGCAGGG 1136

|||||

Db 410 tatcacctgngttctcgggggttccttttcttngaaatggtttcttcttcttctt 469

|||||

Cp 1135 TGTACACCTGTGCTCGGGGCTGCCCTTTTGGCTTT-GGAGATGCTTTTCT-CGATGGG 1078

|||||

Db 470 ggcct 473

|||||

Cp 1077 GGCT 1074

|||||

## RESULT

## LOCUS

R82945

363 bp mRNA

EST

04-AUG-1995

ypl1g03.s1 Homo sapiens cDNA clone 187156 3' similar to gb:M87789

IG GAMMA-1 CHAIN C REGION (HUMAN);

## ACCESSION

R82945

## NID

g927913

## KEYWORDS

EST.

## SOURCE

human clone=187156 library=Soares breast 3NBH8et vector=pt773D

(Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer=Promega -21ml3 Reitel=Not I Rsite2=Eco RI Adult

human. 1st strand cDNA was primed with a Not I - oligo (dT) primer

[5' TGTTACCAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bernaldo.

#### ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcophylli; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

#### REFERENCE AUTHORS

1 (bases 1 to 363)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

#### TITLE JOURNAL COMMENT

The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LINL  
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality.

#### FEATURES source

NCBI gi: 927913  
Location/Qualifiers  
1..363  
/organism="Homo sapiens"  
/clone="187156"  
/note="human"

BASE COUNT 54 a 99 c 115 g 82 t 13 others

Query Match 20.6%; Score 295; DB 69; Length 363;  
Best Local Similarity 92.5%; Pred. No. 0.00e+00;  
Matches 306; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 31 tcattaccgggacaggagaggtcttctgctgtagtggtntgcagagctcatg 90  
|||||

Cp 1431 TCATTTACCGGACAGCGAGAGGCTCTTCTCGGTGTAGTGGTTGTGCAGAGCCTCATG 1372  
|||||

Db 91 catcaggagcatgagaagcgttccctgtgccacctgtcttgcacggtgagctt 150  
|||||

Cp 1371 CATCAGGAGCATGAGAGAGGTTCCCTGTGCGACCTGCTTGTTCACGGTGAGCTT 1312  
|||||

Db 151 nctatagaagaagaagcgtcgtcagcagcagcagcagcagcagcagcagcagc 210  
|||||

Cp 1311 GCTGTAGAGGAAGAGGAGCGCGTCCGAGTCCAGCAGGAGCGTGTCTTCTAGTTGTT 1252  
|||||

Db 211 ctcgggtgcceatgtctcctccatccacggcgatgctcgtgggataagagccttgc 270  
|||||

Cp 1251 CTCGGCTGCCCATGCTCCCATCCACGGCGATGCTCGTGGATAGAGCCTTTGAC 1192  
|||||

Db 271 caaggaggtcaggctna-cgggntcttggcancctcccncggatggggcagggttna 330  
|||||

Cp 1191 CAGCAGCTCAGCTGACCTGGTCTTGGTCAGCTCATCCCGGATGGGGCAGGGTGA 1132  
|||||

Db 331 cacccttggttttcnggnunccttgcctt 363  
|||||

Cp 1131 CACCTGTGTTCTCGGGGCTGCCCTTTGGCTTT 1099  
|||||

#### RESULT 8

LOCUS H62381 473 bp mRNA EST 06-OCT-1995  
DEFINITION yu41a02.s1 Homo sapiens cDNA clone 236330 3' similar to gb:M87789  
IG GAMMA-1 CHAIN C REGION (HUMAN);

#### ACCESSION

NID H62381  
g1015213

#### KEYWORDS

SOURCE

clone=236330 primer=Promega -21ml3 library=Soares ovary tumor  
NBIOT vector=pT7T3D (Pharmacia) with a modified polylinker  
host=DH10B (ampicillin resistant) Reitel=Not I Reite2=Eco RI  
Female. 1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5' TGTTACCAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT7T3 vector (Pharmacia). Library  
constructed by Bento Soares and M.Fatima Bernaldo.

#### ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcophylli; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

#### REFERENCE

1 (bases 1 to 473)

#### AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

#### TITLE JOURNAL COMMENT

The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 284  
Source: IMAGE Consortium, LINL  
This clone is available royalty-free through LINL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

#### FEATURES source

NCBI gi: 1015213  
Location/Qualifiers  
1..473  
/organism="Homo sapiens"  
/clone="236330"

#### mRNA

BASE COUNT 77 a 114 c 158 g 116 t 8 others

#### ORIGIN

Query Match 20.0%; Score 286; DB 22; Length 473;  
Best Local Similarity 91.0%; Pred. No. 0.00e+00;  
Matches 332; Conservative 0; Mismatches 29; Indels 4; Gaps 4;

Db 100 tcattaccggagacaggagaggtcttctgtgtgtagtggttgcaagcctcatg 159  
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Cp 1431 TCATTACCGGAGACGGAGAGGCTCTTCCGTGTAGTGGTTGCGACAGCCTCATG 1372  
 Db 160 catcagagcatgagaagcgtccctgtccacctgctcttgcacggtgagctt 219  
 Cp 1371 CATACGAGCATGAGAGACGTTCCCTGCTGCCACCTGCTTGTCCACGGTAGCTT 1312  
 Db 220 gctgtagagaagaagagcgtccaggtccacatggaggtggtggtcttgatgctt 279  
 Cp 1311 GCTGTAGAGAAAGAGGAGCGCTCCGAGTCCAGCAGGAGGCTGCTTGTAGTTGTT 1252  
 Db 280 ctccggtgccattgctctcccaatccacggcgcatgtcgtggggtagaagcctttna 339  
 Cp 1251 CTCGGCTGCCATTGCTCTCCCACTCCACGG-CGATGTCGCTGGATAGAAGCCTTGA 1193  
 Db 340 ccaggaggtcaggtgancgtggttcttggtcatctctcccggtgattggggcagggt 399  
 Cp 1192 CCAGCGAGTCAAGTCACTGG-TTCTTGCTCAGCTCATCCCGGATCGGGCAGGCTG 1134  
 Db 400 taaacgctngttctcggggtgctccctngt-ttngaaaangttt-tcgatgggntt 457  
 Cp 1133 TACACTGCTGCTTCGCGGGCTCCCTTGGCTTGGAGATGGTTTCTTCATGGGGCT 1074  
 Db 458 ggaag 462  
 Cp 1073 GCGAG 1069

## RESULT 9

LOCUS R66507 358 bp mRNA EST 30-MAY-1995  
 DEFINITION Y132f05.r1 Homo sapiens cDNA clone 140961 5' similar to gb:M87789  
 IG GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION R66507

NID g839145

KEYWORDS EST.

SOURCE human clone=140961 library=Soares placenta Nb2HP vector=pt7T3D  
 (Pharmacia) with a modified polylinker host=DH10B (ampicillin  
 resistant) primer=M13R1 Rsite1=Not I Rsite2=Eco RI Female placenta  
 obtained at birth (full term). 1st strand cDNA was primed with a  
 Not I - oligo(dT) primer [5'  
 AACTGGAGATTCGGCGCGCAGGAATTTTTTTTTTTTTTTT 3'], double-stranded  
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
 I and cloned into the Not I and Eco RI sites of the modified pT73  
 vector. Library went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 358)

## REFERENCE

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Treviskie,E., Waterston,R., Williamson,A., Wohlmann,P. and  
 Wilson,R.

TITLE

JOURNAL

COMMENT

The WashU-Merck EST Project  
 Unpublished (1995)

Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800

Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 219  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 839145

FEATURES

source Location/Qualifiers  
 1..358  
 /organism="Homo sapiens"  
 /clone="140961"  
 /note="human"

BASE COUNT 90 a 109 c 92 g 63 t 4 others

ORIGIN

Query Match 19.9%; Score 285; DB 64; Length 358;  
 Best Local Similarity 97.8%; Pred. No. 0.00e+00;  
 Matches 310; Conservative 0; Mismatches 3; Indels 4; Gaps 4;  
 Db 2 acaagtgaaggtctccaacaagaagcctccagcccccatcgagaaacacatctccaag 61  
 QY 1043 ACAAGTGAAGGTCTCCAACAAGGCCCTCCAGCCCCCATCGAAAAACCATCTCCAAAG 1102  
 Db 62 ccaaggcgagccccgagaaacacacaggtgtacacctgcccccatccccggatgagctga 121  
 QY 1103 CCMAAGGCGAGCCCGGAGAACACAGAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGA 1162  
 Db 122 ccaagaacaggctcagctgacctgctggtcaaggcttctatccacgagcatcgccg 181  
 QY 1163 CCMAACACAGGTGAGCCTGACCTGCCTGCTGAAGGCTTATCCAGCCACATCGCCG 1222  
 Db 182 tggagtggagagcaatggcgagcgagaaacaactacaagaccgctcccggtgctgg 241  
 QY 1223 TGAAGTGGGAGAGCAATGGGCGCGGAGAACAACTACAGACCCAGCGCTCCCGTGTCTG 1282  
 Db 242 gattccgagctctctctctcttcttctacagcaagntaccgtggagacagagctgg 301  
 QY 1283 -ACTCCAGCGCTCCTCTTCTCTCT-ACAGCAAGCTCACCTGG-ACAAGAGCAGGT-GC 1338  
 Db 302 cagcaggggaaacgnttt 318  
 QY 1339 CAGCAGGGGAACGTCTT 1355

## RESULT 10

LOCUS H28084 421 bp mRNA EST 13-JUL-1995  
 DEFINITION Y156d10.s1 Homo sapiens cDNA clone 162259 3' similar to gb:M87789  
 IG GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION H28084

NID g898437

KEYWORDS EST.

SOURCE human clone=162259 library=Soares breast 3NbBst vector=pt7T3D  
 (Pharmacia) with a modified polylinker host=DH10B (ampicillin  
 resistant) primer=Promega -21ml3 Rsite1=Not I Rsite2=Eco RI Adult  
 human. 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 [5' TCTTACCAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
 digested with Not I and cloned into the Not I and Eco RI sites of a  
 modified pT73 vector (Pharmacia). Library went through one round  
 of normalization to a Cot = 20. Library constructed by Bento Soares  
 and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

[illegible]

cp 1251 CTCCGGCTGCCCATTTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAACCTTTGAC 1192

Db 317 caggcagctcagctgacctgggtttcttgctcagctccatcccggatgggaggggt 434  
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Cp 1191 CAGGACAGGTGAGCTGAGTGG-TTCTTGGTCACTCATCCCGGGATGGGGCAGGGT 1135

RESULT 12 T65937 436 bp mRNA EST 20-FEB-1995  
LOCUS yc24f06.e1 Homo sapiens cDNA clone 81635 3' similar to gb:M87789 IG  
DEFINITION GAMMA-1 CHAIN C REGION (HUMAN);  
ACCESSION T65937  
NID g674982  
KEYWORDS EST.  
SOURCE human clone=81635 library=Stratagene lung (#937210)  
vector=pBluescript SK- host=SOIR cells (kanamycin resistant)  
primer=21ml3 Reitel=EcRI Reitel2=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTGGCAGAG-3'; 3' adaptor sequence:  
5'-CTCGAGTTTTTTTTTTTTTTT-3'.  
Homo sapiens  
ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 436)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfs, T., Tan, F., Trevas, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 241  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 674982  
FEATURES  
source Location/Qualifiers  
1..436  
/organism="Homo sapiens"  
/clone="81635"  
/note="human"  
BASE COUNT 74 a 113 c 140 g 104 t 5 others  
ORIGIN  
Query Match 19.2%; Score 275; DB 99; Length 436;  
Best Local Similarity 94.2%; Pred. No. 0.00e+00;  
Matches 310; Conservative 0; Mismatches 15; Indels 4; Gaps 4;  
Db 112 tttcccgagacaggagagctcttcgctgtagtggttgaganc-teatgcatc 170  
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Cp 1427 TTACCCGAGACAGGAGAGGCTCTTCTCGCTGCTAGTGGTTGTCAGAGCCTCATGCTC 1368  
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Db 171 acggagcatgagaaagacttccctgctgcccactctcttgctccacggtgagctt-ctg 229  
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Cp 1367 ACGGAGCATGAGAGACGCTCCCTCTGCTGCCACCTGCTTGTCCACGGTGAGCTTGCTG 1308  
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Db 230 tagaggaagaaggagcgctcgaggtccagcagcgggagcggtgtttagttgtctcc 289

Cp 1307 TAGAGGAAGAAGGAGCGCTCGAGTCCAGGACGGAGCGGTGGTCTTGTAGTTCTTC 1248  
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Db 290 ggtgcccactgtctcccacttcacggcgtgctgctgggataagaagc-tttnaccagg 348  
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Cp 1247 GGTGCCCATTTGCTCTCCACTCCAGCGGAGTCTGCTGGATAGAGGCTTTTCACAGG 1188  
|||||  
Db 349 naagtgaagctgactgggtctcttggttaa-ctcatcccggtgagggcaaggtatacaac 407  
|||||  
Cp 1187 CAGGTCAAGCTGACTGCTGTTCTTGGTCACTCATCCCGGATGGGGCAGGCTGTACACC 1128  
|||||  
Db 408 tgtggtctcgggggttcctccttttgcctt 436  
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Cp 1127 TGTGTTCTCGGGGCTGCCCTTTGGCTTT 1099  
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RESULT 13 T65912 479 bp mRNA EST 20-FEB-1995  
LOCUS yclih01.r1 Homo sapiens cDNA clone 80401 5' similar to gb:M87789 IG  
DEFINITION GAMMA-1 CHAIN C REGION (HUMAN);  
ACCESSION T65912  
NID g674957  
KEYWORDS EST.  
SOURCE human clone=80401 library=Stratagene lung (#937210)  
vector=pBluescript SK- host=SOIR cells (kanamycin resistant)  
primer=M13RPI Reitel=EcRI Reitel2=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTGGCAGAG-3'; 3' adaptor sequence:  
5'-CTCGAGTTTTTTTTTTTTTTT-3'.  
Homo sapiens  
ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 479)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfs, T., Tan, F., Trevas, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 273  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 674957  
FEATURES  
source Location/Qualifiers  
1..479  
/organism="Homo sapiens"  
/clone="80401"  
/note="human"  
BASE COUNT 104 a 140 c 130 g 98 t 7 others  
ORIGIN  
Query Match 19.1%; Score 273; DB 99; Length 479;  
Best Local Similarity 96.7%; Pred. No. 0.00e+00;

Matches 323; Conservative 0; Mismatches 3; Indels 8; Gaps 8;

Db 1 cagccccatcgagaaacaccatctcaagcaagcgaagcagccccgagacacaggtgt 60  
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Qy 1073 CAGCCCCATCGAGAAACCATCTCAAGCCRAAGGGCAGCCCCGAGACACAGGTGT 1132  
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Db 61 atacctgcccccatccccgggatgagctgaccaagaaccaggtcagcctgacctgctgtg 120  
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Qy 1133 ACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTCAACCTGACCTGCTGG 1192  
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Db 121 tcaaggcttctatccagcagcatcgctggagtgagagcaaatggcagccgagaga 180  
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Qy 1193 TCAAGGCTTCTATCCAGGACATCGCGTGGAGTGGGAGCAATGGCAGCCGGAGA 1252  
|||||  
Db 181 acaactacaagaccagctcccgctgctggaactccgagcgtctcttctctctacagca 240  
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Qy 1253 ACAACTACAAGACCAGCCTCCCGTCTGGACTCCGACGGCTCTTCTTCTCTACAGCA 1312  
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Db 241 agctcaactgggacaagcagcgtggcagcagcggggaacgtcttctctcatgttcgt 300  
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Qy 1313 AGCTCACCTGG-ACAGACAGCTGG-CAGCAGGGGAACGTCTT-CT-CATGCT-CCGT 1367  
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Db 301 tgatcatgagagctcttgcaacacattacagc 334  
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Qy 1368 -CATCATG-AGGCTCT-GCACAACCACTACAGC 1398  
|||||

RESULT 14  
LOCUS H61373 297 bp mRNA EST 06-OCT-1995  
DEFINITION yu41d01.r1 Homo sapiens cDNA clone 236353 5' similar to gb:M87789  
IG GAMMA-1 CHAIN C REGION (HUMAN);  
ACCESSION H61373  
NID g1014205  
KEYWORDS EST.  
SOURCE clone=236353 primer=M13RPL1 library=Soares ovary tumor NMHOT  
vector=pT7T3D (Pharmacia) with a modified polyLinker host=DH10B  
(ampicillin resistant) Reitel=Not I Reite2=Eco RI female. 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGGAGCGCGGTTTTTTTTTTTTTTT 3',  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73 vector (Pharmacia). Library  
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 297)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaakis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality.

NCBI gi: 1014205 Location/Qualifiers  
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/clone="236353"  
<1..>297  
BASE COUNT 81 a 92 c 75 g 41 t 8 others  
ORIGIN  
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Best Local Similarity 94.3%; Pred. No. 0.00e+00;  
Matches 280; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
Db 1 cagactngcgaatggcaaggagacaaagtgcgaagctcccaaaagccctccagcc 60  
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Qy 1018 CAGACTCGCTGAATGGCAAGAGTACAAGTGAAGTCTCCAACAAGAGCCCTCCAGCC 1077  
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Db 61 cagatcgagaaacaccatctcaaaagcgaagggcagcccccagacacacaggtgtacac 120  
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Qy 1078 CCATCGAGAAACCATCTCAAAAGCCAAAGGGCAGCCCGGAGACACAGGTGTACACC 1137  
|||||  
Db 121 ctgccccatccccggagagatgacccaaagcagcagctcagcctgacctgctgtcaaa 180  
|||||  
Qy 1138 CTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTCAACCTGCTGCTGTGAAA 1197  
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Db 181 ggcttctatccccagcagcatcgctggagtgagagcaaatggcagccgagancanc 240  
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Qy 1198 GGTTCTATCCAGGACATCGCGCTGGAGTGGGAGCAATGGCGGAGCAAC 1257  
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Db 241 tacaagaccagcttcctgctggactnagcagcgtctcttcttctctatagcaag 297  
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Qy 1258 TACAAGACACCGCTCCGCTGCTGGACTCCGACGGCTCTTCTTCTCTACAGCAAG 1314  
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RESULT 15  
LOCUS T59950 418 bp mRNA EST 09-FEB-1995  
DEFINITION y01907.s1 Homo sapiens cDNA clone 79452 3' similar to gb:M87789 IG  
GAMMA-1 CHAIN C REGION (HUMAN);  
ACCESSION T59950  
NID g661787  
KEYWORDS EST.  
SOURCE human clone=79452 library=Stratagene lung (#937210)

vector=pBluescript SK- host-SOLR cells (kanamycin resistant)  
primer=-21ml3 Reitel=EcoRI Reite2=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:  
5'-CTCGAGTTTTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 418)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaakis,E.,  
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.  
WashU-Merck EST Project

JOURNAL  
COMMENT

Unpublished (1995)

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 339  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 661787

## FEATURES

Location/Qualifiers  
source  
1..418  
/organism="Homo sapiens"  
/clone="79452"  
/note="human"

BASE COUNT 70 a 110 c 136 g 93 t 9 others  
ORIGIN

Query Match 18.4%; Score 264; DB 98; Length 418;  
Best Local Similarity 96.5%; Pred. No. 0.00e+00;  
Matches 277; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

Db 132 tcattaccggagagacaggagaggtcttctgtgtagtgttntgcagagcctcatg 191  
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Cp 1431 TCATTTACCGGACAGGAGGAGGCTCTTCGCTGTAGTGGTTGTGACAGCCTCATG 1372  
|||||

Db 192 catcacggagcatgagaagcgttccctgctgccacctgctcttntccacggtgagctt 251  
|||||

Cp 1371 CATCAGGAGCATGAGAGAGCTTCCCTGCTGCCACCTGCTCTTCTCCAGGCTGAGCTT 1312  
|||||

Db 252 gctntagagaagaaggagcctcggagtcaggacacggaggcgtggtcttgtagtgtt 311  
|||||

Cp 1311 GCTGTAGAGAGAGAGAGGCGCTCGGAGTCCACACGGGAGGGCGTGGTCTTGTAGTGT 1252  
|||||

Db 312 ctccggtgccattgctctccactccacggcgatntcgctgggtagaagccttgac 371  
|||||

Cp 1251 CTCGGGTGCCATTGCTCTCCACTCCACGGCGATGTGGTGGGATAGAAGCCTTGCAC 1192  
|||||

Db 372 caggcaggtcaggtgacctgggttcttgggtcancatcccnnga 418  
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Cp 1191 CAGGAGGTCAGGCTGACCTGG-TTCTTGG-TCAGTCTATCCCGGA 1147  
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Search completed: Tue Dec 17 23:28:56 1996  
Job time : 522 secs.



Qy 7 LLGLLLLPARGCAYELTQPPSVSPQGTARITCGDNRNEVHHYQKPARAPILV 66  
Db 66 vyddsrpsigperfgsgnsgntatliarveagdeadyycqwdssdhvfgggtkl 125  
Qy 67 IYDSDRPSGIPERFSGSGNATLTINGVEAGDEADYYCQWDRASDPVFGGTRVT 126  
Db 126 vlgqkaapvtlfpssseelqankatlvcclisdfypgavtvawkadspvkagvettpp 185  
Qy 127 VLGQKPAAPSVTLFPSSSEELQANKATLVCLISDFYPCAVTVAMKADSPVKAGVETTP 186  
Db 186 skqnnkyaasylltpcqwkshrsyqcvtghegstvektvaptces 233  
Qy 187 SKQNNKYAASSYLSLTPQWKSHRSYSCQVTHGEGSTVEKTVPTECS 234

RESULT 2  
ENTRY S25756 #type complete  
TITLE Ig lambda chain - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change  
ACCESSIONS 26-May-1995  
REFERENCE S25756  
#authors S16439  
#journal Combratio, G.; Klobeck, H.G.  
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.  
#cross-references MUID:91257162  
#accession S25756 preliminary  
#molecule\_type mRNA  
#residues 1-232 ##label COM  
#cross-references EMBL:X57821  
#note translation of nucleotide sequence is not given  
SUMMARY #length 232 #molecular-weight 24489 #checksum 4042

Query Match 80.0%; Score 1319; DB 11; Length 232;  
Best Local Similarity 86.0%; Pred. No. 6.88e-143;  
Matches 196; Conservative 14; Mismatches 16; Indels 2; Gaps 2;  
Db 7 llglsh-ctgavtgyvlcpssvavpqtasitcggnnigskavhwqkpgapvlv 65  
Qy 7 LLGLLLLPARGCAYELTQPPSVSPQGTARITCGDNRNEVHHYQKPARAPILV 66  
Db 66 vyddsrpsigperfgsgnsgntatliarveagdeadyycqwdssdhvfgggtkl 124  
Qy 67 IYDSDRPSGIPERFSGSGNATLTINGVEAGDEADYYCQWDRASDPVFGGTRVT 126  
Db 126 vlgqkaapvtlfpssseelqankatlvcclisdfypgavtvawkadspvkagvettpp 184  
Qy 127 VLGQKPAAPSVTLFPSSSEELQANKATLVCLISDFYPCAVTVAMKADSPVKAGVETTP 186  
Db 186 skqnnkyaasylltpcqwkshrsyqcvtghegstvektvaptces 232  
Qy 187 SKQNNKYAASSYLSLTPQWKSHRSYSCQVTHGEGSTVEKTVPTECS 234

RESULT 3  
ENTRY S25738 #type complete  
TITLE Ig lambda chain - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change

ACCESSIONS 26-May-1995  
REFERENCE S25738  
#authors S16439  
#journal Combratio, G.; Klobeck, H.G.  
#title Eur. J. Immunol. (1991) 21:1513-1522  
V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.  
#cross-references MUID:91257162  
#accession S25738 preliminary  
#status preliminary  
#molecule\_type mRNA  
#residues 1-231 ##label COM  
#cross-references EMBL:X57802  
#note translation of nucleotide sequence is not given  
SUMMARY #length 231 #molecular-weight 24473 #checksum 2186

Query Match 77.1%; Score 1271; DB 11; Length 231;  
Best Local Similarity 81.1%; Pred. No. 6.47e-137;  
Matches 189; Conservative 21; Mismatches 19; Indels 4; Gaps 4;  
Db 3 wipl-flgvla-yctgvasyeltqpsvsvapgtasitcgdtlqdkyacyqkpg 60  
Qy 2 RVPAAQLGLLLLPARGCAYELTQPPSVSPQGTARITCGDNRNEVHHYQKPAR 61  
Db 61 spvlvifqskpsigperfgsgnsgntatliarveagdeadyycqwdssdhvfgggtkl 118  
Qy 62 APILVYDDSDRPSGIPERFSGSGNATLTINGVEAGDEADYYCQWDRASDPVFGG 121  
Db 119 gktitvlgqkaapvtlfpssseelqankatlvcclisdfypgavtvawkadspvkagv 178  
Qy 122 GTRTVLGQKPAAPSVTLFPSSSEELQANKATLVCLISDFYPCAVTVAMKADSPVKAGV 181  
Db 179 ettqskqnnkyaasylltpcqwkshrsyqcvtghegstvektvaptces 231  
Qy 182 ETTTPSKQNNKYAASSYLSLTPQWKSHRSYSCQVTHGEGSTVEKTVPTECS 234

RESULT 4  
ENTRY S25751 #type complete  
TITLE Ig lambda chain - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change  
ACCESSIONS 26-May-1995  
REFERENCE S25751  
#authors S16439  
#journal Combratio, G.; Klobeck, H.G.  
#title Eur. J. Immunol. (1991) 21:1513-1522  
V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.  
#cross-references MUID:91257162  
#accession S25751 preliminary  
#status preliminary  
#molecule\_type mRNA  
#residues 1-231 ##label COM  
#cross-references EMBL:X57816  
#note translation of nucleotide sequence is not given  
SUMMARY #length 231 #molecular-weight 24583 #checksum 4106

Query Match 75.4%; Score 1243; DB 11; Length 231;  
Best Local Similarity 79.8%; Pred. No. 1.96e-133;  
Matches 186; Conservative 20; Mismatches 23; Indels 4; Gaps 4;



Db	3	wipl-flgvia-yctgsvasyeitqpsvsvpqqtasitcsgdklgdkyasewyqkpaq	60
	:	:   :	:     :
Qy	2	RVPALQLGLLLWLPARCAYELTQPSPVSPGQTARITCGGDNSENVEYHHVYQQKPAR	61
Db	61	spvlvyldnrpgisgerfagsngntatlitsetqvmdeadyycqawd--ssi-vvfvgg	118
	:	:   :	:     :
Qy	62	APLIVYDDSDRSGIPERFSGSKSNTATLTINGVACGEADYYCQWRASDHPVFEG	121
Db	119	gtklvtlscpkkaapsvtlfpssseelqankatlvcslidfyppgavtvawkadspvkagv	178
	:	:   :	:     :
Qy	122	GTRVTVLGQPKAAPSVTLFPSPSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGV	181
Db	179	ettptskgnnkyaasaylaltpeqwkhrsycqtthegstvektvaptecs	231
	:	:   :	:     :
Qy	182	ETTTPSKSNKYAASSYLSTPEQWKSHRSYCQVTHEGSTVEKTVAPTPCS	234
RESULT	5	S25753	#type complete
ENTRY		Ig lambda chain - human	
TITLE		#formal_name Homo sapiens #common name man	
ORGANISM		22-Nov-1993 #sequence_revision 26-May-1995 #text_change	
DATE		26-May-1995	
ACCESIONS		S25753	
REFERENCE		S16439	
#authors		Combiato, G.; Klobect, H.G.	
#journal		Eur. J. Immunol. (1991) 21:1513-1522	
#title		V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.	
#cross-references		MUID:91257162	
#accession		S25753	
##status		preliminary	
##molecule_type		mRNA	
##residues		1-231 #label COM	
##cross-references		EMBL:X57818	
##note		translation of nucleotide sequence is not given	
SUMMARY		length 231 #molecular-weight 24724 #checksum 4484	
Query Match		75.4%; Score 1242; DB 11; Length 231;	
Best Local Similarity		79.4%; Pred.No. 2.61e-133;	
Matches		185; Conservative 24; Mismatches 20; Indels 4; Gaps 3;	
Db	3	wipl-flgvia-yctgsvasyeitqpsvsvpqqtasitcsgdklgdkyasewyqkpaq	60
	:	:   :	:     :
Qy	2	RVPALQLGLLLWLPARCAYELTQPSPVSPGQTARITCGGDNSENVEYHHVYQQKPAR	61
Db	61	spvlvyldnrpgisgerfagsngntatlitsetqamdegdyycqawd--antvvfvgg	118
	:	:   :	:     :
Qy	62	APLIVYDDSDRSGIPERFSGSKSNTATLTINGVACGEADYYCQWRASDHPVFEG	121
Db	119	gtklvtlscpkkaapsvtlfpssseelqankatlvcslidfyppgavtvawkadspvkagv	178
	:	:   :	:     :
Qy	122	GTRVTVLGQPKAAPSVTLFPSPSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGV	181
Db	179	ettptskgnnkyaasaylaltpeqwkhrsycqtthegstvektvaptecs	231
	:	:   :	:     :
Qy	182	ETTTTSKSNKYAASSYLSTPEQWKSHRSYCQVTHEGSTVEKTVAPTPCS	234



```

#accession S25741
#status preliminary
#molecule_type mRNA
#residues 1-233 #label COM
#cross-references EMBL:X57805
#note translation of nucleotide sequence is not given
SUMMARY
#length 233 #molecular-weight 24977 #checksum 4094

```

Query Match	73.2%;	Score 1206;	DB 11;	Length 233;
Best Local Similarity	78.0%;	Pred.No. 7.73e-129;		
Matches	177;	Conservative	19;	Mismatches 30; Indels 1; Gaps 1;
Db	8	ltllclci-gsvvseel	tqdtvsevalgtlrlckcqdtkirsyasywqkpgqqaptlli	66
	: :	: :	: :	: :
	: :	: :	: :	: :
Qy	8	LGLILLLPGARCAVELTQP	PSVSPGQTARITCGDMSRNEYVHWYQKGRAPILVI	67
Db	67	ngkdrpsgipdrfgsgtsgntaelitqtqaedaadyncrdesahhlvfggqktlv	126	
	: :	: :	: :	: :
Qy	68	YDDSDRPSSGIPERFSGSKSGNTATLINGVEAGDEADYCQWDRASDPHFVGCGTRVTV	127	
Db	127	leopkaapvtvlfpssaeelqankatlvcldsfypagvtvawkadspvkagvettps	186	
	: :	: :	: :	: :
Qy	128	LQCPKAAPSFTVLPPSSEELQANKATLVCLISDFYPGAVTVAWKADSPVKAGVETTPS	187	
Db	187	kgnnkyaasyylslcpqwkshrsycqvthegstvektvaptcs	233	
	: :	: :	: :	: :
Qy	188	KGSNNKYAASYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTCS	234	

```

RESULT      11
ENTRY
TITLE
S25752      #type complete
lg lambda chain - human
#formal name Homo sapiens #common name man
ORGANISM
DATE        22-Nov-1993 #sequence revision 26-May-1995
#text change

```

S25752  
 May-1993  
 ACCESSIONS  
 REFERENCE  
 #authors  
 #journal  
 #title  
 Combratio, G.; Klobeck, H.G.  
 Eur. J. Immunol. (1991) 21:1513-1522  
 V(Lambda) and J(Lambda)-C(lambda) gene segments of the human  
 immunoglobulin lambda light chain locus are separated by 14  
 kb and rearrange by a deletion mechanism.

```

#cross-references MUID:91257162
#accession S25752
##status preliminary
##molecule_type mRNA
##residues 1-233 ##label COM
#cross-references EMBL:X57817
##note translation of nucleotide sequence is not given
#length 233 #molecular-weight 24516 #checksum 3842
SUMMARY

```

Query Match 70.3%; Score 1158; DB 11; Length 233;  
Best Local Similarity 74.3%; Pred. No. 6.97e-123;  
Matches 171; Conservative 28; Mismatches 29; Indels 2; Gaps 1;

```

4  lltllthcagwagvltqpsasgtpgarvtlscsgssnlgtsntvnwyqqlpgtapk 63
   || || :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
7  LLGLLLWLPGARCAVELTQPPSVSPGGTARTCGGDSNR--NEYVHYQOKPARAPI 64

```

64 Db llyrnrpvgvdfrrfsgkskgtssalrsglasedeadyycaawddslngvvfgggtk 123  
 :|| :||:||||:||||||| :||:|:|:| :||||| || :| :|||:|:  
 65 Qv LVYDDSDRSPGIPERFGSKSGKNTATLTNGVEAGDEADYYCOVWDRADHPVFEGGTR 124

Db 124 ltvlgppkaapsvtlfppsseelqankatlvcldsfypqavtvawkadsspvkaqvett 183

Qy	125	VTVLQGPKAAPSVTLFFPSPSEELQANKATLVCLISDFYFGAVTVAMKADSSPVKAGVETT	184
	:		
Db	184	tpqgknkyaasyalsltpeqwkshrayscqqrthegstvektvaptce	233
Ov	185	TPSKQSNKYYAASYSLLTPPEOMKSHRSYSGVTHFGSTVEKTVAPTEGS	234

```

RESULT      12
ENTRY
TITLE       Ig lambda chain - human
ORGANISM    Homo sapiens
DATE        22-Nov-1993
            #sequence_revision 26-May-1995
            #text_change      26-May-1995
ACCESSIONS  S25750
REFERENCE    S16439
            Combiato, G.; Klobeck, H.G.
            Eur. J. Immunol. (1991) 21:1513-1522
            V(lambda) and J(lambda)-C(lambda) gene segments of the human
            immunoglobulin lambda light chain locus are separated by 14
            kb and rearrange by a deletion mechanism.

```

```

#cross-references MIMD: 91257162
#accession S25750
#status preliminary
#molecule_type mRNA
#residues 1-235 #label COM
#cross-references EMBL:X57815
#note translation of nucleotide sequence is not given
#length 235 #molecular_weight 24710 #checksum 48290
SUMMARY

```

Query Match	70.1%;	Score 1155;	DB 11;	Length 235;
Best Local Similarity	74.3%;	Pred. No. 1.64e-122;		
Matches	171;	Conservative	25;	Mismatches 32;
			Indels	2;
			Caps	2;

6	lltllthcagwaqsvltqpssagtpggrvtiscsgassnigtndvwywqqtlgtapk	65
	:          :    :    :    :    :	
7	lglllllwlpgarcaveltoppssvspsggtaritccgdnsr-ney-vhwyoookparapi	64

Db 66 llyirnnrpsgvprfsgsksgssaslaesglqsedeadyycaawddslegpvfgggtk 125  
 :||| ::|||||:||| |||||:::|||:: ||||| ||| : |||||:  
 Qv 65 lvviyddsrfsgiperefskskgntatlttngveagdeadyvcowdrasdhpfvggtr 124

```

Db      126 ltvlgpkaapsvlfppsseelqankatlvcvlisdfypgavtvawkadapsvkagvett 185
      :|||||
Qv      125 vtvlgopkaapsvtlfpfpssseelqankatlvcvlisdfypgavtvawkadapsvkagvett 184

```

**Db**

186	t p q s n k y a z s y l s i t p e q w k h r s v s c q v t h e g s t v e k t v a p t e c s	235

**Ov**

185	T P Q S O N K Y A Z S Y L S I T P F O W K S H R S V C O V T H E G S T V E K T V A P T E C S	234

RESULT	13
ENTRY	S25759 #text_complete
TITLE	Ig lambda chain - human
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	22-Nov-1993 #sequence_revision 26-May-1995 26-May-1995 #text_change

#authors  
#journal  
#title  
Combrinato, G.; Klobeck, H.G.  
Eur. J. Immunol. (1991) 21:1513-1522  
V(lambda) and J(lambda)-C(lambda) gene segments of the human  
immunoglobulin lambda light chain locus are separated by 14  
kb and rearrange by a deletion mechanism.

Dec 17 15:00

US-08-487-550-2.rpr

11

#cross-references MUID:91257162

#accession S25759

#status preliminary

#molecule\_type mRNA

#residues 1-235 ##label COM

#cross-references EMBL:X57824

#note translation of nucleotide sequence is not given

#summary #length 235 #molecular-weight 24748 #checksum 5527

Query Match

Best Local Similarity 69.7%; Score 1149; DB 11; Length 235;

Matches 178; Conservative 17; Mismatches 32; Indels 5; Gaps 4;

Db 5 llflltlltqgtgswagaltqpasvsgpqsitiscigtssediqayfvwyqyypka 64

||| ||| :: ||||| ||||| ||| : | ||||| ::|

Qy 7 LIGLLLLL-L-PCARCAYELTQPPSVSPGQTARITC-GGDSRNEY--VHWYQKPARA 62

Db 65 pkllifdvgrpsisrfsfgskagntasltisglqaeadeadyycasyarset-vvifggg 123

| :| :| ||||| : ||||| ||||| :| :| ||||| | :| |||||

Qy 63 PILVIYDDSDRPSGIPERFSKSGNTATITINGVEAGDEADYYCQWDRADSPVFGG 122

Db 124 lvtvlqgpkapavtlfppsseelqankatlvclicsfygcqvtthegstvektvaptcs 183

| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 123 TRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAKADSPVKAGVE 182

Db 184 ttpskqsnknyaaasyllstpeqwkshrsycqvtthegstvektvaptcs 235

| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 183 TPTTSKQSNKYAASSYLSTPEQWKSHRSYCQVTHEGSTVEKTVAPECS 234

RESULT 14

ENTRY S14675

TITLE Ig lambda chain - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 19-May-1994 #sequence\_revision 19-May-1994 #text\_change

ACCESSIONS S14675; S12445

REFERENCE S14675

#authors Vasicek, T.J.

#submission submitted to the EMBL Data Library, February 1990

#accession S14675

#molecule\_type DNA

#residues 1-235 ##label VAS1

#cross-references EMBL:X51754

REFERENCE S12440

#authors Vasicek, T.J.; Leder, P.

#journal J. Exp. Med. (1990) 172:609-620

#title Structure and expression of the human immunoglobulin lambda

genes.

#cross-references MUID:90324881

#accession S12445

#molecule\_type DNA

#residues 1-129 ##label VAS2

#cross-references EMBL:X51754

GENETICS

#introns 16/1; 130/1

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

#summary #length 235 #molecular-weight 24859 #checksum 7937

Query Match

Best Local Similarity 69.6%; Score 1147; DB 5; Length 235;

Matches 174; Conservative 25; Mismatches 28; Indels 5; Gaps 5;

Db 5 llflltlltqgtgswagaltqpasvsgpqsitiscigtssediqayfvwyqyypka 64

Dec 17 15:00

US-08-487-550-2.rpr

12

Qy 7 LIGLLLLL-L-PCARCAYELTQPPSVSPGQTARITCGDINS-R-N-EYVHWYQKPARA 62

||| ||| ||:: ||||| ||| : ||| :| :| ||| ||| :| :

Db 65 pkllmyevtkrpsgvprfsgskagntasltisglqaeadeadyycasya-ganellifggg 123

| :| :| ||||| : ||||| ||||| :| :| ||||| | :| |||||

Qy 63 PILVIYDDSDRPSGIPERFSKSGNTATITINGVEAGDEADYYCQWDRADSPVFGG 122

Db 124 trltvlqgpkapavtlfppsseelqankatlvclicsfygcqvtthegstvektvaptcs 183

| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 123 TRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAKADSPVKAGVE 182

Db 184 ttpskqsnknyaaasyllstpeqwkshrsycqvtthegstvektvaptcs 235

| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 183 TPTTSKQSNKYAASSYLSTPEQWKSHRSYCQVTHEGSTVEKTVAPECS 234

RESULT 15

ENTRY S25757

TITLE Ig lambda chain - human (fragment)

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change

ACCESSIONS S25757

REFERENCE S16439

#authors Combiato, G.; Klobbeck, H.G.

#journal Eur. J. Immunol. (1991) 21:1513-1522

#title V(lambda) and J(lambda)-C(lambda) gene segments of the human

immunoglobulin lambda light chain locus are separated by 14

#note kb and rearrange by a deletion mechanism.

#cross-references MUID:91257162

#accession S25757

#status preliminary

#molecule\_type mRNA

#residues 1-234 ##label COM

#cross-references EMBL:X57822

#note translation of nucleotide sequence is not given

#summary #length 234 #checksum 5342

Query Match 69.4%; Score 1143; DB 11; Length 234;

Best Local Similarity 72.6%; Pred. No. 5.04e-121;

Matches 167; Conservative 32; Mismatches 29; Indels 2; Gaps 1;

Db 5 llflltlltqgtgswagaltqpasvsgpqsitiscigtssediqayfvwyqyypka 64

||| ||| :: ||||| ||||| ||| : ||| :| :| ||| ||| :| :

Qy 7 LIGLLLLL-L-PCARCAYELTQPPSVSPGQTARITCGDINSR--NEYVHWYQKPARAPI 64

Db 65 vlylmynerpsvprfsgskagntasltisglqaeadeadyycawddslngllgggtk 124

: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Qy 65 LIVYDDSDRPSGIPERFSKSGNTATITINGVEAGDEADYYCQWDRADSPVFGGTR 124

Db 125 ltvlgqpkapavtlfppsseelqankatlvclicsfygcqvtthegstvektvaptcs 184

: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAKADSPVKAGVET 184

Db 185 tpskqsnknyaaasyllstpeqwkshrsycqvtthegstvektvaptcs 234

| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 185 TPSKQSNKYAASSYLSTPEQWKSHRSYCQVTHEGSTVEKTVAPECS 234

Search completed: Tue Dec 17 15:14:38 1996

Job time : 37 secs.



RP. SEQUENCE (BENCE-JONES PROTEIN KERN).  
 RX MEDLINE; 71150336.  
 RA PONTING L H., HESS M., HILSCHMANN N.J.  
 RL HOPPE-SEYLER' S Z. PHYSIOL. CHEM. 352:247-266(1971).  
 RN [5]  
 RP PARTIAL SEQUENCE (MYELOMA PROTEIN NEMM).  
 RX MEDLINE; 74109253.  
 RA CHEN B.-L., POLJAK R.J.;  
 RL BIOCHEMISTRY 13:1295-1302(1974).  
 RN [6]  
 RP SEQUENCE (DOT).  
 RX MEDLINE; 95255298.  
 RA STOPPINI M., BELLIOTTI V., NEGRI A., MERLINI G., GARVER F., FERRI G.;  
 RL EUR. J. BIOCHEM. 228:886-893(1995).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEMM.  
 RX MEDLINE; 75046825.  
 RA POLJAK R.J., AMZEL L.M., AVEY H.P., CHEN B.-L., PHIZACKERLEY R.P.,  
 RL SAUL F.;  
 RN PROC. NATL. ACAD. SCI. U.S.A. 71:3440-3444(1974).  
 RP [8]  
 RP PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).  
 RX MEDLINE; 75013804.  
 RA FETT J.W., DEUTSCH H.F.;  
 RL BIOCHEMISTRY 13:4102-4114(1974).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.  
 RX EDMUNDSON A.B., ELY K.R., ABOLA E.E., SCHIFFER M.,  
 RA PANAGIOTOPOULOS N.J.  
 RL BIOCHEMISTRY 14:3953-3961(1975).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY OF MCG.  
 RX MEDLINE; 90133913.  
 RA ELY K.R., HERRON J.N., HARKER M., EDMUNDSON A.B.;  
 RL J. MOL. BIOL. 210:601-615(1989).  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 82080680.  
 RA HIEYER P.A., HOLLIS G.F., KORSMEYER S.J., WALDMANN T.A., LEDER P.;  
 RL NATURE 294:536-540(1981).  
 CC -1- THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN FOUND IN PROTEINS  
 CC SH. X, AND NIG-64. THE KERN PROTEIN HAS THE KERN+ MARKER, THE NEMM  
 CC PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN HAS THE KERN+ MARKER,  
 CC AND THE MCG+ MARKER.  
 CC -1- SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE 3 MOST 5' WERE  
 CC SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE (LAMBDA-1), THE  
 CC KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+ SEQUENCE (LAMBDA-3).  
 CC PIR; A02125; L2HU.  
 DR PDB; 2MCG; 15-JUL-92.  
 DR PDB; 7FAB; 31-JAN-94.  
 DR MIM; 147220; 11TH EDITION.  
 DR PROSITE; PS00290; IG MHC.  
 KW IMMUNOGLOBULIN C REGION; 3D-STRUCTURE.  
 FT NON\_TER 1 1  
 FT DISULFID 27 86  
 FT DISULFID 104 104  
 FT VARIANT 5 5  
 FT VARIANT 7 7  
 FT VARIANT 45 45  
 FT VARIANT 56 56  
 FT VARIANT 82 82  
 FT STRAND 4 4  
 FT STRAND 7 11  
 FT HELIX 15 19  
 FT INTERCHAIN (WITH HEAVY CHAIN).  
 A -> N (IN MCG+ MARKER).  
 S -> T (IN MCG+ MARKER).  
 S -> G (IN KERN+ MARKER).  
 T -> K (IN MCG+ MARKER).  
 R -> K (IN OZ+ MARKER).

FT	TURN	20	21	
FT	STRAND	23	33	
FT	STRAND	38	43	
FT	TURN	44	45	
FT	STRAND	46	48	
FT	TURN	50	51	
FT	STRAND	52	54	
FT	STRAND	58	59	
FT	TURN	61	62	
FT	STRAND	65	73	
FT	HELIX	75	79	
FT	TURN	80	80	
FT	STRAND	84	90	
FT	TURN	91	92	
FT	STRAND	93	99	
SEQ	SEQUENCE	105 AA; 11236 MW; 67031 CN;		
Query Match 42.8%; Score 706; DB 5; Length 105;				
Best Local Similarity 100.0%; Pred. No. 1.68e-135;				
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Db	1 qpkaapvtlfpssaeelqankatlvcslisdfypgavtvankadspvkagvetttskq 60			
Qy	130 qpkaapvtlfpssaeelqankatlvcslisdfypgavtvankadspvkagvetttskq 189			
Db	61 snkyaassylsltpqpkshrsycqtrhegatkvektvaptcs 105			
Qy	190 snkyaassylsltpqpkshrsycqtrhegatkvektvaptcs 234			
RESULT 2				
ID	I141 HUMAN STANDARD; PRT; 213 AA.			
AC	P15814;			
DT	01-APR-1990 (REL. 14, CREATED)			
DT	01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)			
DT	01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)			
DE	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
CC	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 89315835.			
RA	HOLLIS G.F., EVANS R.J., STAFFORD-HOLLIS J.M., KORSMEYER S.J.,			
RA	MCKEARN J.P.;			
CC	PROC. NATL. ACAD. SCI. U.S.A. 86:5552-5556(1989).			
CC	-I- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL			
CC	B-CELL LINE (WHICH IS SURFACE IG NEGATIVE).			
CC	-I- THIS LAMBDA LIGHT-CHAIN-RELATED PROTEIN MAY BE THE IMMUN-			
CC	GLOBULIN OMEGA LIGHT-CHAIN.			
CC	-I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY			
CC	AND SHOWS SIMILARITY TO LAMBDA LIGHT CHAIN IN C-TERMINAL HALF			
CC	(J AND C REGIONS).			
CC	EMBL; M27749; M27749.			
DR	PIR; A33911; A33911.			
DR	HSP; P01842; 8FAB.			
DR	PROSITE; PS00290; IG MHC.			
KW	IMMUNOGLOBULIN FOLD; B-CELL; SIGNAL.			
FT	SIGNAL	1	?	
FT	CHAIN	?	213	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN.
FT	DOMAIN	97	108	J REGION (BY SIMILARITY TO LAMBDA
FT				LIGHT-CHAIN).
FT	DOMAIN	109	213	C REGION (BY SIMILARITY TO LAMBDA
FT				LIGHT-CHAIN).





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ID  LACI MOUSE STANDARD; PRT; 105 AA.
AC  P01843;
DT  21-JUL-1986 (REL. 01, CREATED)
DT  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT  01-APR-1988 (REL. 07, LAST ANNOTATION UPDATE)
DE  IG LAMBDA-1 CHAIN C REGION.
OS  MUS MUSCULUS (MOUSE).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; RODENTIA.
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE; 83014953.
RA  SELING E., MILLER J., WILSON R., STORB U.;
RL  PROC. NATL. ACAD. SCI. U.S.A. 79:4681-4685(1982).
RN  [2]
RP  SEQUENCE FROM N.A. (MOPC 315).
RX  MEDLINE; 81148806.
RA  BOTHWELL A.L.M., PASKIND M., SCHWARTZ R.C., SONENSHAIN G.E.,
RA  GEFTER M.L., BALTIMORE D.;
RL  NATURE 290:65-67(1981).
RN  [3]
RP  SEQUENCE FROM N.A. (S43).
RX  MEDLINE; 82220143.
RA  BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJENSKY K.,
RA  BALTIMORE D.;
RL  NATURE 298:380-382(1982).
RN  [4]
RP  SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX  MEDLINE; 71107854.
RA  APPELLA E.;
RL  PROC. NATL. ACAD. SCI. U.S.A. 68:590-594(1971).
CC  -!- THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1 NORMAL LAMBDA-2
CC  CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING A LARGE PART OF
CC  THE V REGION. THE C REGION SEQUENCE (SHOWN HERE) APPEARS COMPLET-
CC  ELY NORMAL.
DR  PIR; A02126; LIMS.
DR  HSP; P01842; LMF.
DR  PROSITE; PS00290; IG MHC.
RW  IMMUNOGLOBULIN C REGION.
FT  NON TER 1 1
FT  DISULFID 27 86
FT  DISULFID 104 104
FT  CONFLICT 19 20
FT  CONFLICT 56 56
FT  CONFLICT 75 75
FT  CONFLICT 81 82
FT  CONFLICT 85 85
FT  CONFLICT 96 96
SQ  SEQUENCE 105 AA; 11575 MW; 63813 CN;

Query Match 33.8%; Score 557; DB 5; Length 105;
Best Local Similarity 71.4%; Pred. No. 3.57e-100;
Matches 75; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

Db 1 gpkaspsvltfppseelgnkatlctidfygsvvtdvkwkdvdpvtggtmtpqsk 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAVKADSSPVKAGVETTPSKQ 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 ennkymassytlktarwerhsycqytheghtveksleradcs 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 190 SNKYAASSYLSLTPEQWKSHRSYSQVTHGEGSTVETKVTAPTECS 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Query Match 32.9%; Score 542; DB 5; Length 105;
Best Local Similarity 72.4%; Pred. No. 1.18e-96;
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ID  LAC2 RAT STANDARD; PRT; 104 AA.
AC  P20767;
DT  01-FEB-1991 (REL. 17, CREATED)
DT  01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT  01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE  IG LAMBDA-2 CHAIN C REGION.
OS  RATTUS NORVEGICUS (RAT).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; RODENTIA.
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE; 87305594.
RA  STEEN M.L., HELLMAN L., PETERSSON U.;
RL  GENE 55:75-84(1987).
DR  ENBL; M22521; M22521.
DR  PIR; B27390; B27390.
DR  HSP; P01842; IBJL.
DR  PROSITE; PS00290; IG MHC.
RW  IMMUNOGLOBULIN C REGION.
FT  NON TER 1 1
FT  DISULFID 27 85
FT  DISULFID 103 103
SQ  SEQUENCE 104 AA; 11318 MW; 58002 CN;

Query Match 32.9%; Score 542; DB 5; Length 104;
Best Local Similarity 65.4%; Pred. No. 1.18e-96;
Matches 68; Conservative 27; Mismatches 8; Indels 1; Gaps 1;

Db 1 gpkstplvtfpsteeelgnkatlclidfydsdvewkangaplegvdtanptkq 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAVKADSSPVKAGVETTPSKQ 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 gn-kylasflrltaeqwcrnsftcqhgtvekelepaec 103
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 190 SNKYAASSYLSLTPEQWKSHRSYSQVTHGEGSTVETKVTAPTEC 233
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
ID  LAC RABBIT STANDARD; PRT; 105 AA.
AC  P01847;
DT  21-JUL-1986 (REL. 01, CREATED)
DT  01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT  01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE  IG LAMBDA CHAIN C REGION.
OS  ORYCTOLAGUS CUNICULUS (RABBIT).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; LAGOMORPHA.
RN  [1]
RP  SEQUENCE.
RX  MEDLINE; 82091105.
RA  GARCIA I., JATON J.-C.;
RL  BIOCHEM. J. 197:177-183(1981).
CC  -!- THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC SPECIFICITY.
DR  PIR; A02130; L7RB.
DR  HSP; P01842; 7FAB.
DR  PROSITE; PS00290; IG MHC.
RW  IMMUNOGLOBULIN C REGION.
FT  NON TER 1 1
FT  DISULFID 27 86
FT  DISULFID 104 104
SQ  SEQUENCE 105 AA; 11484 MW; 62157 CN;

Query Match 32.9%; Score 542; DB 5; Length 105;
Best Local Similarity 72.4%; Pred. No. 1.18e-96;
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Search completed: Tue Dec 17 15:15:16 1996  
Job time : 20 secs.

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.	SUMMARIES	
								†	‡
1	1221	74.1	233	1	P81260	VDJC regions of human		3.63e-84	
2	1172	71.1	217	8	R42163	Anti-HIV-1 recombinan		2.54e-80	
3	1136	68.9	235	6	R31024	Antibody D light chai		1.69e-77	
4	126	44.1	234	7	R38162	Sequence of the kappa		1.52e-45	
5	725	44.0	236	15	R77614	Humanised 5C1.1 VL +		1.82e-45	
6	708	43.0	234	3	R20058	Light chain of 3D6 an		3.74e-44	
7	707	42.9	236	8	R42065	Human anti-HBs light		4.47e-44	
8	696	42.2	106	12	R69093	Anti-HIV Fab rev16/20		3.16e-43	
9	696	42.2	133	12	R69098	Anti-HIV Fab tat16/20		3.16e-43	
10	684	41.5	234	3	R13050	CD4-specific CDR-graf		2.67e-42	
11	681	41.3	234	10	R32951	Human anti-IgE MAb 11		4.54e-42	
12	668	40.5	238	16	R93554	Monoclonal antibody D		4.57e-41	

RESULT	1
ID	P81260 standard; protein; 233 AA.
AC	P81260;
DT	09-NOV-1990 (first entry)
DE	VJJC regions of human sperm-immobilising monoclonal antibody.
KW	Anti-human sperm-immobilising monoclonal antibody; leader region;
KW	variable region; joining region; constant region; sterility;
KW	vaccine; contraceptive.
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	Region 21..115
FT	/label=variable_region
FT	Region 116..127
FT	/label=joining_region
FT	Region 128..233
FT	/label=constant_region
PN	J63126482-A.
PD	30-MAY-1988.
PF	15-NOV-1986; 272412.
PR	15-NOV-1986; JP-272412.
PA	(TOFU) TOA NENRYO KOGYO KK.
DR	WPI; 88-187839/27.
DR	N-PSDB; N81655.
PT	Cell strain producing human sperm-immobilising monoclonal antibody
PT	has at least V-gene in H chain coding genetic family and V gene i
PT	chain of DNA originating from antibody of sterile woman.
PS	Disclosure: : 14pp; Japanese.

Key	Location/Qualifiers
AC	R31024 standard; Protein; 235 AA.
AC	R31024;
DT	19-MAY-1993 (first entry)
DE	Antibody D light chain.
KW	Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;
KW	lymphocyte; hepatitis A virus; HAV; sero; positive; patient;
KW	murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.
OS	Synthetic.
FT	Key
FT	Peptide
FT	/note= "Signal peptide"
FT	Region
FT	/label= FR1
FT	Region
FT	/label= CDR1
FT	Region
FT	/label= FR2
FT	Region
FT	/label= CDR2
FT	Region
FT	/label= FR3
FT	Region
FT	/label= CDR3
FT	Region
FT	/label= FR4
FT	Domain
FT	/label= C lambda
PN	EP-523949-A.
PD	20-JAN-1993.
PF	14-JUL-1992; 306420.
PF	15-JUL-1991; GB-015284.
PR	01-AUG-1991; GB-016594.
PR	23-MAR-1992; GB-006284.
PPA	(WELL ) WELLCOME FOUND LTD.
PI	Crowe JS, Lewis AP;
PI	WPI; 93-019951/03.
DR	N-PSDB; Q35100.
PT	Prodn. of recombinant primate antibodies - useful for treating
PT	infections caused by hepatitis A, B and C, herpes,
PT	cytomegalovirus, AIDS, ARC, also treat multiple sclerosis.

PT arthritis etc.  
 P5 Disclosure; Fig 3; 35pp; English.  
 CC The sequences given in R31023-24 represent the heavy and light chains  
 CC of Antibody D respectively. Antibody D is a monoclonal antibody which  
 CC was derived from peripheral blood lymphocytes from a hepatitis A virus  
 CC (HAV) sero positive patient. Antibody D is closely related in nature  
 CC to murine antibody B5B3. Total RNA was isolated from antibody D  
 CC expressing cells and polyadenylated RNA was extracted. These polyA  
 CC RNA's were used to prepare a cDNA library which was screened for human  
 CC kappa light (L) chains and two positive clones were detected.  
 CC Further heavy (H) chain clones were also isolated.  
 SQ Sequence 235 AA;

Query Match 68.9%; Score 1136; DB 6; Length 235;  
 Best Local Similarity 75.9%; Pred. No. 1.69e-77;  
 Matches 176; Conservative 21; Mismatches 30; Indels 5; Gaps 4;  
 Db 5 llllltlltdgtgwaqeaaltqpaasvsgpqsitctgtndvsgynlvsvyqhqbpka 64  
 Qy 7 LLGULLLWL-PCARCAYELTQPPSVSPQQTARITCGG-DNSRNEY--VHWYQKQPARA 62  
 Db 65 pkimiyevakrpsvsnrfsgskgntasltisglqaeadadyccsya-gsytvvfqgg 123  
 Qy 63 PILVIVDDSDRPSGIPERFSGSKSGNTATITNGVEAGDEADYQCVWDRASHPVFGG 122  
 Db 124 tklvtlqgkaapavtlfpssseelqankatlvcldisdfypgavtvawkadspvkagve 183  
 Qy 123 TRVTVLQGPKAAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVE 182  
 Db 184 ttptskqsnmkyaasyalsltpeqmkshrsyscqvtthegstvektvaptecs 235  
 Qy 183 TTTPTSKQSNMKYAASSYLSLTPEQMKSHRSYSQCVTTHEGSTVEKTVAPTECS 234

## RESULT 4

ID R38162 standard; Protein; 234 AA.  
 AC R38162;  
 DT 01-OCT-1993 (first entry)  
 DE Sequence of the kappa light chain variable region (VK) of human  
 DE immunoglobulin G3 (IgG3) produced by transformed human B-cell line  
 DE 88BV59, ATCC CRL 10624.  
 KW B-cell; immunoglobulin g; cancer; tumour.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Region 1..214  
 FT /\*tag= a  
 FT /label= 1st AA denoted AA#1  
 FT Region 24..49  
 FT /\*tag= b  
 FT /label= CDR 1  
 FT Region 50..88  
 FT /\*tag= c  
 FT /label= CDR 2  
 FT Region 89..108  
 FT /\*tag= d  
 FT /label= CDR 3  
 FT Region 109..214  
 FT /\*tag= e  
 FT /label= CON  
 PN EP-546634-A.  
 PD 16-JUN-1993.  
 PF 09-DEC-1992; 203827.  
 PR 13-DEC-1991; US-807300.  
 PA (ALKU ) AKZO NV.

PI Crichton VZ, Haapel MV, Kobrin BJ;  
 DR WPI; 93-190019/24.  
 DR N-PSDB; Q43773.  
 PT Transformed human B-cell line for monoclonal antibody prodn. for  
 PT cancer diagnosis - prod from peripheral blood B-cells of cancer  
 PT patients actively immunised with autologous tumour antigen, for  
 PT treating cancers  
 PS Claim 9; Fig 3; 18pp; English.  
 CC The 88BV59 kappa light chain sequence is indicated by the poase.  
 CC of the CDRs and the constant region exon. 88BV59 utilises Vx1 and  
 CC Jx5. The first NH2 terminal 22 residues were confirmed by AA  
 CC sequencing.  
 SQ Sequence 234 AA;

Query Match 44.1%; Score 726; DB 7; Length 234;  
 Best Local Similarity 45.3%; Pred. No. 1.52e-45;  
 Matches 107; Conservative 49; Mismatches 74; Indels 6; Gaps 6;  
 Db 1 rqpaelgllllwlpagardqltqspsflsaavdvrtictraeqglssylawyqkpg 60  
 Qy 2 RVPQLLGLULLLWLPGARCAVELTQPPS-VSVSPQQTARITCGGDSNNEYVHWYQKPA 60  
 Db 61 kapkllyaaasslqegypsfagsgqteftltisslqpedfatycqqln-gypriitfg 119  
 Qy 61 RAPILVIVDDSDRPSGIPERFSGSKSGNTATITNGVEAGDEADYQCVWDRASHPVFG 120  
 Db 120 qqtrelt-rttvaapsvflfpssdeqlkqstasvcllnmfypreakvqkvdnalqsgn 178  
 Qy 121 GGRVTVLQGPKAAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAG 180  
 Db 179 ggesvteqskdstyslsstltlskadyekhkvyacevthqglsepytksfnrqec 234  
 Qy 181 VETTPTSKQSNMKYAASSYLSLTPEQMKSHRSYSQCVTTHEG-ST-VEKTVAPTEC 233

## RESULT 5

ID R77614 standard; Protein; 236 AA.  
 AC R77614;  
 DT 15-MAR-1996 (first entry)  
 DE Humanised 5G1.1 VL + 012.  
 KW Complement C5; haemolysis; kidney; glomerulonephritis;  
 KW monoclonal antibody; antiinflammatory; antibody engineering;  
 KW humanised antibody; complementarity determining region; CDR;  
 KW ds.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..23  
 FT /label= sig peptide  
 FT Peptide 23..236  
 FT /label= mat peptide  
 FT Region 47..57  
 FT /label= CDR-L1  
 FT Region 73..79  
 FT /label= CDR-L2  
 FT Region 112..120  
 FT /label= CDR-L3  
 PN W09529697-A1.  
 PD 09-NOV-1995.  
 PF 01-MAY-1995; U05688.  
 PR 02-MAY-1994; US-236208.  
 PA (ALEX-) ALEXION PHARM INC.  
 PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins SJ;  
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;  
 PI Wang Y, Wilkins JA;



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DR WPI1; 95-392923/50.
DR N-PSDB; T08486.
PT Treating glomerulonephritis with antibody against complement C5
PS Claim 40; Page 132-34; 181pp; English.
CC A humanised CDR-grafted light chain, designated 5G1.1 VL + 012
CC (R77614), includes CDRs derived from mouse anti-C5 monoclonal
CC antibody 5G1.1. DNA (T08486) coding for the light chain can be
CC subcloned together with DNA (T08484) coding for a humanised Fd
CC (R77611) into vector APEX-3P (T08476) for expression of humanised
CC antibody in human 293 ERNA cells. Such recombinant antibodies retain
CC the ability of mAb 5G1.1 to block human complement C5a generation and
CC thus to reduce glomerular inflammation and kidney dysfunction
CC associated with glomerulonephritis.
SQ Sequence 236 AA;

Query Match 44.0%; Score 725; DB 15; Length 236;
Best Local Similarity 44.3%; Pred. No. 1.82e-45;
Matches 105; Conservative 53; Mismatches 72; Indels 7; Gaps 6;

Db 3 mrpqaqlgllllwlgarcdiqtpasleasvqdrvticcaseniynalnwqqkp 62
Qy 1 MRVPAQLLGLLLLPQARCAVELTQPPS-VSVSPGQTARITCGDNRNEYVHYQQKP 59

Db 63 kpaqklliyatnldavprrfsgsgtgdfcltiselpedfatyycc--nvIntpltf 120
Qy 60 ARAPILIVYDSDRPPSGIFERFSGSKSGNTATLTINGVEAGDEADYVCQWDRASDHPVF 119

Db 121 qggktkvei-krtvaapsvfifppsdqksgtasvvccllnnfyreakvqkvdnalqsg 179
Qy 120 GCGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAWKADSPVKA 179

Db 180 neqsvteqdkdstylastltilekadyekkhkyacevthglspsvtfksfngcc 236
Qy 180 GVEITTPSKQSN--KYAASSYLSLTPQWKSHRSYSCQVTHEG-ST-VEKTVAPTEC 233

RESULT 6
ID R20058 standard; Protein; 234 AA.
AC R20058;
DT 25-MAR-1992 (first entry)
DE Light chain of 306 anti-HIV antibody.
KW Plasmid pUC3D61C; human immunodeficiency virus; AIDS;
KW complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= signal 23..234
FT Protein 23..45
FT Region 23..45
FT /label= Framework_1 46..56
FT Region 46..56
FT /label= CDR_1 57..71
FT Region 57..71
FT /label= Framework_2 72..78
FT Region 72..78
FT /label= CDR_2 79..110
FT Region 79..110
FT /label= Framework_3 111..117
FT Region 111..117
FT /label= CDR_3 118..127
FT Region 118..127
FT /label= Framework_4 128..234
FT Region 128..234

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FT /label= Constant_region
PN W09118983-A.
PD 12-DEC-1991.
PF 28-MAY-1991; 100067.
PR 29-MAY-1990; AT-001178.
PA (JUNG/) JUNGBAUER A.
PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;
DR WPI1; 92-007468/01.
DR N-PSDB; Q20067.
PT Recombinant protein which binds to complex viral antigen and
PT HIV-1 - contains variable region of antibody derived from 3D6
PT cell line, used for detecting HIV-1 antigen
PS Claim 3; Page 28; 52pp; German.
CC The variable region of the light chain is used in a recombinant
CC protein with the variable region from the heavy chain of 3D6,
CC the two V regions being joined by a linker. The recombinant
CC protein binds to HIV gp160.
CC See also Q20066 and Q20068.
SQ Sequence 234 AA;

Query Match 43.0%; Score 708; DB 3; Length 234;
Best Local Similarity 45.1%; Pred. No. 3.74e-44;
Matches 107; Conservative 49; Mismatches 72; Indels 9; Gaps 8;

Db 3 mrpqaqlgllllwlgakcdiqtpasleasvqdrvticcaseniynalnwqqkp 62
Qy 1 MRVPAQLLGLLLLPQARCAVELTQPPS-VSVSPGQTARITCGDNRNEYVHYQQKP 59

Db 63 kvpklliykaaslesqvsrfsgsgtgftltiselpddfatyyccqyn--s-ys-f 118
Qy 60 ARAPILIVYDSDRPPSGIFERFSGSKSGNTATLTINGVEAGDEADYVCQWDRASDHPVF 119

Db 119 qpgtkvdi-krtvaapsvfifppsdqksgtasvvccllnnfyreakvqkvdnalqsg 177
Qy 120 GCGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAWKADSPVKA 179

Db 178 neqsvteqdkdstylastltilekadyekkhkyacevthglspsvtfksfngcc 234
Qy 180 GVEITTPSKQSN--KYAASSYLSLTPQWKSHRSYSCQVTHEG-ST-VEKTVAPTEC 233

RESULT 7
ID R42065 standard; Protein; 236 AA.
AC R42065;
DT 29-APR-1994 (first entry)
DE Human anti-HBs light chain.
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= sig_peptide 23..236
FT Protein 23..236
FT /label= mat_protein W09320205-A.
PN W09320205-A.
PD 14-OCT-1993.
PF 30-MAR-1993; J00396.
PR 30-MAR-1992; JP-074678.
PA (SUNR ) SUNTORY LTD.
PI Arima K, Kurihara T, Mateukura S, Nishihara T, Teuruoka N;
DR WPI1; 93-336913/42.
DR N-PSDB; Q49943.
PT Human anti-hepatitis B surface antigen antibody gene - can be
PT used to produce L and H chains of the antibody in large quantity

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PS Disclosure; Fig 4-5; 46pp; Japanese.  
CC Polynucleotides encoding the L and H chains of human anti-HBs  
CC Ab are given in Q4943-Q4944. The Ab can be easily produced in  
CC large quantities for therapeutic use.  
SQ Sequence 236 AA;

Query Match 42.9%; Score 707; DB 8; Length 236;  
Best Local Similarity 43.7%; Pred. No. 4.47e-44;  
Matches 104; Conservative 54; Mismatches 71; Indels 9; Gaps 9;  
Db 3 mrvpaqlgllllwfpqacdiqmtgpaamaasvqdrvtictcrasgignylwfgqkp 62  
Qy 1 MRPVPAQLGLLLLWPCARCAYELTPQPS-VSVSPQATRTTCGDNSRNEYVHYQOKP 59  
Db 63 gkvpkrliyaasellqevpferfsgesgctfcltislrlqpedfatyycc-l-hh-nnypls 119  
Qy 60 ARAPILVIYDDSDRPSGIPERFSGKSGNTATLTINGVEAGDEADYVCQWDRASDHPV- 118  
Db 120 fgggtkvei-krtvaapsvfifpsdeqlsgtaavvcllnfnfybreakvqkvdnalqs 178  
Qy 119 FGGGTRVTVLGQPKAAPSVTLPFSPSEELQANKATLVCLISDFYPGAVTVAMKADSSPVK 178  
Db 179 gnsqevteqdkdstyslsltlslkadyekthkvacvethqglspvtskfnrgec 236  
Qy 179 AGVETTPSKQSNM-KYMASSYLSTPEQWKSHRSYSCQVTHEG-ST-VEKTVAPTEC 233

## RESULT 8

ID R69093 standard; Protein; 106 AA.  
AC R69093;  
DT 30-AUG-1995 (first entry)  
DE Anti-HIV Fab rev16/20 light chain.  
KW HIV-1; human immunodeficiency virus type 1; AIDS; Rev protein;  
KW intracellular immunization; gene therapy; single chain antibody;  
KW Fab; antibody engineering; resistance; cell immunity.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Misc\_difference 68  
FT /note= "not known"  
FT Misc\_difference 86  
FT /note= "not known"  
FT Misc\_difference 101  
FT /note= "not known"  
PN W09503832-A.  
PD 09-FEB-1995.  
PF 28-JUL-1994; U08448.  
PR 30-JUL-1993; US-099870.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
PI Duan L, Pomerantz R;  
DR WPI; 95-082039/11.  
PT Method for conducting gene therapy - comprises using recombinant  
PT gene encoding antibody binding antigen associated with a disease;  
PT useful for providing cell immunity.  
PS Example 11; Page 32-33; Table 2; 62pp; English.  
CC A phagemid library was constructed using lymphocyte RNA from  
CC a long-term asymptomatic HIV-1 positive donor. Heavy and light  
CC chain genes were cloned and a combinatorial library was prepared  
CC and screened to select antigen (HIV rev or tat) binders. Human  
CC soluble anti-HIV Fabs were obtained. Heavy chain VH sequences are  
CC given in R69084-87, light chain VL in R69088-92 and light chain CL  
CC in R69093-97.  
SQ Sequence 106 AA;

Query Match 42.2%; Score 696; DB 12; Length 106;

Best Local Similarity 96.2%; Pred. No. 3.16e-43;  
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 gqkaapsvtlfpssseelqankatlvcclisdfypgavtvawkadsspvkagvetttsk 60  
Qy 129 GQKAAPSVTLPFSPSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTPSK 188  
Db 61 gnmkyaxsylvltpsqkshkshkxycqthegstvektvxptecs 106  
Qy 189 QSNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPECS 234

## RESULT 9

ID R69088 standard; Protein; 133 AA.  
AC R69088;  
DT 30-AUG-1995 (first entry)  
DE Anti-HIV Fab tat16/20 (VL5-FR1, CDR1, CL).  
KW HIV-1; human immunodeficiency virus type 1; AIDS; Tat protein;  
KW intracellular immunization; gene therapy; single chain antibody;  
KW Fab; antibody engineering; resistance; cell immunity.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Region 1..20  
FT /label= FR1  
FT Region 21..27  
FT /label= CDR1  
FT Region 28..97  
FT /label= FR2  
FT Misc\_difference 95  
FT /note= "not known"  
FT Region 98..133  
FT /label= CDR2  
FT Misc\_difference 113  
FT /note= "not known"  
FT Misc\_difference 128  
FT /note= "not known"  
PN W09503832-A.  
PD 09-FEB-1995.  
PF 28-JUL-1994; U08448.  
PR 30-JUL-1993; US-099870.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
PI Duan L, Pomerantz R;  
DR WPI; 95-082039/11.  
PT Method for conducting gene therapy - comprises using recombinant  
PT gene encoding antibody binding antigen associated with a disease;  
PT useful for providing cell immunity.  
PS Example 11; Page 32-33; Table 2; 62pp; English.  
CC A phagemid library was constructed using lymphocyte RNA from  
CC a long-term asymptomatic HIV-1 positive donor. Heavy and light  
CC chain genes were cloned and a combinatorial library was prepared  
CC and screened to select antigen (HIV rev or tat) binders. Human  
CC soluble anti-HIV Fabs were obtained. Heavy chain VH sequences are  
CC given in R69084-87, light chain VL in R69088-92 and light chain CL  
CC in R69093-97.  
SQ Sequence 133 AA;

Query Match 42.2%; Score 696; DB 12; Length 133;  
Best Local Similarity 96.2%; Pred. No. 3.16e-43;  
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 28 gqkaapsvtlfpssseelqankatlvcclisdfypgavtvawkadsspvkagvetttsk 87  
Qy 129 GQKAAPSVTLPFSPSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTPSK 188



RESULT 12  
 ID R33554 standard; Protein; 238 AA.  
 AC R33554;  
 DT 20-AUG-1996 (first entry)  
 DE Monoclonal antibody DNA light chain against 65 kD hCMV antigen.  
 KW Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;  
 KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /note= "Signal peptide"  
 FT Protein 21..238  
 FT /note= "Mature light chain"  
 PN J08038178-A.  
 PD 13-FEB-1996.  
 PF 20-FEB-1995; 030742.  
 PR 18-FEB-1994; JP-021628.  
 PA (NISN ) NISSHINBO IND INC.  
 PA (TANA/) TANAKA H.  
 DR MPI; 96-154852/16.  
 DR N-PSDB; T18060.  
 PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -  
 PT produced by primer amplification, used in the diagnosis of hCMV  
 PT infection  
 PS Claim 5; Page 19; 22pp; Japanese.  
 CC The sequences given in R33553-54 represent the heavy and light chains  
 CC respectively of a monoclonal antibody against a 65 kD antigen of human  
 CC cytomegalovirus (hCMV). The DNA's encoding these sequences were  
 CC amplified using the sequences given in T18040-58. The monoclonal  
 CC antibody may be used in the diagnosis of hCMV.  
 SQ Sequence 238 AA;

Query Match 40.5%; Score 668; DB 16; Length 238;  
 Best Local Similarity 43.0%; Pred. No. 4,57e-41;  
 Matches 104; Conservative 56; Mismatches 69; Indels 13; Gaps 9;  
 Db 1 mrvpallglmlwlpqsgadivmtqtalsvtpgpaaiscksgslldhgdgtylyw 60  
 Qy 1 mrvpallglmlwlpqsgadivmtqtalsvtpgpaaiscksgslldhgdgtylyw 60  
 Db 61 ylkpqsqplliyevenfsgvdrfsgegetdftklksrveadvgvyco-m--rsi 117  
 Qy 55 YQOKPARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYQCQWDRAS 114  
 Db 118 qfatfgqgktlei-krtvaapsvfifpdsdeqlksgtasvvccllnnfypreakvgkvkd 176  
 Qy 115 DHPVFGGTRVTVLGQPKAAPSVTLFPPSSEELQNKATLVCLISDFYPGAVTVAKRADS 174  
 Db 177 alqegsqesvteqdsdtsyalstltlskadyekkhkyacevthqgleapvtsfnrg 236  
 Qy 175 SPVACGVETTTFSKOSNN-KYAASYSLSLTPEQWKSRSYSQVTHEG-ST-VEKTVAPT 231  
 Db 237 ec 238  
 Qy 232 EC 233

RESULT 13  
 ID R28809 standard; Protein; 241 AA.  
 AC R28809;  
 DT 02-APR-1993 (first entry)  
 DE Vector pMDR1007.  
 KW Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;  
 KW pMDR986; BglII; pMDR1003; JA221(Iq); E. coli; ampicillin resistance;

KW NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;  
 KW melting agarose; immunoglobulin; kappa chain; signal peptide; LC;  
 KW humanised; 5A8; light chain; variable region; LV; genomic; constant  
 KW antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+;  
 KW lymphocyte; helper; inducer; HIV; syncytia; formation.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..22  
 FT /note= "Immunoglobulin kappa chain signal peptide"  
 FT Region 23..134  
 FT /note= "Humanised 5A8 LV"  
 FT Region 135..241  
 FT /note= "Human kappa chain LC"  
 PN W09209305-A.  
 PD 11-JUN-1992.  
 PF 27-NOV-1991; U08843.  
 PR 27-NOV-1990; US-618542.  
 PA (BIO ) BIOGEN INC.  
 PI Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;  
 DR MPI; 92-398399/48.  
 DR N-PSDB; Q30920.  
 PT New anti-CD4 antibody homologues - which bind CD4, do not block  
 PT binding of HIV gp120 to CD4 but block HIV-induced syncytia  
 PT formation between CD4+ cells  
 PS Disclosure; Page 166-7; 205pp; English.  
 CC The sequence given is encoded by the insert of the vector pMDR1007.  
 CC pMDR1006 (see Q30919) and pSAB132 (see Q30906) were used in the  
 CC construction of this vector. Three fragments were ligated together  
 CC to generate pMDR1006; a 572 bp fragment of pMDR985 (see Q30913), a  
 CC 344bp AatII/EcoRV fragment of pMDR986 (see Q30918) and a 326 bp  
 CC EcoRV/BglII fragment of pMDR1003 (see Q30900). The ligation mixture  
 CC was used to transform E. coli JA221(Iq) to ampicillin resistance.  
 CC pMDR1006 was cleaved with NotI and the 1693 bp fragment isolated was  
 CC ligated into NotI linearised pSAB132 which had been dephosphorylated  
 CC by calf alkaline phosphatase. This generates the plasmid pMDR1007.  
 CC The dephosphorylated mixture was fractionated through low temperature  
 CC melting agarose and used to transform E. coli JA221(Iq) to ampicillin  
 CC resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3'  
 CC order, the immunoglobulin kappa chain signal peptide, amino acid (AA)  
 CC 1-AA112 of the humanised 5A8 light chain variable region (LV) followed  
 CC by genomic DNA encoding AA108-AA214 of the human kappa light chain,  
 CC ie. the light chain constant region (LC). This polypeptide is an  
 CC antibody homolog which was shown to bind to CD4 but did not block the  
 CC binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+  
 CC lymphocytes (helper/inducer cells). The homolog blocked HIV-induced  
 CC syncytia formation. This homolog can be used in the detection,  
 CC prophylaxis and treatment of diseases caused by infective agents whose  
 CC primary targets are CD4+ cells.  
 SQ Sequence 241 AA;

Query Match 40.3%; Score 664; DB 5; Length 241;  
 Best Local Similarity 45.7%; Pred. No. 9,29e-41;  
 Matches 111; Conservative 48; Mismatches 70; Indels 14; Gaps 10;  
 Db 3 mrvnaqlglmlwlpqsgadivmtqtalsvtpgpaaiscksgslldhgdgtylyw 62  
 Qy 1 mrvnaqlglmlwlpqsgadivmtqtalsvtpgpaaiscksgslldhgdgtylyw 62  
 Db 63 wyqkqpgppkillywastresgvpdrfsgegetdftklksrveadvgvyccqy-y 120  
 Qy 54 WYQKPARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYQCQWDR 113  
 Db 121 s-ytfggktlei-krtvaapsvfifpdsdeqlksgtasvvccllnnfypreakvgkvkd 178



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Q1 - 202 LTPEOMKSHRSYSCQVTHEC-ST-VEKTVAPTEC 233

Search completed: Tue Dec 17 15:13:42 1996  
Job time : 28 secs.

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2339	67.4	330	2	GHHU	Ig gamma-1 chain C r	0.00e+00
2	2335	67.3	329	5	S36861	Ig gamma-1 chain C r	0.00e+00
3	2135	61.5	470	5	S22080	Ig heavy chain precu	6.82e-301
4	2133	61.4	326	2	G2HU	Ig gamma-2 chain C r	1.39e-300
5	2133	61.4	327	2	G4HU	Ig gamma-4 chain C r	1.39e-300
6	2126	61.2	472	12	S31459	Ig gamma-1 chain - s	1.70e-299
7	1913	55.1	469	12	S37493	Ig gamma-2a chain -	1.85e-266
8	1832	52.8	446	12	S40295	Ig gamma-2a chain (m	6.41e-254
9	1817	52.3	475	12	S01321	Ig gamma-2b chain pr	1.34e-251
10	1792	51.6	474	14	S25057	Ig gamma-2b chain -	9.89e-248
11	1747	50.3	377	5	A23511	Ig gamma-3 chain C r	8.96e-241
12	1747	50.3	377	5	A60764	Ig gamma-3 chain C r	8.96e-241

```

1
RESTART
ENTRY
TITLE
ORGANISM
DATE
GHRU
#type complete
Ig gamma-1 chain C region - human
#formal name Homo sapiens #common name man
31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change
08-Dec-1994
ACCESSIONS
REFERENCE
#authors
#journal
#title
A93433; B90563; A90564; B91668; A91723; A02146
A93433
Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. (1982) 10:4071-4079
The nucleotide sequence of a human immunoglobulin C-gamma1
gene.
#cross-references MUID:82274238
#accession A93433
#molecule_type DNA
1-330 #label ELL
this sequence has the Glm(17) allotypic marker, 97-Lys
and the Glm(1) markers, 239-Asp and 241-Leu
Lys-330 is removed after translation
A90563
Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb,
P.D.; Waxdal, M.J.; Edelman, G.M.
Biochemistry (1970) 9:3161-3170
The covalent structure of a human gammaG-immunoglobulin. V1
Amino acid sequence of heavy-chain cyanogen bromide
fragments H-1-H-4.
#cross-references MUID:71064024

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#contents      myeloma protein Eu
#accession     B90563
##molecule_type protein
##residues     1-96,'R',98-135 ##label CUN
##note         this sequence has the G1m(3) marker, 97-Arg
REFERENCE
#authors       Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg,
                W.H.; Edelman, G.M.
#journal        Biochemistry (1970) 9:3171-3181
#title          The covalent structure of a human gammaG-immunoglobulin.
                VIII. Amino acid sequence of heavy-chain cyanogen bromide
                fragments H-5-H-7.
#cross-references M01D:71064025
#contents      Eu
#accession     A90564
##molecule_type protein
##residues     136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,
                'D',199-238,'E',240,'M',242-267,'DGEPE',273-329
                ##label RUT
##note         this sequence has the G1m(non-1) markers, 239-Glu and
                241-Met
REFERENCE
#authors       Ponstingl, H.; Hilschmann, N.
#journal        Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1571-1604
#title          Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins
                (Myelomprotein Nie), III. Die chymotryptischen Peptide der
                H-Kette, Anordnung der tryptischen Peptide und Diskussion
                der vollstaendigen Primaerstruktur.
#cross-references M01D:77070269
#contents      myeloma protein Nie
#accession     B91668
##molecule_type protein
##residues     1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',
                240,'L',242-268,'E',270-271,'D',273-330 ##label PON
##note         this sequence has the G1m(17) and G1m(1) markers
REFERENCE
#authors       Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
#journal        Hoppe-Seyler's Z. Physiol. Chem. (1983) 364:713-747
#title          Die Primaerstruktur des kristallisierbaren monoklonalen
                Immunglobulins IgG1 KOL, I.
#cross-references M01D:83289131
#contents      myeloma protein KOL; disulfide bonds
#accession     A91723
##molecule_type protein
##residues     1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',
                268-271,'D',273-330 ##label SCH
##note         this sequence has the G1m(3) and G1m(non-1) markers
REFERENCE
#authors       Gall, W.E.; Edelman, G.M.
#journal        Biochemistry (1970) 9:3188-3196
#title          The covalent structure of a human gammaG-immunoglobulin. X.
                Intrachain disulfide bonds.
#cross-references M01D:71064027
#contents      annotation; disulfide bonds
#accession     A91667
REFERENCE
#authors       Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
#journal        Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1515-1540
#title          Rule of antibody structure. The primary structure of
                monoclonal IgG1 immunoglobulin (myeloma protein Nie), I:
                purification and characterization of the protein, the L-
                and H-chains the cyanogenbromide cleavage products, and the
                disulfide bridges.
#cross-references M01D:77070267
#contents      annotation; disulfide bonds

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GENETICS
#gene          GDB:IGHG1
#map_position  14q32.33
#introns       99/1; 114/1; 224/1
CLASSIFICATION
#superfamily  immunoglobulin C region; immunoglobulin homology
#glycoprotein
FEATURE
20-85          #domain immunoglobulin homology #label IGG1\
137-206        #domain immunoglobulin homology #label IGG2\
243-310        #domain immunoglobulin homology #label IGG3\
27-83,144-204, #disulfide bonds #status experimental\
250-308        #disulfide bonds interchain (to light chain) #status
103            experimental\
109,112        #disulfide bonds interchain (to heavy chain) #status
180            #binding site carbohydrate (Asn) (covalent) #status
                experimental
SUMMARY        #length 330 #molecular-weight 36106 #checksum 8773
Query Match    67.4%; Score 2339; DB 2; Length 330;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 askgsvfplapskatsgtgaalgclvdyfpepvtvsmngaltsgvhtfpavlgss 60
               |||||
Qy 147 ASTKGSVFPLAPSSKTSGGTAAIGCLVKDYFPEPTVVSNNSGALTSGVHTFPAVLQSS 206
               |||||
Db 61 gylslasvvtvpssslgtqtyicnvnhkpsntkvdkkvepkcdkthtccpccpapellg 120
               |||||
Qy 207 GLYSLSVVTPVSSSLGTQTYICNVNHKPSNTKVDKKAEKASCDKTHTCPPCPAPELLGG 266
               |||||
Db 121 psvflfpkpkdltlmsrtpevtcvvvdvshdpevkfnwvdygvevhnaktkpreeqyn 180
               |||||
Qy 267 PSVFLFPKPKDILTMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
               |||||
Db 181 styrvsvltvlhqdwlngkeyckvsnkalpapietkistakgpprepqvytlpparde 240
               |||||
Qy 327 STRVSVSLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQRPQVYTLPPSRDE 386
               |||||
Db 241 ltnqsvslclvkgfypsdiavewengpennnykttppvldsdgsfflyskltvdkerw 300
               |||||
Qy 387 LTNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPTPVLDSDGSGFFLYSKLTVDKSRW 446
               |||||
Db 301 qqgnvfscvmhealhhnytkslslspgk 330
               |||||
Qy 447 QQGNVFCVMHEALHHNYTKSLSLSPGK 476

RESULT 2
ENTRY      S36861      #type fragment
TITLE      Ig gamma-1 chain C region - human (fragment)
ORGANISM   #formal name Homo sapiens #common name man
DATE       31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change
                02-Aug-1994
ACCESSIONS S36861; S33887
REFERENCE   S33904
#authors    Harris, L.J.
#submission submitted to the EMBL Data Library, October 1992
#accession  S36861
#molecule_type DNA
#residues   1-329 ##label HAR
##cross-references EMBL:217370
REFERENCE   S33887

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#authors Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.;  
Honjo, T.  
#journal Cell (1987) 29:671-679  
#title Structure of human immunoglobulin gamma genes: implications  
for evolution of a gene family.  
#accession 533887  
#molecule\_type DNA  
#residues 87-112;234-329 #label TAK  
#cross-references EMBL:217370

GENETICS  
#introns 98/1; 113/1; 223/1  
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology  
FEATURES  
#length 329 #checkum 6336

Query Match 67.3%; Score 2335; DB 5; Length 329;  
Best Local Similarity 99.7%; Pred. No. 0.00e+00;  
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 stgpsvflpasektsqgtaalqclvdyfpepvtvswnsqaltsgvhtfpavlgsg 60  
Qy 148 STKGPSVFLPAPSSKTSQGTAAALQCLVDYFPEPVTVSWNSGALTSGVHTFPVAVLQSSG 207  
Db 61 lyelssvtpvseelgtqyicnvnhkpentkvdkvepkscdtkhcpcpapelggp 120  
Qy 208 LYSLSWVTPVSSLSGTQYICNVNHPKSNITKVDKAEPSKDKTHTCPPCPAPELLGCP 267  
Db 121 avflfpkpkdtlmartpevtcvvdvshedevkfnwvvgdvevhnaktpreeqyns 180  
Qy 268 SVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWVGDVEVHNAKTPREEQYNS 327  
Db 181 tyrvsvltvlhqdlnqkeyckvsnkalpapietkiskakgpgpvytlpssrdel 240  
Qy 328 TYRVSVTLVLHQDLNQLNGKEYCKVSNKALPAPIETKISKAKGPREPQVYTLPSRDEL 387  
Db 241 tkngvaltlkvqfypedvawesngqpennykttpvldsdgdefflyskltvdksrwq 300  
Qy 388 TKNQVSLTCLVKRGYPSDIAVWESNGQPENNYKTTPVLDSDGSFELYSKUTVDKSRWQ 447  
Db 301 qgnvfscsymhealhhnyctelspgk 329  
Qy 448 QGNVFCSYMHEALHHNYTKQSLSPGK 476

RESULT 3  
ENTRY S22080 #type complete  
TITLE Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine  
ALTERNATE\_NAMES Ig gamma-1 chain C region (clone 8.10)  
ORGANISM #formal name Bos primigenius taurus #common name cattle  
DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 26-May-1995  
ACCESSIONS S22080; S06610; A31303  
REFERENCE S22080  
#authors Sanders, P.G.  
#submission submitted to the EMBL Data Library, November 1991  
#accession S22080  
#status preliminary  
#molecule\_type mRNA  
#residues 1-470 #label SAN  
#cross-references EMBL:X62916  
REFERENCE S06610  
#authors Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
#journal Mol. Immunol. (1989) 26:841-850  
#title Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2 genes.

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#cross-references MUID:90097956  
#accession S06610  
#molecule\_type DNA  
#residues 142-470 #label SYM  
#cross-references EMBL:X16701  
#note the sequence was determined from the germline gene

GENETICS  
#gene Ig CH gamma-1  
#introns 98/1; 111/1; 221/1  
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology  
KEYWORDS antibody; complement; immunoglobulin; membrane protein  
FEATURES  
#binding\_site carbohydrate (Asn) (covalent) #status predicted  
#length 470 #molecular-weight 50625 #checkum 2181

Query Match 61.5%; Score 2135; DB 5; Length 470;  
Best Local Similarity 62.6%; Pred. No. 6.82e-301;  
Matches 299; Conservative 84; Mismatches 85; Indels 10; Gaps 8;

Db 1 mmpwlcllvisapigvleqvqlresgplvksptqlslctctvgfslssyal-twvrqa 59  
Qy 1 MKHLWFLLLVAAPRWLSQVKLQWGEGLQPSSETLSRTCVCVSGSGISGYVWVIRQT 60  
Db 60 pqkalewvvgi-taggttyvnpalkrslsitkenskeqvalavsvtpeatatyccarat 118  
Qy 61 PQRGLMIGHYTGATNTNPSLKSRSVITSKDTSKQFFLNLSVTDADTAVYCARGP 120  
Db 119 ygevvd---galadawggllvtvseastapkvplaseccgdkassstvlglcvssymp 175  
Qy 121 RDCCTTCYGMVDVMDGDLVTVSSASTKGPSVFP LAPSSKTSQGTAAALGCLVKDTP 180  
Db 176 epvtvtwmgalksgvhtfpavlgseglylesmvtvpgtag-qftcnvahpasetkv 234  
Qy 181 EPVTVSMGALTSGVHTFPVAVLQSSGLYSLSVVTVPSSSLGCTQYICNVNHPKSNITK 240  
Db 235 dkavdp-tc-kpspcdcppepplpgpsvfiifppkpkdltisgtpevtcvvvvghddp 292  
Qy 241 DKAEKPSKDKTHTCPPCPAPELLGSGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDP 300  
Db 293 evkfswfvdvdeventattkpreeqfnetyrvvsalriqhdwtgdkfckvhneglpap 352  
Qy 301 EVKENWYVDGVEVHNAKTPREEQYNSYRVVSVLTVLHQDLNQLNGKEYCKVSNKALPAP 360  
Db 353 ivrtisrtkparepvyvllappqeelsketvslctmvtsefypdyiavewgrngqpeaed 412  
Qy 361 TEKTSKAKGPREPQVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPEN-N 419  
Db 413 kygtppqladssyflysklrvdrnswqgdtytcvmhealhhnythqstkeagk 470  
Qy 420 -YKTPPVLDSGDSFFLYSKLTVDKSRWQGNVFCSYMHEALHHNYTKQSLSPGK 476

RESULT 4  
ENTRY G2HU #type complete  
TITLE Ig gamma-2 chain C region - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 08-Dec-1994  
ACCESSIONS A93906; A92809; A90752; A93132; A02148  
REFERENCE A93906  
#authors Ellison, J.; Hood, L.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1982) 79:1984-1988  
#title Linkage and sequence homology of two human immunoglobulin

```

#cross-references MUID:82197621
#accession A93906
#molecule_type DNA
#residues 1-326 ##label ELL
#note Lys-326 is probably removed posttranslationally
REFERENCE A92809
#authors Wang, A.C.; Tung, E.; Fudenberg, H.H.
#journal J. Immunol. (1980) 125:1048-1054
#title The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.
#cross-references MUID:81007873
#contents myeloma protein Til
#accession A92809
#molecule_type protein
#residues 1-19,'Q','21-57','2','59','A','61-193','D','195-325 ##label WAN
#note Trp-156 is at or near the complement-binding site
REFERENCE A90752
#authors Connell, G.E.; Parr, D.M.; Hofmann, T.
#journal Can. J. Biochem. (1979) 57:758-767
#title The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.
#cross-references MUID:80001357
#contents myeloma protein Zie
#accession A90752
#molecule_type protein
#residues 1-24,'E','26-57','EV','60-85;132-171,'ZZZ','175','B','177-193,'D','195-196,'Q','198-234,'Z','236-263,'BGEFZ',269-325
#label CON
#note this sequence has since been revised
REFERENCE A93132
#authors Hofmann, T.; Parr, D.M.
#journal Mol. Immunol. (1979) 16:923-925
#title A note on the amino acid sequence of residues 381-391 of human immunoglobulin gamma chains.
#cross-references MUID:80114419
#contents Zie
#accession A93132
#molecule_type protein
#residues 238-275 ##label HOF
REFERENCE A94591
#authors Hofmann, T.; Parr, D.M.
#submission submitted to the Atlas, March 1980
#contents annotation; Zie, revisions to residues 25, 59, 60, and 264-268
#note the revised sequence differs from that shown in having 60-Ala and in the amidation states of residues 58, 194, and 197; the amidation states of residues 172-174, 176, and 235 were not determined
REFERENCE A90253
#authors Milstein, C.; Frangione, B.
#journal Biochem. J. (1971) 121:217-225
#title Disulphide bridges of the heavy chain of human immunoglobulin G2.
#cross-references MUID:72033500
#contents annotation; myeloma protein Sa, disulfide bonds
REFERENCE A93157
#authors Frangione, B.; Milstein, C.; Pink, J.R.L.
#journal Nature (1969) 221:145-148
#title Structural studies of immunoglobulin G.
#cross-references MUID:69064124
#contents annotation; Sa, disulfide bonds
GENETICS
#gene GDB:IGHG2

```

```

#map_position 14q32.33
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-85 #domain immunoglobulin homology #label IGG1\
133-202 #domain immunoglobulin homology #label IGG2\
239-306 #domain immunoglobulin homology #label IGG3\
14 #disulfide_bonds interchain (to light chain) #status experimental\
27-83,140-200, #disulfide_bonds #status experimental\
246-304 #disulfide_bonds interchain (to heavy chain) #status experimental
102,103,106,109 #disulfide_bonds interchain (to heavy chain) #status experimental
SUMMARY #length 326 #molecular-weight 35884 #checksum 7982

Query Match 61.4%; Score 2133; DB 2; Length 326;
Best Local Similarity 90.9%; Pred. No. 1.39e-300;
Matches 300; Conservative 15; Mismatches 11; Indels 4; Gaps 3;

Db 1 aatkqpsvfplapcstsestaalgclvkdypcpvtvswngaltsgvhtfpavlgss 60
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Qy 147 ASTKGSVEPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 206
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Db 61 glyalsavvtvpssnfgtdytcnvdhkpsentkvdktverkc--ve-cpccpappv-ag 116
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Qy 207 GLYSLASVVTVPSSSLGTQTYICNVNHRPSNTKYDKAEFKCDKTHTCPPAPPELLGG 266
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Db 117 psvfllppkpkdtlmisrtpevtcvvvdshedpevqfnwydvgevhnaktkpreeqfn 176
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Qy 267 PSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Db 177 stfrvsvltvvhqdwlngkeyckvkenkglpapietk.tsktkgprepqvvtlpsree 236
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Qy 327 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPTEKTSKAKGQPREPOVYTLPPSRDE 386
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Db 237 mtknqvslctclvkgfypsdiavewesnggennykttppmlsdsgsflyskltvdkerw 296
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Qy 387 LTRKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSLKLTVDKSRW 446
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Db 297 qqgnvfscsvmhhealhnhytqkalslpqk 326
||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Qy 447 QQGNVFSCSVMHHEALHNHYTQKSLSLSPGK 476

RESULT 5
ENTRY G4HU #type complete
TITLE Ig gamma-4 chain C region - human
ORGANISM #formal name Homo sapiens #common name man
DATE 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 23-Mar-1995
ACCESSIONS A90933; A90249; A02150
REFERENCE A90933
#authors Ellison, J.; Buxbaum, J.; Hood, L.
#journal DNA (1981) 1:11-18
#title Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
#cross-references MUID:83157104
#accession A90933
##molecule_type DNA
##residues 1-327 ##label ELL
#note the sequence was determined from the germline gene
REFERENCE A90249
#authors Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
#journal Biochem. J. (1970) 117:33-47
#title Human immunoglobulin subclasees. Partial amino acid sequence of the constant region of A gamma4 chain.

```

```
#cross-references MUID:70207560
#accession A90249
#molecule_type protein
#residues 1-30;81-326 #label PIN

GENETICS
#gene GDB:IGHG4
#map_position 14q32.33
#introns 99/1; 111/1; 221/1

CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-85 #domain immunoglobulin homology #label IGHG\
99-110 #region hinge\
134-203 #domain immunoglobulin homology #label IGHG2\
240-307 #domain immunoglobulin homology #label IGHG3\
14 #disulfide bonds interchain (to light chain) #status experimental\

27-83,141-201,
247-305 #disulfide bonds #status predicted\
106,109 #disulfide bonds interchain (to heavy chain) #status experimental\

SUMMARY #length 327 #molecular-weight 35940 #checksum 907

Query Match 61.4%; Score 2133; DB 2; Length 327;
Best Local Similarity 90.6%; Pred. No. 1.39e-300;
Matches 299; Conservative 17; Mismatches 11; Indels 3; Gaps 3;

Db 1 astkgsveplapscststaalgclvckdyfpepvtvwnsgaltesghvtfpavlqss 60
Qy 147 ASTKGSVEPLAPSSKSTSGTAAALGCLVKDYFPEPVTVMNSGALTSVHTFPAVLQSS 206

Db 61 glyslsvvtpssslgtkytcnvdkhpsntckvdkrvesk-yg-p-pcpscpapeflgg 117
Qy 207 GLYSLSSVTVPPSSSLGTQYICNVNHPKNTKYDKKAEKSCDKTCTCPPCPAPELLGG 266

Db 118 psvflfpkpkdtlmartpevtcvvvdsqebvqfnwvdgvvhnaktkpreeqfn 177
Qy 267 PSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYDGVGVHNKTKPREQYN 326

Db 178 styrvsvltvlhgdwlngkyckvknkqlpslektiekakgpreqvytlpsqee 237
Qy 327 STYRVSVLTVLRDHWLNGKYCKVKNKQLPSLEKTIKAKGPREPOVYTLPPSRDE 386

Db 238 mtknqvslclvkgfypsdiaveesngpennykttppvldsdgsfflysriltvdkerw 297
Qy 387 LTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRW 446

Db 298 qegnvfscvsmhealnhhytqkslelglk 327
Qy 447 QEGNVFSCVSMHEALNHHTYQKSLSLSPCK 476

RESULT 6 S31459 #type fragment
ENTRY Ig gamma-1 chain - sheep (fragment)
TITLE #formal name Ovis orientalis aries, Ovis ammon aries
ORGANISM #common name domestic sheep
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995

ACCESSIONS S31459
REFERENCE S31459
#authors Patri, S.; Nau, F.
#submission submitted to the EMBL Data Library, December 1992
#accession S31459
#status preliminary
```

```
#molecule_type mRNA
#residues 1-472 #label PAT
#cross-references EMBL:X69797
SUMMARY #length 472 #checksum 9485

Query Match 61.2%; Score 2126; DB 12; Length 472;
Best Local Similarity 61.8%; Pred. No. 1.70e-299;
Matches 294; Conservative 85; Mismatches 89; Indels 8; Gaps 8;

Db 2 lwtllfvsaprvlsqvlqesgpalatlqltsvtctisgfalnnvgv-dwvtrgapgk 60
Qy 4 LWFLLLVAAAPRWLSQVKLQWGEGLQLPSETLSRTCVCVSGSISGYSYTWIRQTPGR 63

Db 61 alewlqgs-gydedidvnpvkarlsatiktksqvaltlstvttedtavyycarvdyds 119
Qy 64 GLEWIGHIYGNGATTNPNPSLKSRTVITISKDTSKNQFFNLNLSVTDADTVYVCARGRPD 123

Db 120 shafayasy-dfwpgllisvlaasttpkvypltsccgdtassivtlgclivesympv 178
Qy 124 CTTICYGWVDVWGPDLVTVSSASTKGSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPV 183

Db 179 tvtnsegaltsegvhtfpailgesglvlesvvtvpastagadtfcicnvahpasstkvdkr 238
Qy 184 TVSNNSCALTSCTVHTFPAVLQSSGLYSLSVTVPPSSSLGTQYICNVNHPKNTKYDKK 243

Db 239 vep-gcpdkchcr-cppelpggpsvfifppkpkdtltisgtpevtcvvvdvgddp 296
Qy 244 AEPKSC-DKHTCTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEV 302

Db 297 qfsvfdvnevartarkpreeqfnstfrvvsalpiqgdwtgkfkckvhnalpapiv 356
Qy 303 KENYVDGVGVHNKTKPREQYNSTYRVVSLTVLHQDLNKGKETYKCRVSNKALPAPIE 362

Db 357 rtisrtkgarepvyvlpapeqelsktlsvtclvtgfydpdiavevknqngpseedy 416
Qy 363 KTIISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEESNGQPEN-N-Y 420

Db 417 gtttsqlsdagdyflyerlrvdknswqegdtvacvnmhealnhhytqkslekppak 472
Qy 421 KTTPTPVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVSMHEALNHHTYQKSLSLSPCK 476

RESULT 7 S37483 #type complete
ENTRY Ig gamma-2a chain - mouse
TITLE #formal name Mus musculus
ORGANISM #common name house mouse
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

ACCESSIONS S37483
REFERENCE S37483
#authors Duncanson, F.F.D.
#submission submitted to the EMBL Data Library, February 1993
#accession S37483
#status preliminary
#molecule_type mRNA
#residues 1-469 #label DUC
#cross-references EMBL:X70423
SUMMARY #length 469 #molecular-weight 51549 #checksum 7833

Query Match 55.1%; Score 1913; DB 12; Length 469;
Best Local Similarity 56.3%; Pred. No. 1.85e-266;
Matches 267; Conservative 89; Mismatches 107; Indels 11; Gaps 6;

Db 5 wfiflllegtagvhcqlqgqgpevlvkgasvkiackeaegyftdyi-nwvkdqpgg 63
```

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```
1:||||: 1 1: ||| 1 1: : : 1 || : : 1 || : : 1 ||: ||:
Qy 5 WFFLLVAPRWLSQVKLQWGGELQLQSETLSRTCVSGSGISGYVYWTWIRTPERG 64
Db 64 lkwlgwypasgntkynenfkgatltvdsastaymqleasteedavycata-ngat 122
Qy 65 LEWIGHYNGATNTNPNISKRTYISKTQKNOFFINLINSVTDADTAVYCYARGPRDC 124
Db 123 atl-----ldywggttlvtvasakttapsvplapvcgdtgssvtlqclvkgyfpepvt 177
Qy 125 TTICYGWVDWVCGF GDLVTVSSATKGPVFLAPSSKSTSGCTAALGCLVKDYFPEPVT 184
Db 178 ltwmsglsesvghfavlqsd-lytlesavtvtstwpseiccnvahpasstkvdki 236
Qy 185 VSNNSGALTSGVHFFPAVLQSGSLYSLSVWVTPSSSLGTQYICNVNHNKPSNTKVDKA 244
Db 237 eprg-ptikpcpcckpapnllggpsvfifppkikdvlmislepivtcvvdvseddpgv 295
Qy 245 EPKSCDKTHTCPCC--PAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEV 302
Db 296 qiafwvnnvvhvtaqtqthredynstlrvesalpiqhdqmsqefkckvnnkdlpapie 355
Qy 303 KENMYVDGVEVHNAKTPREQYNSTRVSVLVTLHQDLINGKEYCKVSNKALPAIE 362
Db 356 rtiakpkgsravapvylpppeemtkkqvtltcmvtdfmpediyvewtngktelnykn 415
Qy 363 KTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 422
Db 416 tepvladgsyfmysklrvckknwvnsyscvvhgelnhhttkafstpgk 469
Qy 423 TPVLDSDSGSFYLSKLTVDKSRHQQGVFSCVWHEALHNHYTKQSLSLSPCK 476

RESULT 8 S40295 #type complete
ENTRY Ig gamma-2a chain (mAb735) - mouse
TITLE #formal name Mus musculus #common name house mouse
ORGANISM 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
DATE 20-Aug-1994
ACCESSIONS S40295
REFERENCE S40295
#authors Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.;
Frosch, M.; Weisegerber, C.; Bitter-Suermann, D.;
Hiltschmann, N.
#submission submitted to the EMBL Data Library, January 1993
#description Primary structure of the murine monoclonal IgG2a antibody
mAb735 against '(2-8) polysialic acid. 2. Amino acid
sequence of the heavy (H-) chain Fd' region.
#accession S40295
#molecule_type protein
#residues 1-446 #label KIE
GENETICS
#map_position 12
KEYWORDS disulfide bond; glycoprotein; immunoglobulin; pyroglutamic
acid
FEATURE
1-446 #product Ig gamma-2a chain #status experimental #label
MAT\
1-117 #domain V-D-J region #label VDJ\
118-446 #domain C region #label CHR\
118-214 #domain C1 region #label CH1\
215-230 #region hinge\
231-340 #domain C2 region #label CH2\
341-446 #domain C3 region #label CH3\
1 #modified_site pyrrolidone carboxylic acid (Gln) #status
```

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```
22-96,144-199, experimental\
261-321,367-425 #disulfide bonds #status predicted\
132 #disulfide_bonds interchange (to light chain) #status
predicted\
224,227,229 #disulfide bonds interchange #status predicted\
297 #binding_site carbohydrate (Asn) (covalent) #status
experimental
SUMMARY #length 446 #molecular-weight 49108 #checksum 6356
Query Match 52.8%; Score 1832; DB 12; Length 446;
Best Local Similarity 57.0%; Pred. No. 6.41e-254;
Matches 261; Conservative 83; Mismatches 100; Indels 14; Gaps 6;
Db 1 qiclqgqelrvprgavskieckasgytfdyyl-hwtkrpggelewigwypgsntk 59
Qy 20 QVKLQWGGELQLQSETLSRTCVSGSGISGYVYWTWIRTPGRGLEWIGHYNGATTN 79
Db 60 ynekfkkgatltvdsastaymqleasteedavycarggk-----fa--mdywgqg 110
Qy 80 YNPSIKSRVTISKDTSKNOFFINLINSVTDADTAVYCYARGPRDCTTICYGWVDWVCGP 139
Db 111 tevtsasakttapsvplapvcgdtgssvtlqclvkgyfpepvtltwmsglsesvghf 170
Qy 140 DLVTVSSATKGPVFLAPSSKSTSGCTAALGCLVKDYFPEPVTVSNNSGALTSGVHTF 199
Db 171 pavlqsd-lytlesavtvtstwpseiccnvahpasstkvdkiieprg-ptikpcpcpk 228
Qy 200 PAVLQSGSLYSLSVWVTPSSSLGTQYICNVNHNKPSNTKVDKAEKPSCKDTHTCPPC- 258
Db 229 cpapnllggpsvfifppkikdvlmislepivtcvvdvseddpgvqlswfvnnvvltaq 288
Qy 259 -PAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKNWYVDGVEVHNK 317
Db 289 tqthredynstlrvesalpiqhdqmsqefkckvnnkdlpapieritiskpkgsravqv 348
Qy 318 TKPREQYNSTRVSVLVTLHQDLINGKEYCKVSNKALPAIEKTIKAKGQPREQV 377
Db 349 yvlpppeemtkkqvtltcmvtdfmpediyvewtngktelnykntepvladgsyfmys 408
Qy 378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDSGSF 437
Db 409 klrvckknwvnsyscvvhgelnhhttkafstpg 446
Qy 438 KLTVDKSRHQQGVFSCVWHEALHNHYTKQSLSLSPG 475

RESULT 9
ENTRY S01321 #type complete
TITLE Ig gamma-2b chain precursor - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change
23-Mar-1993
ACCESSIONS S01321
REFERENCE S01321
#authors de Haële, P.; Feys, V.; van de Voorde, A.; Molenans, F.;
Fiers, W.
#journal Eur. J. Biochem. (1988) 176:287-295
#title Expression in non-lymphoid cells of mouse recombinant
immunoglobulin directed against the tumour marker human
placental alkaline phosphatase.
#crosse-references MUID:88329081
#accession S01321
#molecule_type mRNA
```



CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology  
SUMMARY #length 377 #molecular-weight 41287 #checksum 8588

Query Match 50.3%; Score 1747; DB 5; Length 377;  
Best Local Similarity 82.8%; Pred. No. 8,96e-241;  
Matches 312; Conservative 15; Mismatches 3; Indels 47; Gaps 9;

Db 1 astkgpsvfplapcstsgtgaalgcclvkdyfpepvtvsnsgaltgcvhvfpaqlqs 60  
|||||  
Qy 147 ASTKGPSVFPLAPSKSTSGCTAALGCLVKDYFPEPVTVSNNGALTSGVHFFPAVLQSS 206  
|||||

Db 61 gylvesvvtvpssslgtctytcnvnkpsntkvdkrvelktplgdtthtcprcpepksc 120  
|||||  
Qy 207 GLYLSVVTPVSSSLGTCTYTCNVNHKPSNTKVDK-----KA-----EPKSC 249  
|||||

Db 121 dtpppcprcpepkcdtpppcprcpepkcdtpppcprcpepkcdtpppcprcpepkcdt 180  
|||||  
Qy 250 D-----K---T-----H-----TC-----P-P-CPAPELLGGPSVFLFPPKPKDT 279  
|||||

Db 181 lmsrtpevtcvvvdshedpevfkwvdygvevhnaktkpreeqnystfrvsvltvlh 240  
|||||  
Qy 280 LMSRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYNSTYRVSVLTVLH 339  
|||||

Db 241 qdwlngkyckvknkalpapiaktiaktkgprepqvtylppseemtknqvslclvk 300  
|||||  
Qy 340 QDWLNGKEYKCKVSNKALPAPTEXTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 399  
|||||

Db 301 gfpysdiavessggpennnttppmlsdsgsflyskltvdkrsrqgnlfscsvmhe 360  
|||||  
Qy 400 GFPSDIAVENESGQPENNYKTPPVLDSDGSFELYSKLTVDKSRQGNLFSCSVMHE 459  
|||||

Db 361 alhnrfqkalelspgk 377  
|||||

Qy 460 ALNHHYTKQSLSLSPGK 476  
|||||

## RESULT 12

ENTRY A60764 #type complete  
TITLE Ig gamma-3 chain C region, form LAT - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 12-Apr-1995

## ACCESSIONS A60764

## REFERENCE A60764

#authors Huck, S.; Leftanc, G.; Leftanc, M.P.

#journal Immunogenetics (1989) 30:250-257  
#title A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 converted region and three hinge exons.

## #accession A60764

#status preliminary

#molecule\_type DNA

#residues 1-377 #label HUC

CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology

SUMMARY #length 377 #molecular-weight 41270 #checksum 9390

Query Match 50.3%; Score 1747; DB 5; Length 377;  
Best Local Similarity 82.8%; Pred. No. 8,96e-241;  
Matches 312; Conservative 15; Mismatches 3; Indels 47; Gaps 9;

Db 1 astkgpsvfplapcstsgtgaalgcclvkdyfpepvtvsnsgaltgcvhvfpaqlqs 60  
|||||  
Qy 147 ASTKGPSVFPLAPSKSTSGCTAALGCLVKDYFPEPVTVSNNGALTSGVHFFPAVLQSS 206  
|||||

Db 61 gylvesvvtvpssslgtctytcnvnkpsntkvdkrvelktplgdtthtcprcpepksc 120  
|||||

Qy 207 GLYLSVVTPVSSSLGTCTYTCNVNHKPSNTKVDK-----KA-----EPKSC 249  
|||||

Db 121 dtpppcprcpepkcdtpppcprcpepkcdtpppcprcpepkcdtpppcprcpepkcdt 180  
|||||  
Qy 250 D-----K---T-----H-----TC-----P-P-CPAPELLGGPSVFLFPPKPKDT 279  
|||||

Db 181 lmsrtpevtcvvvdshedpevfkwvdygvevhnaktkpreeqnystfrvsvltvlh 240  
|||||  
Qy 280 LMSRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYNSTYRVSVLTVLH 339  
|||||

Db 241 qdwlngkyckvknkalpapiaktiaktkgprepqvtylppseemtknqvslclvk 300  
|||||  
Qy 340 QDWLNGKEYKCKVSNKALPAPTEXTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 399  
|||||

Db 301 gfpysdiavessggpennnttppvldsdsgsflyskltvdkrsrqgnlfscsvmhe 360  
|||||  
Qy 400 GFPSDIAVENESGQPENNYKTPPVLDSDGSFELYSKLTVDKSRQGNLFSCSVMHE 459  
|||||

Db 361 alhnrfqkalelspgk 377  
|||||

Qy 460 ALNHHYTKQSLSLSPGK 476  
|||||

## RESULT 13

ENTRY S31866 #type complete  
TITLE Ig gamma-G4 chain C region - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

## ACCESSIONS S31866

## REFERENCE S31866

#authors Filipula, D.

#submission submitted to the EMBL Data Library, February 1993  
#description Screening method for protein-protein interactions of cloned gene products.

## #accession S31866

#status preliminary

#molecule\_type mRNA

#residues 1-255 #label FIL

#cross-references EMBL:X70421

SUMMARY #length 255 #molecular-weight 28325 #checksum 2783

Query Match 48.6%; Score 1686; DB 11; Length 255;  
Best Local Similarity 99.6%; Pred. No. 2.37e-231;  
Matches 231; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 eskcdkthtcpcpapellggsvfllppkpkdtlmsrtpevtcvvvdshedpevkf 83  
|||||

Qy 245 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 304  
|||||

Db 84 nwydgvvhnaktkpreeqnystyrsvsvltvlhqdwlngkyckvknkalpapiakt 143  
|||||

Qy 305 NWYDGVVHNKTKPREEQYNSTYRVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKT 364  
|||||

Db 144 iskagqprepqvtylppardeltnqvslclvkgyfypediavenesngqpennkyttp 203  
|||||  
Qy 365 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVENESNGQPENNYKTTT 424  
|||||

Db 204 pvlstdsgsflyskltvdkrsrqgnlfscsvmhealhnhytqkalelspgk 255  
|||||

Qy 425 PVLSDSGSFELYSKLTVDKSRQGNLFSCSVMHEALHNHYTQKSLSLSPGK 476  
|||||



\* RESULT 14

```
ENTRY      PT0207      #type complete
TITLE      Ig gamma chain C region - chimpanzee
ORGANISM   #formal_name Pan troglodytes #common_name chimpanzee
DATE       23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change
          12-Apr-1995
ACCESSIONS PT0207
REFERENCE   PT0207
#authors   Ethlich, P.H.; Moustafa, Z.A.; Oestberg, L.
#journal   Mol. Immunol. (1991) 28:319-322
#title     Nucleotide sequence of chimpanzee Fc and hinge regions.
#cross-references MIMD:91287716
#accession PT0207
#molecule_type mRNA
#residues  1-234 #label EHR
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY      #length 234 #molecular-weight 26330 #checksum 6128

Query Match      48.3%; Score 1677; DB 5; Length 234;
Best Local Similarity 98.3%; Pred. No. 5.82e-230;
Matches 230; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1  entkvdkvpekcadtcttccpaapellgqpsvflfppkpkdktlmisrtpevtcvvdv 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 236  SNTKDKKAEPKSKDTHCTPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTVVDV 295

Db 61  shedpevfwnydvgevhnaaktprcegnstyrsvvltvlhqdlnqkcykcvnsk 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 296  SHEDPEVFENWYDVGEVHNKTKPREQYNSTYRVVSVLTVQLQDWLNKREYKCVSNK 355

Db 121  alpalektiskagqprepqwtlpsrdeltknqslctclvkgyfypdiavesssq 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 356  ALPAPTEKTSKAGQPREPQVTLPPSDELTKNQSVLTCVKGFFPSDIAVENESNQ 415

Db 181  pennykttppvldsgsflysklvtkdrwqgnvfscsvnhealhnhytqks 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 416  PENNYKTPPVLDSDGSFSLYSLKLTVDKSRMQGNVFSCSVNHEALHNHYTQKS 469

RESULT 15
ENTRY      GHRB      #type complete
TITLE      Ig gamma chain C region - rabbit
ORGANISM   #formal_name Oryctolagus cuniculus #common_name domestic
          rabbit
DATE       #sequence_revision 15-Nov-1984 #text_change 04-Nov-1994
ACCESSIONS A91749; A90290; A93928; A90245; A94416; A90161
REFERENCE   A91749
#authors   Bernslein, K.E.; Alexander, C.B.; Mage, R.G.
#journal   Immunogenetics (1983) 18:387-397
#title     Nucleotide sequence of a rabbit IgG heavy chain from the
          recombinant F-I haplotype.
#cross-references MIMD:84030930
#accession A91749
#molecule_type mRNA
#residues  1-323 #label BER
#note      this sequence has the d12 allotypic marker, 104-Thr, and
          the e14 marker, 185-Thr

REFERENCE   A90290
#authors   Pratt, D.M.; Mole, L.E.
#journal   Biochem. J. (1975) 151:337-349
#title     Sequence studies on the constant region of the Fd sections of
          rabbit immunoglobulin G of different allotype.
#cross-references MIMD:76135469
#accession A90290
```

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#molecule_type protein
#residues  1-47, 'E', 49-71, 'PV', 72-128 #label PRA
REFERENCE   A93928
#authors   Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight,
          K.L.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1982) 79:6018-6022
#title     Heavy chain genes of rabbit IgG; isolation of a cDNA encoding
          gamma heavy chain and identification of two genomic C-gamma
          genes.
#cross-references MIMD:83299917
#accession A93928
#molecule_type mRNA
#residues  88-103, 'W', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266
          #label MAR
#note      this sequence has the d11 allotypic marker, 104-Met, and
          the e15 allotypic marker, 185-Ala

REFERENCE   A90245
#authors   Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
#journal   Biochem. J. (1970) 116:249-259
#title     Sequence studies of the Fd section of the heavy chain of
          rabbit immunoglobulin G.
#cross-references MIMD:70110015
#accession A90245
#molecule_type protein
#residues  132-143, 'E', 145-161 #label FRU
          A94416
#authors   Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
          in Gamma Globulins, Nobel Symp. 3, Killander, J., ed.,
          pp.109-127, Almqvist and Wiksell, Stockholm, 1967
#accession A94416
#molecule_type protein
#residues  129-131;155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D',
          202-217, 'E', 219-232, 'Q', 234-245, 'D', 247-255, 'C',
          257-259, 'D', 261-265, 'D', 267-279, 'W', 281-283, 'S',
          285-322 #label HIL
#note      this has the e15 allotypic marker, 185-Ala
          #superfamily immunoglobulin C region; immunoglobulin homology

CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-82      #domain immunoglobulin homology #label IGG1\
130-199    #domain immunoglobulin homology #label IGG2\
236-303    #domain immunoglobulin homology #label IGG3
SUMMARY    #length 323 #molecular-weight 35404 #checksum 1467

Query Match      48.1%; Score 1669; DB 2; Length 323;
Best Local Similarity 70.0%; Pred. No. 9.99e-229;
Matches 229; Conservative 46; Mismatches 45; Indels 7; Gaps 3;

Db 4  kapsvflapccgdtspstvtlglvkgylpepvtvtnsgtltngvrtfsvrqsagly 63
    |:||||| |:::| :||| |::| |::| |::| |::| |::| |::| |::| |::|
Qy 150  KGSVEPIAPSSKTSGGTAALGLVDRDYFPEPVTVSNWNSGALTSVGHVTFPAVLQSSGLY 209

Db 64  slsrsvsvtss---qpvtcnvhpattntkvdktvaptcscpk-tcpp---pellgpsv 116
    ||||| | | | | |::| | | | |::| | | | |::| | | | |::| | | | |::|
Qy 210  SLSSVVTVPSSSLGTQTYICNNHKPSNTKYDKKAEKSCDKTHTCPCPAPELLGGSV 269

Db 117  fifppkpktlmisrtpevtcvvsvsqddpevftwyinneqvrtarplrqgfnsti 176
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Qy 270  FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREQYNSTY 329

Db 177  rwstlptlthqdlrqefkckvhnkalpaplektiskargplekvymgppreels 236
    |||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Qy 330  RVSVSLTVLHQDWLNKREYKCVSNKALPAPTEKTSKAGQPREPQVTLPPSDELTK 389

Db 237  rsvaltcmfngypsdisvewekngkaednyktttppvldsgsflylnklsvptsewqrg 296
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QY 390 NQVSLTCLVRGFTPSDIAVENESGQPNNTTPPVLDSDGSEFFLYSKLTVDKSRMQOG 449

Db 297 dvftcevmhealhnhytqkqkqk 323

QY 450 NVFSCVMHEALHNHYTQKSLSPGK 476

Search completed: Tue Dec 17 15:20:21 1996  
Job time : 63 secs.



[14]  
RN SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE; 77070269.  
RA PONSTINGL H., HILSCHMANN N.;  
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1571-1604 (1976).  
[5]  
RN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE; 83289131.  
RA SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N.;  
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 364:713-747 (1983).  
[6]  
RN DISULFIDE BONDS.  
RX MEDLINE; 71064027.  
RA GALL W.E., EDELMAN G.M.;  
RL BIOCHEMISTRY 9:3188-3196 (1970).  
[7]  
RN DISULFIDE BONDS.  
RX MEDLINE; 77070267.  
RA DREKER L., SCHWARZ J., REICHEL W., HILSCHMANN N.;  
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1515-1540 (1976).  
[8]  
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE; 81208100.  
RA DEISENHOFER J.;  
RL BIOCHEMISTRY 20:2361-2370 (1981).  
CC -!- NIE HAS THE GIM(17) ALLOTYPE MARKER, 97-K, & THE GIM(1) MARKERS,  
239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM  
(NON-1) MARKERS.  
CC -!- NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.  
CC -!- EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177,  
195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.  
CC -!- KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198,267&272.  
DR EMBL; J00228; J00228.  
DR PIR; A02146; GHU.  
DR PDB; 1FC1; 15-JUL-92.  
DR PDB; 1FC2; 15-JUL-92.  
DR PDB; 147100; 11TH EDITION.  
DR PROSITE; PS00290; IG MHC.  
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; 3D-STRUCTURE.  
FT NON TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 223 CH2.  
FT DOMAIN 224 330 CH3.  
FT DISULFID 27 83  
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).  
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT CARBOHYD 180 180  
FT VARIANT 97 97 K -> R (IN GIM(3) MARKER).  
FT VARIANT 239 239 D -> E (IN GIM(NON-1) MARKER).  
FT VARIANT 241 241 L -> M (IN GIM(NON-1) MARKER).  
FT MOD RES 330 330 REMOVED POST-TRANSLATIONALLY.  
FT STRAND 123 126  
FT HELIX 130 134  
FT TURN 136 137  
FT STRAND 141 148  
FT STRAND 158 162  
FT TURN 163 164  
FT STRAND 165 166  
FT STRAND 175 178  
FT STRAND 183 190

FT HELIX 193 197  
FT TURN 198 199  
FT STRAND 202 206  
FT STRAND 215 219  
FT STRAND 227 227  
FT STRAND 230 234  
FT HELIX 238 240  
FT TURN 241 242  
FT STRAND 245 256  
FT STRAND 260 266  
FT TURN 267 268  
FT STRAND 269 270  
FT STRAND 274 276  
FT STRAND 280 281  
FT TURN 283 284  
FT STRAND 287 296  
FT HELIX 297 301  
FT TURN 302 303  
FT STRAND 306 312  
FT TURN 313 314  
FT TURN 316 317.  
FT STRAND 320 324  
SQ SEQUENCE 330 AA; 36106 MW; 642285 CN;  
  
Query Match 67.4%; Score 2339; DB 3; Length 330;  
Best Local Similarity 99.7%; Pred. No. 0.00e+00;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Db 1 aetkqpsvflapsksetsgtgaalgcLvkdYfpepvtvwnsgaltsgvhtfpavlgss 60  
|||||  
Qy 147 ASTKGSVFELAPSSKSTSGGTAALGCLVKDYFEPEPVTVMNSGALTSGVHTFPVAVLQSS 206  
|||||  
Db 61 glyelassvtpesslgtctyicnnhhkpsntkvdkvpepkacdtkhtccppcapellgg 120  
|||||  
Qy 207 GLYSLSVVTPVPSLSLGTQTYICNVNHRPSNTKYDKKAEPKSCDKTHTCPPCPAPPELLGG 266  
|||||  
Db 121 pavflfpkpkdltmIertpevtcvvvdvshdedpevkfnwvdgvevhnaktkpreeqyn 180  
|||||  
Qy 267 PSVFLFPPPKPDITLISRPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYN 326  
|||||  
Db 181 atyrvsvltvlhqdwlngkeyckvsnkalpapiektiskakgqpreqvylpparde 240  
|||||  
Qy 327 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 386  
|||||  
Db 241 ltknqvltclvkfypsdiaveeengqpennykttppvldsdgsfflyskltvdkerw 300  
|||||  
Qy 387 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRW 446  
|||||  
Db 301 qqgnvfscsvmhcalhnhytqklsleppok 330  
|||||  
Qy 447 QQGNVFCSCVMHEALHNNHYTKQKLSLSPGK 476  
|||||  
  
RESULT 2  
ID GC2 HUMAN STANDARD; PRT; 326 AA.  
AC P01859;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE IG GAMMA-2 CHAIN C REGION.  
GN IGHG2.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.

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5

RN [1] SEQUENCE FROM N.A.  
 RP MEDLINE; 82197621.  
 RA ELLISON J.W., HOOD L.E.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 79:1984-1988(1982).  
 RN [2]  
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
 RX MEDLINE; 81007873.  
 RA WANG A.-C., TUNG E., FUDENBERG H.H.;  
 RL J. IMMUNOL. 125:1048-1054(1980).  
 RN [3]  
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
 RX MEDLINE; 80001357.  
 RA CONNELL G.E., PARR D.M., HOFMANN T.;  
 RL CAN. J. BIOCHEM. 57:758-767(1979).  
 RN [4]  
 RP SEQUENCE OF 238-275 (ZIE).  
 RX MEDLINE; 80114419.  
 RA HOFMANN T., PARR D.M.;  
 RL MOL. IMMUNOL. 16:923-925(1979).  
 RN [5]  
 RP ZIE, REVISIONS TO 25; 59; 60 AND 264-268.  
 RA HOFMANN T., PARR D.M.;  
 RL SUBMITTED (MAR-1980) TO THE PIR DATA BANK.  
 RN [6]  
 RP SEQUENCE OF 1-121 (DOT).  
 RA STOPPINI M., BELLOTTI V., NEGRI A., MERLINI G., GARVER F., FERRI G.;  
 RL EUR. J. BIOCHEM. 0:0-0(1995).  
 RN [7]  
 RP MYELOMA PROTEIN SA, DISULFIDE BONDS.  
 RX MEDLINE; 72033500.  
 RA MILSTEIN C., FRANGIONE B.;  
 RL BIOCHEM. J. 121:217-225(1971).  
 RN [8]  
 RP SA, DISULFIDE BONDS.  
 RX MEDLINE; 69064124.  
 RA FRANGIONE B., MILSTEIN C., PINK J.R.L.;  
 RL NATURE 221:145-148(1969).  
 DR EMBL; V00554; V00554.  
 DR PIR; A02148; G2HU.  
 DR HSP; P01857; 1BBJ.  
 DR MIM; 147110; 11TH EDITION.  
 DR PROSITE; PS00290; IG.MHC.  
 KW IMMUNOGLOBULIN C REGION.  
 FT NON TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 219 CH2.  
 FT DOMAIN 220 326 CH3.  
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 140 200  
 FT DISULFID 246 304  
 FT VARIANT 60 60  
 FT SITE 156 156  
 FT MOD RES 326 326  
 SQ SEQUENCE 326 AA; 35884 MW; 629390 CN;  
 S -> A (IN MYELOMA PROTEINS TIL & ZIE).  
 AT OR NEAR THE COMPLEMENT-BINDING SITE.  
 REMOVED POST-TRANSLATIONALLY (PROBABLE).  
 Query Match 61.4%; Score 2133; DB 3; Length 326;  
 Best Local Similarity 90.9%; Pred. No. 0.00e+00;

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Matches 300; Conservative 15; Mismatches 11; Indels 4; Gaps 3;  
 Db 1 astkqsvflapacsrsteestaalgclvkdypetvtnvmsgaltsgvhtfpavlaqss 60  
 Qy 147 ASTKGSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 206  
 Db 61 glyalsavvtvpssnfgtqtcnvdhkpentkydktverkc--ve-cpccpappv-ag 116  
 Qy 207 GLYSLSVWVTPSSSLGTQTYICNVNHRPSNTKYDKRAEPKSCOKTHTCPCPAPELLGG 266  
 Db 117 psvflfppkpkdtlmisrtpevtcvvvdvshdpevqfnwydvghvhnaktkpreeqfn 176  
 Qy 267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 326  
 Db 177 etfrvsvltvvhqdwlngkeyckvkcnklpapiekt.lsktkgqprepvytlppree 236  
 Qy 327 STYRVSVLTIVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386  
 Db 237 mtknqvaltlvkgfypsdiavewengpennykttppmlsdsgsflyskltvdkerw 296  
 Qy 387 LTRKQVSLTLCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLKLTVDKSRW 446  
 Db 297 qqgnvfscsvmhcalhnyhtqkslsapok 326  
 Qy 447 QQGNVFCVSMWHEALHNHYTQKSLSLSPGK 476  
 RESULT 3  
 ID GC4 HUMAN STANDARD; PRT; 327 AA.  
 AC P01861;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)  
 DE IG GAMMA-4 CHAIN C REGION.  
 GN 1GHG4.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 83157104.  
 RA ELLISON J.W., BUXBAUM J.N., HOOD L.E.;  
 RL DNA 1:11-18(1981).  
 RN [2]  
 RP SEQUENCE OF 1-30 AND 81-326.  
 RX MEDLINE; 70207560.  
 RA PINK J.R.L., BUTTERY S.H., DE VRIES G.M., MILSTEIN C.;  
 RL BIOCHEM. J. 117:33-47(1970).  
 DR PIR; A02150; G4HU.  
 DR HSP; P01857; 1BBJ.  
 DR MIM; 147130; 11TH EDITION.  
 DR PROSITE; PS00290; IG.MHC.  
 KW IMMUNOGLOBULIN C REGION.  
 FT NON TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 220 CH2.  
 FT DOMAIN 221 327 CH3.  
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 141 201  
 FT DISULFID 247 305



DE	IG GAMMA-2 CHAIN C REGION.
OS	CAVIA PORCELLUS (GUINEA PIG).
OC	EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE OF 1-3.
RP	TRISCHMANN T.M.;
RA	SUBMITTED (APR-1975) TO THE PIR DATA BANK.
RL	[2]
RN	SEQUENCE OF 4-68.
RP	MEDLINE; 71058471.
RX	BIRSSTEIN B.K., HUSSAIN Q.Z., CEBRA J.J.;
RA	BIOCHEMISTRY 10:18-25(1971).
RL	[3]
RN	SEQUENCE OF 69-133 AND 312-329.
RP	MEDLINE; 71058486.
RX	TURNER K.J., CEBRA J.J.;
RA	BIOCHEMISTRY 10:9-17(1971).
RL	[4]
RN	SEQUENCE OF 134-226.
RP	MEDLINE; 75036072.
RX	TRACEY D.E., CEBRA J.J.;
RA	BIOCHEMISTRY 13:4796-4803(1974).
RL	[5]
RN	SEQUENCE OF 227-311.
RP	MEDLINE; 75036073.
RX	TRISCHMANN T.M., CEBRA J.J.;
RA	BIOCHEMISTRY 13:4804-4811(1974).
RL	[6]
RN	DISULFIDE BONDS.
RP	MEDLINE; 71058474.
RX	OLIVEIRA B., LAMM M.E.;
RA	BIOCHEMISTRY 10:26-31(1971).
RL	-I- THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED
CC	GUINEA PIGS.
CC	PIR; A02151; G2GP.
DR	HSP; P01857; 1FC1.
DR	PROSITE; PS00290; IG.MHC.
DR	IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.
KW	NON TER 1 1
FT	DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID 28 79
FT	DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 142 202
FT	CARBOHYD 178 178
FT	DISULFID 248 308
SQ	SEQUENCE 329 AA; 36074 MW; 630420 CN;

	Query Match	46.5%	Score 1616;	DB 3;	Length 329;
	Best Local Similarity	70.1%;	Pred. No. 0.00e+00;		
	Matches 234;	Conservative 39;	Mismatches 52;	Indels 9;	Gaps
Db	1	eaattapevfpaaacvdtagsmmtlgcllkgvfppevtvkmagaltagvhtfpavqls	60		
		:   :			
Qy	146	SASTKGSVFPLAPSSKTSGCTAALGCLLVKDYPPPEPVTVSNNGALTSGVHTFPVQLS	205		
		:			
Db	61	-glyaltsmvtvpsq--kat--cnvaphaaastkvdktvepirtzpbbctpcpkppen	115		
		:			
Qy	206	SGLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKVOKKAEP-KSCDKTH-TCPCPAPEL	263		
		:			
Db	116	lqgpavfifppkpkdtlmisltpvtcvvdvsqdepevqftwfvdnkpvgaetkprve	175		
		:			

QY	264	LGPSVFLFPKPKDTLMI	SRTEPTEVCVVWDVSHEDPEVKENMYDGVGVHNNAKTKPREE	323
Db	176	qynttfrrveevipichdwlr	gkfkckvynkalpaiektiektgacmpdytclpø	235
QY	324	QYNSTYRVSVELTFLHQD	WLNGKEYKCKVSNKALPALTEKTSKAGQPREPQVYTIIPS	383
Db	236	rdelesekavrtcliniiffad	ihveasnrpvveekeykntpiedadgsyflyekltv	295
QY	384	RDELTKQVSLTCLVKGYFSD	IAVENESGQP--ENNYTKTPVLDSDGSFFLYSKLTV	441
Db	296	dksawdggtvctsvmhleah	nhnhtqkaierspg	329
QY	442	DKSRMQQGNFVSCSVMH	EALHNHYTKSLSPG	475
RESULT 6				
ID	GC3 HUMAN	STANDARD;	PRT;	290 AA.
AC	PO1860;			
DT	21-JUL-1986 (REL. 01,	CREATED)		
DT	21-JUL-1986 (REL. 01,	LAST SEQUENCE UPDATE)		
DT	01-FEB-1991 (REL. 17,	LAST ANNOTATION UPDATE)		
DE	IG GAMMA-3 CHAIN C	REGION (HEAVY CHAIN DISEASE PROTEIN) (HDC) .		
DE	IGHG3.			
GN	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA;	CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RX	SEQUENCE (DISEASE PROTEIN WIS).			
RP	MEDLINE; 81021548.			
RA	FRANGIONE B., ROSENWASSER E., PRELLI F., FRANKLIN E.C.;			
RL	BIOCHEMISTRY 19:4304-4308 (1980).			
RL	[2]			
RP	NORMAL GAMMA-3 CHAINS, REVISIONS TO 12-97 OF PROTEIN WIS.			
RA	MEDLINE; 71118561.			
RL	MICHAELSEN T.E., FRANGIONE B., FRANKLIN E.C.;			
RL	J. BIOL. CHEM. 252:883-889 (1977).			
RL	[3]			
RP	DISEASE PROTEIN ZUC, REVISIONS TO 59-289 OF PROTEIN WIS.			
RA	MEDLINE; 17021516.			
RX	WOLFSTEIN-TODEL C., FRANGIONE B., PRELLI F., FRANKLIN E.C.;			
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 71:907-914 (1976).			
RL	[4]			
RP	SEQUENCE FROM N.A. (DISEASE PROTEIN OMW).			
RX	MEDLINE; 82247835.			
RA	ALEXANDER A., STEINMETZ M., BARRITAU D., FRANGIONE B.,			
RA	FRANKLIN E.C., HOOD L., BUxbaUM J.N.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 79:3260-3264 (1982).			
CC	-1- THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.			
CC	-1- THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE REF. 2.			
CC	-1- DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE CHI REGION.			
CC	-1- DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.			
CC	-1- DISEASE PROTEIN OMW MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLASS.			
CC	-1- THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).			
CC	-1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.			
DR	EMBL; J00231; J00231.			
DR	PIR; A02149; G3HUM1.			



DR HSP; P01857; IFC1.  
DR MIM; 147120; 11TH EDITION.  
DR PROSITE; PS00290; IG MHC.  
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.  
FT DOMAIN 12 73 HINGE.  
FT DOMAIN 74 183 CH2.  
FT DOMAIN 184 289 CH3.  
FT REPEAT 29 43  
FT REPEAT 44 58  
FT REPEAT 59 73  
FT MOD RES 1 1  
FT CARBOHYD 6 6

## PYRROLIDONE CARBOXYLIC ACID.

FT DISULFID 7 7 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT CARBOHYD 140 140  
FT MOD RES 290 290  
FT VARIANT 126 127  
FT VARIANT 134 134  
FT VARIANT 139 139  
FT VARIANT 182 182  
FT VARIANT 227 227  
FT VARIANT 227 227  
FT VARIANT 279 279  
SQ SEQUENCE 290 AA; 32331 MW; 485009 CN;

## REMOVED POST-TRANSLATIONALLY.

QV -&gt; EB (IN ZUC).

P -&gt; L (IN OHM).

F -&gt; Y (IN OHM).

T -&gt; A (IN OHM).

S -&gt; N (IN OHM).

MISSING (IN ZUC).

F -&gt; Y (IN OHM).

Query Match 45.8%; Score 1590; DB 3; Length 290;

Best Local Similarity 90.1%; Pred. No. 0.00e+00;

Matches 210; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 58 pepscdtpcpapellggspsvflfppkpkdtlmisrtpevtcvvvdshdpevq 117  
:||||| || |||||

Qy 244 AEPKSCDTHTCPPCAPPELLGGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHDEPK 303  
:||||| || |||||

Db 118 fkyvdygvghnaktkpreqgnstfrvsvltvlgqwlldgkeyckkvankalpapie 177  
:||||| || |||||

Qy 304 FNWYDGVGEVHNAKTKPREQYNSYTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEK 363  
:||||| || |||||

Db 178 tiestkgtgppqvyltppsreentknqslctlvkfypsdiaveesagqpenyntt 237  
:||||| || |||||

Qy 364 TISKAGQPREPQVYLTIPSRSDELTKNQSLCLVKGFPYSDIAVEESNGQPENNYKT 423  
:||||| || |||||

Db 238 pmlsdsgsflyskltvdksrwaggnifscvnmhealnhrftqkslsppok 290  
:||||| || |||||

Qy 424 PPVLDSDGSFFLYSKLTVDKSRMQGNVFCVNMHEALHNHYTQKSLSLSPGK 476  
:||||| || |||||

RESULT 7  
ID GC1 RAT STANDARD; PRT; 326 AA.  
AC P20759;

DT 01-FEB-1991 (REL. 17, CREATED)  
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)  
DE IG GAMMA-1 CHAIN C REGION.  
OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89232738.  
RA BRUEGGEMANN M.;  
RL GENE 74:473-482 (1988).  
DR PIR; PS0017; PS0017.  
DR HSP; P01857; IFC1.  
DR PROSITE; PS00290; IG MHC.  
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.  
FT NON TER 1 1  
FT DOMAIN 1 97 CHI.  
FT DOMAIN 98 112 HINGE.  
FT DOMAIN 113 219 CH2.  
FT DOMAIN 220 326 CH3.  
FT DISULFID 27 82  
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 140 200  
FT DISULFID 246 304  
FT CARBOHYD 176 176  
SQ SEQUENCE 326 AA; 35946 MW; 630958 CN;

Query Match 45.8%; Score 1582; DB 3; Length 326;

Best Local Similarity 63.3%; Pred. No. 0.00e+00;

Matches 209; Conservative 60; Mismatches 57; Indels 4; Gaps 4;

Db 1 aettapsvylapgtalkenmvltgclvkgypcvvtvtnsgalagshgvtfpavlgq- 59  
:||||| || |||||

Qy 147 ASTKGFSVFPPLAPSSKSTSGCTAALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVLQSS 206  
:||||| || |||||

Db 60 glyltltsvtpsetwpsqvtcnavhpaastkvdkiivprncg-gd-ckpcictgs-ev 116  
:||||| || |||||

Qy 207 GLYSLSVSVVTPSSSLGTQTYICNVNHRPSNTKYDKRAEPKSCDKTHTCPCPAPPELLGG 266  
:||||| || |||||

Db 117 asvfiipkpkdvlitltpkvtcvvvdisdqddpevhfawfvdvdehtaqtrpseeqfn 176  
:||||| || |||||

Qy 267 PSVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 326  
:||||| || |||||

Db 177 stfrsvselplhqdwlngtrfcrckvtsaafpspietkiskpegrtqvphvymptkee 236  
:||||| || |||||

Qy 327 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPVYTIIPPSRDE 386  
:||||| || |||||

Db 237 mtqneaitcmvkgfpyppdiyvewqmgqgqenykntpmtmdtdqsyflysklnvkkew 296  
:||||| || |||||

Qy 387 LTKNQSLCLVKGFPYSDIAVEESNGQPENNYKTTPPVLDSDGSFELYSLKLTVDKSRW 446  
:||||| || |||||

Db 297 cagntfcsvheglhnhhtekslshpgk 326  
:||||| || |||||

Qy 447 QQGNVFCVNMHEALHNHYTQKSLSLSPGK 476  
:||||| || |||||

RESULT 8  
ID GC3 MOUSE STANDARD; PRT; 329 AA.  
AC P22436;

DT 01-AUG-1991 (REL. 19, CREATED)  
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)  
DT 01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)  
DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC	EUTHERIA; ROENTIA.
{1}	
RN	SEQUENCE FROM N.A.
RP	MEDLINE; 85027161.
RX	WELLS J.A., WORD C.J., RIMM D., DER-BALAN G.P., MARTINEZ H.M.,
RA	TUCKER P.W., BLATTNER F.R.;
RL	EMBO J. 3:2041-2046(1984).
DR	EMBL; J00451; J00451.
DR	PIR; B02156; G3MSC.
DR	HSSP; P01857; 1FC1.
DR	PROSITE; PS00290; IG_MHC.
KW	IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; TRANSMEMBRANE;
KW	ALTERNATIVE SPLICING.
FT	NON TER 1 1
FT	D0A1N 1 97 CH1.
FT	D0A1N 98 113 HINGE.
FT	D0A1N 114 223 CH2.
FT	D0A1N 224 327 CH3.
SQ	SEQUENCE 329 AA; 36228 MW; 617081 CN;
	Query Match 45.6%; Score 1584; DB 3; Length 329;
	Best Local Similarity 63.8%; Pred. No. 0.00e+00;
	Matches 210; Conservative 61; Mismatches 57; Indels 2; Gaps 2;

Db	1	t	t	t	p	a	v	y	p	v	p	g	s	d	t	s	g	s	a	v	t	i	g	c	v	k	g	y	f	p	e	p	v	t	k	v	n	y	g	a	l	s	g	v	t	v	e	s	v	l	q	-	g	59	
Qy	148	S	T	K	G	S	V	F	L	A	P	S	K	S	T	S	G	T	A	L	G	L	V	K	D	Y	F	P	E	P	V	T	V	S	N	S	C	A	L	T	S	G	V	H	T	F	A	V	L	Q	S	G	207		
Db	60	f	y	e	s	e	l	t	v	p	s	e	t	w	s	e	t	v	i	c	n	v	a	h	p	a	k	t	e	l	k	r	i	e	p	r	i	k	p	a	t	p	p	g	s	e	c	p	p	n	i	l	g	119	
Qy	208	L	Y	S	L	S	V	T	P	S	S	L	G	T	Q	T	Y	I	C	N	V	N	H	K	P	S	N	T	R	V	D	K	A	E	P	S	C	O	-	K	T	H	T	C	P	C	P	A	E	L	L	G	266		
Db	120	p	s	v	i	f	f	p	p	k	d	a	l	m	i	s	t	p	k	v	t	c	v	v	d	v	s	e	e	d	p	d	v	h	s	v	f	v	d	n	k	e	v	t	a	w	t	g	r	e	a	q	v	n	179
Qy	267	P	S	V	F	F	P	P	K	D	T	I	M	I	S	R	P	E	V	T	C	V	V	D	V	S	H	E	D	E	V	K	F	N	Y	V	D	G	V	E	V	N	N	A	K	T	P	R	E	E	Q	N	326		
Db	180	s	t	f	r	v	s	a	p	i	q	h	d	m	t	g	k	e	f	c	k	v	n	k	a	p	i	a	r	t	i	e	s	k	p	a	r	a	d	t	p	q	v	y	t	i	p	p	r	e	q	239			
Qy	327	S	T	R	V	S	V	T	V	L	H	Q	M	I	N	G	K	E	T	C	K	S	N	A	L	P	A	P	I	E	K	T	I	S	K	A	G	Q	P	R	E	P	Q	V	T	T	P	S	R	D	386				
Db	240	m	s	t	k	v	a	l	t	c	l	r	n	t	f	f	e	s	e	i	s	e	v	e	r	n	e	l	e	q	d	y	n	t	k	p	i	l	d	e	d	t	y	f	y	s	k	t	v	d	t	d	s	w	299
Qy	387	L	T	N	Q	S	V	T	C	L	V	R	G	F	S	D	I	A	V	E	S	G	O	P	E	N	N	Y	K	T	T	P	V	L	S	D	G	S	F	F	L	S	K	T	V	D	K	S	R	W	446				
Db	300	l	q	e	a	f	t	c	s	v	e	a	h	n	h	t	t	q	n	i	s	a	p	k	329																														
Qy	447	Q	O	C	N	F	S	C	S	V	N	H	E	A	L	N	H	T	O	K	S	L	S	P	K	476																													

RESULT	9
ID GC3M MOUSE STANDARD; PRT; 398 AA.	
AC AC	P03987;
DT DT	23-OCT-1986 (REL. 02, CREATED)
DT DT	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT DT	01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE DE	IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
OS OS	MUS MUSCULUS (MOUSE).
OC OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC OC	EUTHERIA; RODENTIA..
RN RN	[1]
RP RP	SEQUENCE FROM N.A.
RX RX	MEDLINE; 85027161.
RA RA	WELS J.A., WORD C.J., RIMM D., DER-BALAN G.P., MARTINEZ H.M., TUCKER P.W., BLATTNER F.R.;

RL	EMBO J. 3:2041-2046(1984).	
[2]		
RN	SEQUENCE OF 328-398 FROM N.A.	
RP	MEDLINE; 84041483.	
RX	KOMAROMY M., CLAYTON L., ROGERS J., ROBERTSON S., KETTMAN J.,	
RA	WALL R.;	
RA	NUCLEIC ACIDS RES. 11:6775-6785(1983).	
DR	EMBL; J00451; J00451.	
DR	EMBL; V01526; V01526.	
DR	PIR; A02155; G3NSM.	
DR	HSSP; P01857; 1FC1.	
DR	PROSITE; PS00290; IG_MHC.	
KW	IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; TRANSMEMBRANE;	
KW	ALTERNATIVE SPLICING.	
FT	NON_TER 1 97	
FT	DOMAIN 1 FT CH1.	
FT	DOMAIN 98 113 HINGE.	
FT	DOMAIN 114 223 CH2.	
FT	DOMAIN 224 327 CH3.	
FT	TRANSMEM 346 362 POTENTIAL.	
FT	DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).	
FT	CONFLICT 333 333 E -> G (IN REF. 2).	
FT	CONFLICT 342 342 E -> Q (IN REF. 2).	
FT	CONFLICT 388 388 P -> F (IN REF. 2).	
SQ	SEQUENCE 398 AA; 43929 MW; 896835 CN;	

Query Match	45.2%;	Score 1570;	DB 3;	Length 398;
Best Local Similarity	63.4%;	Pred. No. 0.00e+00;		
Matches	208;	Conservative	61;	Mismatches 57;
			Indels	2;
			Gaps	2;
Db	1	tttapswplvgcsdtesgsavtlgclvkvqfpevptvkvkmvgalaeqgvtvsvvlqe-g 59		
	:	:		
	:	:		
	:	:		
Qy	148	STGQPSVFLPAPSKSTSGCTGAALGCUKVDPEPVTVSNNGALTSQVHTFPVAVLQSSG 207		
Db	60	fyslslavltvpstwpstqvticnvahpaakteelikrielpktpetpggscppgnilgg 119		
	:	:		
	:	:		
Qy	208	LYSLSSWTVTPSSLSGTQYICNVNKKPNTNKDKAEPKSCD-KTHCTPCPCAPPELLGG 266		
Db	120	psvifipbpkdaImIsLtpkvctvvvdseddphdvhwfvdnkvehtawtqpreagyn 179		
	:	:		
	:	:		
Qy	267	PSVFIFPPKPKDITLISRPEVTVCVVVDYSHEDYEVKENWYVDGVEVNNAKTKPREEQYN 326		
Db	180	stfrvvsalpiqhdvmrgkafckvnnkalpapiertiskpgractpqwtipppreq 239		
	:	:		
	:	:		
Qy	327	STRVSVVLITWHDQWNGKEYCKVSNKALPAIETKTSKAGQPREPQVYTLTPSPRDE 396		
Db	240	mskkksvltclvntffseaiswerngelegdykntppildsdqtyfyskltvdtcsw 299		
	:	:		
	:	:		
Qy	387	LTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYTKTTPPVLDSGSGFFLYSKLTVDKSRW 446		
Db	300	lqgeiftcsvvhcaalnhhntqknlresp 327		
	:	:		
	:	:		
Qy	447	OQGNVPECSVMHEALNHYTOKSLISLSP 474		

RESULT	10	STANDARD;	PRT;	324 AA.
ID	GC1 MOUSE			
AC	P01868;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
DE	IG GAMMA-1 CHAIN C REGION.			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			

OC	EUTHERIA; RODENTIA.
(1)	
RN	SEQUENCE FROM N.A.
RP	MEDLINE; 80045036.
RX	HONJO T., OBATA M., YAMAWAKI-KATAOKA Y., KATAOKA T., KAWAKAMI T.,
RA	TAKAHASHI N., MANO Y.;
RA	CELL 18:559-568 (1979).
RL	
(2)	
RN	SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX	MEDLINE; 80202559.
RX	OBATA M., YAMAWAKI-KATAOKA Y., TAKAHASHI N., KATAOKA T., SHIMIZU A.,
RA	MANO Y., SEIDMAN J.G., PETERLIN B.M., LEDER P., HONJO T.;
RL	GENE 9:87-97 (1980).
(3)	
RN	SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX	MEDLINE; 80012837.
RA	ROGERS J., CLARKE P., SALSER W.;
RL	NUCLEIC ACIDS RES. 6:3305-3321 (1979).
(4)	
RN	SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX	MEDLINE; 78242288.
RA	ADETUGBO K.;
RL	J. BIOL. CHEM. 253:6068-6075 (1978).
(5)	
RN	DISULFIDE BONDS (MOPC 21).
RX	MEDLINE; 73008889.
RA	SVASTI J., MILSTEIN C.;
RL	BIOCHEM. J. 126:837-850 (1972).
DR	EMBL; V00793; V00793.
DR	EMBL; V00795; V00795.
DR	PIR; A02159; GIMS.
DR	HSPP; P01679; IBAF.
DR	PROSITE; P50290; IG_MHC.
KW	IMMUNOGLOBULIN C REGION; ALTERNATIVE SPLICING; GLYCOPROTEIN.
1	
1	NON TER
1	FT DOMAIN
1	FT DOMAIN
1	FT DOMAIN
1	FT DOMAIN
1	FT DOMAIN
1	FT DISULFID
1	FT DISULFID
1	FT DISULFID
1	FT DISULFID
1	FT DISULFID
1	FT DISULFID
1	FT CARBOHYD
1	FT DISULFID
1	FT MOD RES
1	SEQUENCE
1	Query Match
1	Best Local Similarity
1	Matches
1	Db
1	Qy
1	Db
1	Qy
1	Db

[illegible]

RESULT	12
ID	GCM MOUSE STANDARD; PRT; 393 AA.
AC	P01869;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE	IG GAMMA-I CHAIN C REGION, MEMBRANE-BOUND FORM.
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA..
RN	[1]
RX	SEQUENCE FROM N.A.
RX	MEDLINE; 80045036.
RA	HONJO T., OBATA M., YAMAOKI-KATAOKA Y., KATAOKA T., KAWAKAMI T.,
RA	TAKAHASHI N., MANO Y.;
RL	CELL 18:559-568(1979).
RN	[2]
RP	SEQUENCE OF 323-393 FROM N.A.
RX	MEDLINE; 82197626.
RA	TYLER B.M., COMMAN A.F., GERONDAKIS S.D., ADAMS J.M., BERNARD O.;
RL	PROC. NATL. ACAD. SCI. U.S.A. 79:2008-2012(1982).
RN	[3]
RP	SEQUENCE OF 323-366 FROM N.A.
RX	MEDLINE; 82115295.
RA	ROGERS J., CHOI E., SOUZA L., CARTER C., WORD C.J., KUEHL M.,
RA	EISENBERG D., WALL R.;
RL	CELL 26:19-27(1981).
RN	[4]
RP	SEQUENCE OF 1-44 FROM N.A.
RX	MEDLINE; 82222190.
RA	YAMAOKI-KATAOKA Y., NAKAI S., MIYATA T., HONJO T.;
RL	PROC. NATL. ACAD. SCI. U.S.A. 79:2623-2627(1982).
CC	-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC	SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC	GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC	BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC	IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC	SEGMENT OF MU CHAINS.
DR	EMBL; V00793; V00793.
DR	PIR; B02159; GINSM.
DR	HSSP; P01857; IBAF.
DR	PROSITE; PS00290; IG_MHC.
KW	IMMUNOGLOBULIN C REGION; ALTERNATIVE SPLICING; TRANSMEMBRANE;
KW	GLYCOPROTEIN.
FT	NON TER 1 1
FT	DOWAN 1 97 CH1.
FT	DOWAN 98 110 HINGE.
FT	DOWAN 111 217 CH2.
FT	DOWAN 218 324 CH3.
FT	DISULFID 27 82
FT	DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN) .

RESULT	13
ID	GCAA MOUSE STANDARD; PRT; 330 AA.
AC	P01863;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE	IG GAMMA-2A CHAIN C REGION, A ALLELE.
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC	EUTHERIA; RODENTIA.
RN	{1}
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 81076554.
RA	SIKORAV J.-L., AUFRAY C., ROUGEON F.;
RL	NUCLEIC ACIDS RES. 8:3143-3155(1980).
RN	{2}
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 81198976.
RA	YAWAKAWI-KATAOKA Y., MIYATA T.;
RL	NUCLEIC ACIDS RES. 9:1365-1381(1981).
RN	{3}
RP	.SEQUENCE FROM N.A.
RX	MEDLINE; 81223894.
RA	OLLO R., AUFRAY C., MORCHAMPS C., ROUGEON F.;
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:2442-2446(1981).

RESULT	14	STANDARD;	PRT; 333 AA.
ID	GCB RAT		
AC	P20761;		
DT	01-FEB-1991 (REL. 17, CREATED)		
DT	01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)		
DT	01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)		
DE	IG GAMMA-2B CHAIN C REGION.		
OS	RATTUS NORVEGICUS (RAT).		
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		

RESULT	15
ID	GCAM MOUSE STANDARD; PRT; 399 AA.
AC	P01865;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT	01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE	IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC	EUTHERIA; RODENTIA.
RN	[1]
RC	SEQUENCE FROM N.A.
RP	
RX	MEDLINE; 8222190.
RA	YAMAWAKI-KATOKA Y., NAKAI S., MIYATA T., HONJO T.;

```

RL PROC. NATL. ACAD. SCI. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
CC -!- THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH
CC THE CORRESPONDING REGION OF THE SECRETED FORM OF THE A ALLELE.
DR EMBL; J00471; J00471.
DR PIR; A02154; G2MSAM.
DR HSP; P01857; IFC1.
DR PROSITE; PS00290; IG MHC.
KW IMMUNOGLOBULIN C REGION; ALTERNATIVE SPLICING; TRANSMEMBRANE.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT TRANSMEM 346 363
FT DOMAIN 364 399 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 399 AA; 44020 MW; 926112 CN;

Query Match 44.4%; Score 1542; DB 3; Length 399;
Best Local Similarity 63.4%; Pred.No. 0.00e+00;
Matches 210; Conservative 52; Mismatches 65; Indels 4; Gaps 3;

Db 1 aktapsvylapvcddtgssvtlclvkvgyfpepvtltwnsgslssgyhtfpavlqsd 60
Qy 147 ASTKGSVPFLAPSSKSTSGGTALGCLVKDYFPEPTVWNSGALTSVGHTEPAVLQSS 206

Db 61 -lytlassvvtstwpqstcnavhasstkvdkieprg-ptlkcpcckcpapnll 118
Qy 207 GLYSLSVWVTPSSSLGTQTYIGNVHKFSNKKVKAEPKSCDKTHTCPPC--PAPELL 264

Db 119 ggsqvfiipkikdvimlsapivtcvvdvseddqdvglwfvnnvevhtaqtqhred 178
Qy 265 GGSVFLFPKPKDITLMTSRTPEVTCVVDVSHEDPEVKENMYDGVFNNAKTPREEQ 324

Db 179 ynstlrsvsalpighdmsgskfckvnmkdlpapiertiskpkgsavrapqvylpppe 238
Qy 325 YNSTYRWVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 384

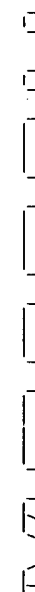
Db 239 eeatkkqvtltcmvtdfmpediyvwtngktelnkntepvldsgsfmysklrvekk 298
Qy 385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPTPPVLDSDGSFELYSLYDKS 444

Db 299 nwvemsyscavhheglhnhhttkfsertpg 329
Qy 445 RWQGNVFCSVWHEALHNHYTKSLSPG 475

```

Search completed: Tue Dec 17 15:21:10 1996  
Job time : 33 secs.

(TUL)



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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

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Run on: Tue Dec 17 15:18:11 1996; MasPar time 10.33 Seconds
438.806 Million cell updates/sec
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Tabular output not generated.

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Title: >US-08-487-550-4
Description: (1-476) from US08487550 pep
Perfect Score: 3472
Sequence: 1 MKHLMFFLLLVAPRWLSQ.....

```

Scoring table: PAM 150  
Gap 11

Searched: 81589 seqs, 9523651 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

a-geneseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16

Statistics: Mean 35.425; Variance 166.647; scale 0.213

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query			ID	Description	Pred. No.
			Match	Length	DB			
1	3004	86.5	475	16	R3553	Monoclonal antibody D	4.04e-258	
2	2787	80.3	470	4	R22757	Reshaped CAMPATH-1 an	2.168e-238	
3	2785	80.2	481	5	R24442	Sequence of antibody	4.08e-238	
4	2774	79.9	467	4	R22759	Reshaped CD4 antibody	4.12e-237	
5	2772	79.8	467	4	R22758	Reshaped CD4 antibody	2.67e-237	
6	2744	79.0	453	6	R33311	Humanised Ma11 Vse1	2.26e-234	
7	2717	78.3	475	3	R20057	Heavy chain of 3D6 an	6.58e-232	
8	2714	78.2	476	6	R31023	Antibody D heavy chai	1.24e-231	
9	2689	77.4	449	7	R43339	Completely humanised	2.36e-229	
10	2689	77.4	461	8	R42162	Anti-HIV-1 recombinan	2.36e-229	
11	2653	76.4	459	8	R42066	Human anti-HBs heavy	4.56e-226	
12	2642	76.1	477	8	R47453	chIT94.12 H3 heavy ch	4.60e-225	

1313	2613	75.3	466	5	R24812	Sequence encoded by t	2.04e-222
1415	2599	74.9	466	7	R40750	Sequence encoded by t	3.86e-221
1515	2594	74.7	454	6	R30774	H524H-160 murine anti	1.10e-220
1616	2577	74.2	470	3	P60351	Chimeric human-mouse	3.92e-219
1717	2577	74.2	470	2	P70547	Sequence of novel mou	3.92e-219
1818	2526	72.8	467	15	R08617	Anti-human IL-4 human	1.76e-214
1919	2506	72.2	468	5	R28808	pre-5A8 humanised hea	1.17e-212
2020	2459	70.8	371	1	P91918	Sequence of the linke	2.26e-208
2121	2453	70.7	371	1	P93558	Linkered human IgG1 (	7.97e-208
2222	2353	67.8	534	5	R26531	Sequence of CD4-IgG1	1.04e-198
2323	2341	67.4	351	8	R43685	Human kappa immunogl	1.29e-197
2424	2340	67.4	729	4	P93008	Sequence encoded by a	1.58e-197
2525	2316	66.7	528	10	R52952	Human anti-IgE MAb he	2.44e-195
2626	2276	65.6	330	1	R81026	C region of H chain (	1.07e-191
2727	2267	65.1	337	8	P41045	Peptide for linking c	3.07e-190
2828	2251	64.8	337	3	R20129	SEQ ID No. 4 of the c	2.03e-189
2929	2226	64.1	330	3	R26130	SEQ ID No. 5 of the c	3.83e-187
3030	2147	61.8	530	5	R26783	CD4-IgG2 chimeric hea	5.95e-180
3131	2138	61.6	530	9	R46679	CD4-IgG2 chimeric hea	3.92e-179
3232	1996	57.5	452	6	R30775	ph52-8.0 humanised mu	3.22e-166
3333	1923	55.4	464	13	R76088	MAb 55.1 heavy chain.	1.39e-159
3434	1913	55.1	469	8	R40384	Monoclonal antibody M	1.12e-158
3535	1903	54.8	445	12	R66758	Anti-tobacco mosaiv v	9.10e-158
3636	1888	54.4	465	13	R76085	MAb 55.1 heavy chain.	2.10e-156
3737	1884	54.3	468	3	R13061	Monoclonal antibody O	4.84e-156
3838	1874	54.3	599	16	R40937	3B1 single chain anti	4.84e-156
3939	1874	54.0	461	8	R44494	Sequence of the immun	3.92e-155
4040	1868	53.8	448	8	R43673	Mouse anti-bovine gro	1.37e-154
4141	1858	53.5	466	4	P40032	Gamma anti-carcinoemb	1.11e-153
4242	1850	53.3	477	8	R74750	T84.12 Heavy chain.	5.92e-153
4343	1848	53.2	448	2	R06476	Heavy chain of anti-b	8.99e-153
4444	1777	51.2	464	3	R13049	CD4-specific CD8-graf	2.50e-146
4545	1719	49.5	447	1	P93037	Chimeric antibody hea	4.56e-141

## ALIGNMENTS

RESULT	1	
ID	R03553 standard; Protein; 475 AA.	
AC	R03553;	
DT	20-AUG-1996 (first entry)	
DE	Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.	
KW	Polymertase chain reaction; primer; amplify; PCR; light chain; MAB;	
KW	65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.	
OS	Synthetic.	
Key	Location/Qualifiers	
FT	Peptide	1..19
FT	/note= "Signal peptide"	
FT	Protein	20..475
FT	/note= "Mature heavy chain"	
PN	J08038178-A.	
PD	13-FEB-1996.	
PF	20-FEB-1995; 030742.	
PR	18-FEB-1994; JP-021628.	
PA	(NIN ) NISSHINO IND INC.	
PA	(TANA/) TANAKA H.	
DR	WPI; 96-154852/16.	
DR	N-PSDB; T18059.	
PT	Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -	
PT	produced by primer amplification, used in the diagnosis of hCMV	
PT	infection	
PS	Claim 4; Page 16-18; 22pp; Japanese.	
CC	The sequences given in R03553-54 represent the heavy and light chains	
CC	respectively of a monoclonal antibody against a 65 kD antigen of human	



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CC cytomegalovirus (hcmv). The DNA's encoding these sequences were  
 CC amplified using the sequences given in T18040-58. The monoclonal  
 CC antibody may be used in the diagnosis of hcmv.  
 SQ Sequence 475 AA;

Query Match 86.5%; Score 3004; DB 16; Length 475;  
 Best Local Similarity 89.7%; Pred. No. 4,04e-258;  
 Matches 428; Conservative 15; Mismatches 31; Indels 3; Gaps 3;  
 Db 1 mklhfflllvaaprwlsqqlqesgqlvpsqtlslctvsgdsrsesysgcirg 60  
 QY 1 MKHLHFFLLVLAAPRWLSQQLQEGGLQPSLTSRTCWVSGGSIS-GYYTWTIRQ 59  
 Db 61 ppkglewigtlyyagst-yynpslksrvtsjvsdaannqfklksvtaadtavycart 119  
 QY 60 TPGRGLEIGHYGCATTNPNPSIKSRVTISKQFFLNLSVTDADTAVYTCARG 119  
 Db 120 s-pqydydlitgsfpywgqgtltvssastkpsvflapsakstsggtaalgclvdyf 178  
 QY 120 PREDTTTCYCGWVDWGPGLVTVSSASTKGPVPEPLAPSSKSTSGCTAALGCLVKDYF 179  
 Db 179 pepvtvsnegaltsgvhtfpavlgsglylsavvtvpssslgtgttyicnvhkpsntk 238  
 QY 180 PEPVTVSNAGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNKHPSNTH 239  
 Db 239 vdkkvepkacdkthtccpcapeallggpsvflppkpkdtlmlertpevtcvvvdvshed 298  
 QY 240 VDKKAEPRKCDKTHTCPCPAPELLGGPSVFLFPKPKDMLISRTPEVTCVVDVSHED 299  
 Db 299 pevknwydgvevhnaktkpreeqnystyrsvltvlhqdwlngkeyckvsnkalpa 358  
 QY 300 PEVKNWYDGVVEVHNKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPA 359  
 Db 359 piektiskakgprepyvtlpperdeltknqvalclvkgfypsdiavewesngqpenn 418  
 QY 360 PIEKTISKAKGPREPYVTLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419  
 Db 419 ykttppvladsgsflyskltvdkserwqgnvfscsvmhhealnhhnytqkslslepgk 475  
 QY 420 YKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHHEALNHHTQKSLSLSPCK 476

RESULT 2

ID R22757 standard; Protein; 470 AA.  
 AC R22757;  
 DT 20-OCT-1992 (first entry)  
 DE Reshaped CAMPATH-1 antibody heavy chain.  
 KW Antigen; CD8; complementarity determining region; graft rejection;  
 KW autoimmune diseases; rheumatoid arthritis; allergy.  
 OS Rattus rattus.  
 FT Key Location/Qualifiers  
 FT Region 50..54  
 FT /note= "Complementarity determining region 1"  
 FT Region 69..87  
 FT /note= "Complementarity determining region 2"  
 FT Region 101..110  
 FT /note= "Complementarity determining region 3"  
 FT Peptide 1..19  
 FT /note= "signal peptide"  
 FT Peptide 20..470  
 FT /note= "mature peptide"  
 PN W09205274-A.  
 PD 02-APR-1992.  
 PF 16-SEP-1991; G01578.

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PR 17-SEP-1990; GB-020282.  
 PA (GORM/) GORMAN S D.  
 PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.  
 DR WPI; 92-132139/16.  
 DR N-PSDB; Q23570.  
 PT Humanisation of antibodies binding to human CD4 antigen - by  
 PT mutation of framework-encoding regions of DNA encoding variable  
 PT domain of rat or mouse antibody chain  
 PS Disclosure; Fig 5; 74pp; English.  
 CC The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.  
 CC Reshaped CD4 antibody can be used to induce tolerance against an  
 CC antigen. It can also be used to alleviate autoimmune diseases such  
 CC as rheumatoid arthritis, and to prevent graft rejection. Tolerance  
 CC to a graft, e.g. an organ graft or a bone marrow transplantation can  
 CC also be useful to alleviate allergies. Tolerance to allergens could  
 CC also be achieved. See also R22754-R22763.  
 SQ Sequence 470 AA;

Query Match 80.3%; Score 2787; DB 4; Length 470;  
 Best Local Similarity 86.3%; Pred. No. 2.68e-238;  
 Matches 408; Conservative 25; Mismatches 30; Indels 10; Gaps 6;  
 Db 6 ililfvataatgvhsqvlqesgqlvrpsqtlslctvsgfttdfym-nwrcppqrgl 64  
 QY 6 FFLLVLAAPRWLSQQLQEGGLQPSLTSRTCWVSGGSISGYTWTIRQTPGRGL 65  
 Db 65 ewigfirdkagkyteynpsvkgvrtmlvtdsknfslrlesvtaadtavycareghta 124  
 QY 66 EWIGHI-Y-GNGATTNPNPSIKSRVTISKQFFLNLSVTDADTAVYTCARGPRPD 123  
 Db 125 -ap---f-----dywggsllvtvseastkpsvflapsakstsggtaalgclvdyf 177  
 QY 124 CTTTCYCGWVDWGPGLVTVSSASTKGPVPEPLAPSSKSTSGCTAALGCLVKDYFPEV 183  
 Db 178 tvsnsgaltsgvhtfpavlgsglylsavvtvpssslgtgttyicnvhkpsntkvd 237  
 QY 184 TVSNNSGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNKHPSNTH 243  
 Db 238 vepkscdkthtccpcapeallggpsvflppkpkdtlmlertpevtcvvvdvshedpevk 297  
 QY 244 AEPKCDKTHTCPCPAPELLGGPSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVK 303  
 Db 298 fnwydgvevhnaktkpreeqnystyrsvltvlhqdwlngkeyckvsnkalpapiek 357  
 QY 304 FNNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAIEK 363  
 Db 358 tiskakgprepyvtlpperdeltknqvalclvkgfypsdiavewesngqpenn 417  
 QY 364 TISKAKGPREPYVTLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 423  
 Db 418 ppvladsgsflyskltvdkserwqgnvfscsvmhhealnhhnytqkslslepgk 470  
 QY 424 PPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHHEALNHHTQKSLSLSPCK 476

RESULT 3

ID R24442 standard; Protein; 481 AA.  
 AC R24442;  
 DT 02-JAN-1992 (first entry)  
 DE Sequence of antibody molecule IgG1.  
 KW Antibody; immunoglobulin G1.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Misc difference 308

FT	/label= N	
FT	/note= "Substn. to create glycan addition site"	
FT	Misc difference 310	
FT	/label= S	
FT	/note= "see above"	
FT	Misc difference 321	
FT	/label= N	
FT	/note= "see above"	
FT	Misc difference 329	
FT	/label= N	
FT	/note= "see above"	
FT	Misc difference 331	
FT	/label= S	
FT	/note= "see above"	
FT	Misc difference 356	
FT	/label= N	
FT	/note= "see above"	
FT	Misc difference 369	
FT	/label= N	
FT	/note= "see above"	
PN	W09209293-A.	
PD	11-JUN-1992.	
PD	18-NOV-1991; U08605.	
PR	23-NOV-1990; US-618314.	
PA	(GCHO ) GEN HOSPITAL CORP.	
PI	Seed B, Walz G;	
DR	WPI; 92-216789/26.	
DR	N-PSDB; Q25443.	
PT	Inhibition of cell adhesion mediated through ELAM-1 mol. binding	
PT	- used in treating chronic inflammation, rheumatoid arthritis,	
PT	psoriasis, etc.	
PS	Disclosure; Fig 1; 46pp; English.	
CC	The IgG1, in its nascent form, bears no sialyl-Lex side chains. The	
CC	inventors designed a molecule including several such sites for	
CC	attachment of sialyl-Lex side chains (see R2442, FT). The	
CC	additional N-linked glycosylation sites are introduced at locations	
CC	which impair complement fixing and Fc receptor binding ability. They	
CC	are preferably located in the CH2 region of the Ig molecule.	
CC	Antibodies bearing multiple sialyl-Lex determinants are useful for	
CC	disrupting undesirable interactions between cells or proteins.	
CC	Disrupting this interaction has therapeutic applications, for	
CC	example, in minimising inflammation following tissue injury.	
SQ	Sequence 481 AA;	

Query Match	80.2%;	Score 2785;	DB 5;	Length 481;
Best Local Similarity	82.8%;	Pred. No. 4, 08e-238;		
Matches	396;	Conservative	30; Mismatches 49; Indels 3; Gaps 3;	
Db	5 mdwtwrlffvvaatvgsgqvqlvgsgeavkpgskpsvkscaggtfesyai-swrrq	63		
Qy	:           :         :         :			
	1 MKHLFFELLV-AAPRWLSQVLQQWGEGLLOPSETLSNTCSWGSGISCYYYWTWRQ	59		
Db	64 apggclwmvggipifigtanyaqkfgrvtitadestetaymelaesledtavyycard	123		
Qy	:         :         :         :			
	60 TPGRGLEIGHIYCGNAGATTNNPSLKSRYVTLSKOTSKNOFFNLNSVTDADTAVYYCARG	119		
Db	124 ngaycsgegsyegwfddwgqqtllrvtsaatkpsevfplapaskateggtaalgcilvdy	183		
Qy	:   :     :     :     :     :     :     :     :			
	120 PRPDCTT--ICYGGMVDVMVGDPDLTVTSASATKGSPVFPLAPSSTSGSTAALGCLLVKDY	178:		
Db	184 fpeprtvenmgaltsgvhtfpavlgesglvlservtpvsaslgctqtcicnvnhkpent	243		
Qy	179 FPEPTVSWNSGALTSGVHTFPVALVASGLYSLSGVTPVSSSLGTQTYICNVNHKPSNT	238		

Db	244	kvdvkvepscdkthccppapeilggpsvflfppkpktlmisrtpvtcvvdvshe	303
Qy	239	KVDKRAEPKSCDKTHCCPCAPPELLGGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE	298
Db	304	dpevkfnwydgvevhnahtkpteeqgnatyrvsvltvlhgdwlngkyckckvkanalp	363
Qy	299	DPEVKFNWYDGVGVEVHNAHTKPREEQYNSTRVSVSLTVLHQDWLNGKEYCKCKVNKALP	358
Db	364	apiektiskakgagrepqvyltpps-deltknqvalctci kvfpesdiavewesngqpen	423
Qy	359	APIEKTISKAKGAPREPQVYLTPPSDRLTKNQVSLTCLIVKGFPYSIDIAVEVESNGPEN	418
Db	424	nykttppvldadgesfflyskitlvdkerwqaqnvfscvmbeahlnhytkqlslspgk	481
Qy	419	NYKTTTPVLDSGSFFLYSKITLVDKSRWGQNVFSCVMBEAHNHYTKQSLSLPQG	476

RESULT	4
ID	R22759 standard; Protein; 467 AA.
AC	R22759;
DT	20-OCT-1992 (first entry)
DE	Reshaped CD4 antibody heavy chain CD04VHNEW-Ser30.
KW	Antigen; CDR; complementarity determining region; graft rejection; autoimmune diseases; rheumatoid arthritis; allergy.
OS	Rattus rattus.
Key	Location/Qualifiers
FT	Peptide 1..19
FT	/note= "signal peptide"
FT	Peptide 20..467
FT	/note= "mature peptide"
FT	Region 50..54
FT	/note= "Complementarity determining region 1"
FT	Region 69..85
FT	/note= "Complementarity determining region 2"
FT	Region 118..126
FT	/note= "Complementarity determining region 3"
PN	W09205274-A.
PD	12-APR-1992.
PF	16-SEP-1991; G01578.
PR	17-SEP-1990; GB-020282.
PI	(GORM/) GORMAN S D.
PI	Clark M R, Cobbold S P, Gorman S D, Waldmann H.
DR	WPI; 92-132139/16.
DR	N-PSDS; Q23581.
PT	Humanisation of antibodies-binding to human CD4 antigen - by
PT	mutation of framework-encoding regions of DNA encoding variable
PT	domain of rat or mouse antibody chain
PS	Disclosure; Fig 7; 74pp; English.
CC	The sequence is that of the reshaped CD4 antibody heavy chain
CC	CD04VHNEW-Ser30. Reshaped CD4 antibody can be used to induce tolerance
CC	against an antigen. It can also be used to alleviate autoimmune diseases
CC	such as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC	to a graft, e.g. an organ graft or a bone marrow transplantation can
CC	also be useful to alleviate allergies. Tolerance to allergens could
CC	also be achieved. See also R22753-R22763.
SQ	Sequence 467 AA;

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Query Match      79.9%;      Score 2774;  DB 4;  Length 467;
Best Local Similarity 86.8%;
Matches 408;  Conservative 23;  Mismatches 31;  Indels 9;  Gaps 6;

Db 6 liilvatgvisqvqesgplvrpqtllaitctvgaftfnygm-awrvqpgrgl 64
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Ov 6 FELLIVAPRWLSOKVLOONGEGLLPSETLSRTCVSGGSIYYVWTWTRPGRGL 65

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CC Residues were selected from MaE11 and inserted or substituted into  
CC a human Fab antibody background (Vh region Kabat subgroup III and V1  
CC region kappa subgroup I). A first version, humaellv1 or version 1 is  
CC given below. The affinity of version 1 was assayed and found to be  
CC ca. 100 times lower than that of the donor antibody MaE11.  
CC Therefore, further modifications in the sequence of version 1  
CC were made.  
SQ Sequence 453 AA;

Query Match 79.0%; Score 2744; DB 6; Length 453;  
Best Local Similarity 85.7%; Pred. No. 2,26e-234;  
Matches 395; Conservative 25; Mismatches 29; Indels 12; Gaps 6;

Db 1 evqlvesggglvcpaggelrlacavgsyaltsgyswnlrcapqgkglewvasity-dqst- 58  
QY 20 QVKLAQWGEGLQPSSETLSRTCVVSGSISGYYYWTWIRQTPCRGLEWIGHI-YGNGATT 78

Db 59 nyadvskgrftierdskntfylvmslraedtaavyycargh-----yfgwhfawvg 112  
QY 79 NYNPSLKSRVTISKDTSKNOFFLINSVTDADTAVYYCARGPRPDCTTTCYCGW-VDVWG 137

Db 113 qgtlvtsesaetkqkpsvflpasesktsqgtaalgclvkdvfpepytvswnsegaltsg 172  
QY 138 PGDLTVSSASTKG--PSVFP LAPSSKTSGGTAALGCLVKDYPPEPVTVMNSGALTSG 195

Db 173 vhtfpavlqesqlyslsvvtvpssalgtqyicnvnhkpkntkvdckvepkcdkthtc 232  
QY 196 VHTFPAVLQSSGYLSLSSVTVPSSSLGTQTYICNVNHKPSNTKDKAEPKSCDKTHTC 255

Db 233 pccpapellqgpavflfppkpkdtlmiartpevtcvvvdshedpevkfmyvvdgvevhn 292  
QY 256 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHEDPEVKFNMYVDGVEVHN 315

Db 293 attkpreeqynstyrvsvltvlhqdwlngkeyckvkenkalpapietkiskakgqprep 352  
QY 316 AKTKPREQYNSTYRWISVLTVLHQDLWLNKGYCKVSNKALPAP IETKTISKAKGQPREP 375

Db 353 qvvtlppreemtknqvslctclvkgyfypediaveesngqpennykttppvldsdgdfll 412  
QY 376 QVYTLPPSRDELTKNOVSLTCLVKGYFSPDIAVEMESNGQPENNYKTTTPFVLDSDGSFEL 435

Db 413 yskltvdkerwqgnvfscsvmhealhnhytqkslslepqk 453  
QY 436 YSKLTVDKSRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 476

RESULT 7  
ID R20057 standard; Protein; 475 AA.  
AC R20057;  
DT 25-MAR-1992 (first entry)  
DE Heavy chain of 3D6 anti-HIV antibody.  
KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;  
KW complementarity determining region.  
OS Homo sapiens.

FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= signal  
FT Region 20..49  
FT /label= Framework 1  
FT Region 50..54  
FT /label= CDR-1  
FT Region 55..68  
FT /label= Framework 2  
FT Region 69..85

FT /label= CDR\_2  
FT Region 86..117  
FT /label= Framework 3  
FT Region 118..134  
FT /label= CDR\_3  
FT Region 135..145  
FT /label= Framework 4  
FT Region 146..475  
FT /label= Constant\_region  
PN W09118983-A.

PD 12-DEC-1991. 100067.  
PF 28-MAY-1991; 100067.  
PR 29-MAY-1990; AT-001178.  
PA (JUNG/) JUNGHAUER A.  
PI Felgenhauer M, Himmel G, Kohl J, Steindl F;  
DR WPI; 92-007468/01.  
DR N-PSDB; Q20066.

PT Recombinant protein which binds to complex viral antigen and  
PT HIV-1 - contains variable region of antibody derived from 3D6  
PT cell line, used for detecting HIV-1 antigen  
PS Claim 2; Page 24; 52pp; German.  
CC The variable region of the heavy chain is used in a recombinant  
CC protein with the variable region from the kappa light chain of 3D6,  
CC the two V regions being joined by a linker. The recombinant protein  
CC binds to HIV gp160.  
CC See also Q20067 and Q20068.  
SQ Sequence 475 AA;

Query Match 78.3%; Score 2717; DB 3; Length 475;  
Best Local Similarity 81.6%; Pred. No. 6,58e-232;  
Matches 386; Conservative 33; Mismatches 49; Indels 5; Gaps 4;

Db 7 wifllailkg--vqceqlvesggglvqpggrslrlscaasgftfndyam-hwvraqpgk 63  
QY 5 WFFLLVAAPRWVLQVLAQWGEGLQPSSETLSRTCVVSGSISGYYYWTWIRQTPGRG 64

Db 64 lewsgiedssigvadvskgrftisrdhaknslylvmslraedmaalyvcvkgrdy 122  
QY 65 LEWIGHYGNATTNYPNLSKSRVTISKDTSKNOFFLINSVTDADTAVYYCARGPRPD 124

Db 123 dsqgyftvafdiwggtmtvseastkqpsvflpasesktsqgtaalgclvkdyppep 182  
QY 125 TTICY-GGVVDVWGPCDILVTVSSASTKGPSVFP LAPSSKTSGGTAALGCLVKDYPPEV 183

Db 183 tvswnsqaltsgvhtfpavlqesqlyslsvvtvpssalgtqyicnvnhkpkntkvdck 242  
QY 184 TVSWNSGALTSQVHTFPAPVLAQSSGLYLSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK 243

Db 243 vepkcdkthtcppcpapellggpsvflfppkpkdtlmiartpevtcvvvdshedpevk 302  
QY 244 AEPKCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHEDPEVK 303

Db 303 fnwydvdvshnaktpreeqynstyrvsvltvlhqdwlngkeyckvkenkalpapietk 362  
QY 304 FNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDLWLNKGYCKVSNKALPAP IETK 363

Db 363 tiakakgqprepqvvtlppsrdeitknqvslctclvkgyfypediaveesngqpennyktt 422  
QY 364 TISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGYFSPDIAVEMESNGQPENNYKTT 423

Db 423 ppvldsdgdfllyskltvdkerwqgnvfscsvmhealhnhytqkslslepqk 475  
QY 424 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 476

Query Match 78.2%; Score 2714; DB 6; Length 476;  
Best Local Similarity 81.8%; Pred. No. 1.24e-231;  
Matches 390; Conservative 28; Mismatches 57; Indels 2; Gaps 2;

Db	1	mdwtwrlfvvaatqvgsmqvwgvaegvkkpssvtsvcksaeggtfenvyal-swvrga	59
Qy	1	MKHLAFELLVAAPRWLSQVKLQWGEGLQPSLETSRLTCVSSGGSISGYIYWTWIRQT	60
Db	60	pggglwmggiipfctpyeqnfgqrvtitadktsahmetelrseadtavvycatdr	119
Qy	61	PGGLELGHLYNGATYNNPISLKSRTVTSKOTSKOFFNLINSLNSVTDADTAVYVCARG	120
Db	120	yrqanfdrarvqfdpwgqgtlvtvsaastkqpsvfplapasketsaggtaalqclvkdyf	179
Qy	121	-RDCCTTCYGGWVDVWVGPGDGLTVSSASTKGPSVFLAPSSKTSGGTAAIGCLVKDYF	179
Db	180	pepvtvsnsgaltsgvhtfpavqlsqeglylselsavrtvpsaslgctqtiycnvhhkpank	239
Qy	180	PEPVTVSNSGALTSQVHTFPAVLQSSGLYLSLSVTVPSSSLGTQTYICNVNHPKSNTK	239
Db	240	vdtkvpekscdkhtcpcpapelggpsevfllppkpkdtlmierptevtcvvdvshed	299
Qy	240	VDKKAEPKSCDKHTCPCPAPELLGSPSVFLPPPKDTLMISRTPEVTCVVDVSHED	299
Db	300	pevkfnvywgdvvevhnaktprceegynatyrvasvltvlhqdmlngkeyckkvenkalpa	359
Qy	300	PEVKFNWYVDCVEVHNAKTPREEQYNSTRVVSVLTVLHQDMLNGKEYCKKVSNNKALPA	359
Db	360	plektiskagpqppepyvtlppserdeltnqnvalctlvkgyfpsdlavewesngpenn	419
Qy	360	PIEKTISKAGQPREPYVTLPPSRDELTKNQVSLTCLVKGFPSDIAVHESNGQPENN	419
Db	420	yktptpvidsgafflysklvtvdkerwqgggnvfscvmmhealnhvhtqkalelspgk	476
Qy	420	YKTPPVLDSDGFFLYSKLTVDKSRWQGGNVFSCVMHEALNHVHTQKLSLSPGK	476
RESULT	9		
ID	R43339	standard; Protein; 449 AA.	
AC	R43339;		
DT	27-NOV-1993	(first entry)	
DE	Completely humanised C4G1 Ig heavy chain.		
KW	Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIa/IIb;		
KM	monoclonal antibody; platelet agglutination; humanised antibody.		
OS	Synthetic.		
PN	W09313133-A.		
PD	08-JUL-1993.		
PF	15-DEC-1992; J01630.		
PR	20-DEC-1991; US-812111.		
PR	09-JUN-1992; US-895952.		
PR	11-SEP-1992; US-944159.		
PA	(PROT-) PROTEIN DESIGN LABS INC.		
PA	(YAMA) YAMANOUCHI PHARM CO LTD.		
PI	Co MS, Tso JY;		
PI	WPI; 93-227275/28.		
DR	Compen. contg. immunoglobulin specific for the GP-IIb and -IIIA		
PT	protein - for treating disorders related to vascular thrombosis		
PS	Claim 26; Fig 5C; 54pp; Japanese.		
CC	This is the sequence of the humanised C4G1 immunoglobulin heavy		
CC	chain fragment. See R43338 for the light chain sequence. The		
CC	antibody is specific for the platelet membrane glycoprotein		
CC	GPIIa/IIb and inhibits platelet agglutination. The Ig is thus		
CC	useful in the treatment of thrombosis.		
SQ	Sequence 449 AA;		
Query Match	77.4%;	Score 2689;	DB 7; Length 449;
Best Local Similarity	84.7%;	Pred No. 2.36e-229;	



DR N-PSDB; Q45944.  
PT Human anti-hepatitis B surface antigen antibody gene - can be  
PT used to produce L and H chains of the antibody in large quantity  
PS Disclosure; Fig 6-8; 46pp; Japanese.  
CC Polynucleotides encoding the L and H chains of human anti-HBs  
CC Ab are given in Q49943-Q49944. The Ab can be easily produced in  
CC large quantities for therapeutic use.  
SQ Sequence 459 AA;

[illegible]

RESULT	12	
ID	R47453	standard; Protein; 477 AA.
AC	R47453;	
DT	24-JUN-1994	(first entry)
DE	chi184.12 H3	heavy chain.
KW	Chimeric; carcinoembryonic antigen; CCA;	murine; mouse; constant;
KW	region; transform; myeloma cell; light chain;	tumour.
OS	Synthetic.	
PN	W09325237-A.	
PD	23-DEC-1993.	
PF	15-JUN-1993; U05709.	
PR	15-JUN-1992; US-904074.	
PA	(CITY ) CITY OF HOPE.	
PA	(YANG/) YANG Y.	
PI	Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;	
PI	Yang YH;	
DR	WPI; 94-007204/01.	
DR	N-PSDB: Q54655.	

PT New chimaeric T84.12 antibody active against carcinoembryonic  
PT antigen - has murine variable and human constant regions, also  
PT DNA encoding it and transformed myeloma cells  
PS Claim 1; Page 22-23; 27pp; English.  
CC The sequences (054651-52) show the light and heavy chain cDNAs  
CC of murine T84.12. The T84.12 antibody is directed against the  
CC tumour marker carcinoembryonic antigen, and is useful for  
CC tumour imaging and immunotherapy.  
CC The amino acid sequence given in the specification has been  
CC incorrectly identified as a nucleic acid sequence, therefore  
CC unacceptable characters have been represented as an 'N'.  
CC The amino acid sequence given below has been derived from the  
CC cDNA, by the indexer.  
SO Sequence 477 AA:

Query Match	76.1%	Score 2642;	DB 8;	Length 477;
Best Local Similarity	81.4%;	Pred. No. 4,60e-225;		
Matches	384;	Conservative 32;	Mismatches 47;	Indels 9;
Gaps	7;			
Db	14	felifivlvkvgcveklveseggvfkvgpggalklscasagftfesyam--ewrqtqpekr	72	
Qy	6	FFLL--LVAAPRWLVSVKQLQWGGELQIQLSELTSTCVSGSGISGYYIWTWIRQTPGRG	64	
Db	73	lewvasiasdg--itfydvskgrftvrdnarniilylqmsslrsestdamyyca--i-dy	128	
Qy	65	LEWIGHIYGNCAATTNTPSLKSRVTISKOTSKNOFFLNLNSVTDADTAIVYVCARGPRPDC	124	
Db	129	ygg--ggf--gywggglatvsaactkpsvfplapsaketsaggtaaqlcivkdyfppevt	185	
Qy	125	TTICYGWVDWVGFDGLVTVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVT	184	
Db	186	vsmnsгалтсgvhtfcpavlqesglsyleavttvpssslgtqtcyicnvnhkpsntkvdkkv	245	
Qy	185	VSMNSGALTSGVHTFPFPAVLQSSGLYSLSSVWTVPSSSLGTQTVIQNVNHKPSNTKVDKKA	244	
Db	246	epkscdkthtccpcpapelllgpavflfpkpdkdtlmisrtpevtcvvvdashedpevkf	305	
Qy	245	EPKSCDKHTCCPCPAPELLLGPSVFLFPKPKOTLMISRTPEVTCVVVDVSHEDPEVKF	304	
Db	306	nwyvdgvevhnaktkpreeqnystyrvvavltvlhqdlngkeyckvsnkalpapiekt	365	
Qy	305	NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT	364	
Db	366	iskakqgprepyvtlpperdeltknqvaltcclvkgfyppedlaveweengqpennykttp	425	
Qy	365	ISKAKQGPQEPQVYTLPPSRDELTKNQVSLTCLVKGYPSDIAVEWESNGQPENNYKTTTP	424	
Db	426	pvlidedgafflysklvtvdksrwqgnvfacsvmhealhmhytqkelslggk	477	
Qy	425	PVLDSGCSFFLYSKLVTVDKSRWQGNVFCSSVMHEALRHNYTKOISLSLSPCK	476	

RESULT	13	
ID	R24812 standard; Protein; 466 AA.	
AC	R24812;	
DT	28-DEC-1992 (first entry)	
DE	Sequence encoded by the chimeric H chain cDNA contained in pTB1373	
KW	Chimeric monoclonal antibody; anti-fibrin antibody; primer;	
KW	antithrombotic agent; myocardial infarction therapy.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	Peptide	13..19
FT	/label= Leader	
FT	Region	20..134



\* FT /Label= VH 135..232  
FT /Label= CH1 233..247  
FT /Label= hinge 248..357  
FT /Label= CH2 358..464  
FT /Label= CH3  
FT Misc difference 465  
FT /note= "translated stop codon"  
PN EP-491351-A.  
PD 24-JUN-1992.  
PF 17-DEC-1991; 121591.  
PR 18-DEC-1990; JP-413829.  
PR 11-NOV-1991; JP-294464.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
PI Iwasa S, Taka H, Watanabe T, Tada H;  
DR WPI; 92-209528/26.  
DR N-PSDB; Q25692.  
PT Chimeric monoclonal antibodies - contain anti-human fibrin  
PT antibody light and heavy chain variable and constant for treating  
PT thrombotic conditions e.g. myocardial infarction  
PS Example; Figure 11; 87pp; English.  
CC Plasmid pTB1373 contains the whole length of a mouse-human  
CC chimeric anti-human fibrin heavy chain cDNA open reading  
CC frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin  
CC chimeric Ab-producing transformant FIB1-H01/X63 as a template  
CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as  
CC a primer for first strand cDNA synthesis and the 5'CZH and 3'EH  
CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding  
CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain  
CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader  
CC peptide cDNA were amplified using the primers 3'EH, 3'CZH and 3'CIH  
CC respectively as a primer for first strand cDNA synthesis and the  
CC primer combination of 5'CIH and 3'CZH, of 5'LIH and 3'CIH and of  
CC 5'SH and 3'LIH respectively as primers for PCR. The amplified gene  
CC products were isolated and used to produce plasmids. After  
CC confirmation of the cDNA sequence of each plasmid, the cDNA  
CC encoding LH, VH, CH1 and CH2CH3 were joined together to give  
CC plasmid pTB1373 contg. the whole length chimeric H chain  
CC (LH, VH, CH1, CH2CH3), also abbreviated as Igh-FIB,  
SQ Sequence 466 AA;  
Query Match 75.3%; Score 2613; DB 5; Length 466;  
Best Local Similarity 81.5%; Pred. No. 2,046-222;  
Matches 383; Conservative 33; Mismatches 42; Indels 12; Gaps 6;  
DB 7 lvflvlllkqvdcvqlveagggllvkgpgslklscasagftfanydm-swrrqtperlle 65  
QY 7 FLLVAPRWVLSQVKLQOQWEGCLLPQSETLSRTCWVSGSISGYIYTWIRQPGGLE 66  
DB 66 wvasi-svgtctyypdemkgrfiardnarnilylqlslrsedtamyc--gnfad-am 121  
QY 67 WIGHYNGATTNYPNSLKSRVTISKDTSKNQFFLNLSVTDADTAVYCARCPDCTT 126  
DB 122 d-y-----wgggtlvtvsaastkpgsvflapssktsaggttaalgcivkdyfp 174  
QY 127 ICYGGWDMVGPDLVTVSSASTKGPVFLAPSSKTSAGTAAALGCIVKDYFPVTVS 186  
DB 175 wnsagtsagvhtfpavlgagsglylsavvtvpssslgtctyictvnhkpsntkvrp 234  
QY 187 WNSGALISGVHTFPVAVLJSSGLSLSVSVVVPSSSLGTCTYICNVNHRPSTKVDKAE 246

DB 235 kcdtkhtccpccpapeilggpsvflfppkpkdtlmistpvtcvvvdshedpevkf 294  
QY 247 KSCDKTHTCCPCPEAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 306  
DB 295 yvdgvevhnaktprceegynstyrsvvsvltvlhqdwlngkeyckvsnkalpapiaktia 354  
QY 307 YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 366  
DB 355 kagqprepqvtylppsreemtknqslclvkgfypadiavewangpennykttppv 414  
QY 367 KAGQPREPQVYTLPPSDELTKNQSVLTCVKGFPYPSDIAVENSNGQPNYKTTTPV 426  
DB 415 lddgsfflysklvtvdkerwqgnvfscsvmhealhnhytqkslalepgk 464  
QY 427 LDDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476  
RESULT 14  
ID R40750 standard; Protein; 466 AA.  
AC R40750;  
DT 01-OCT-1993 (first entry)  
DE Sequence encoded by the heavy chain expression  
DE vector pAG4235.  
KW Chimeric monoclonal antibody; expression plasmid.  
OS Synthetic.  
PN W09311252-A.  
PD 10-JUN-1993.  
PF 24-NOV-1992; U10207.  
PR 26-NOV-1991; US-798696.  
PA (REGC ) UNIV CALIFORNIA.  
PI Hastings A, Morrison SL, Wims L;  
DR WPI; 93-197069/24.  
DR N-PSDB; Q43497.  
PT Expression plasmids and derivs. - used to produce protein  
PT molecules esp. chimaeric monoclonal antibodies  
PS Disclosure; Fig 3; 54pp; English.  
CC The expression plasmid pAG4235 (ATCC No. 75038) is claimed. It is  
CC used to express chimeric monoclonal antibodies. It contains genes  
CC with leader sequences and is functional. The variable region and  
CC constant regions exons were sequenced, however the other sequences  
CC are from published references and have not been verified for this  
CC particular plasmid. Regions for which there is no sequence  
CC information are indicated by N's with the length determined by sizes  
CC of fragments observed on agarose gels.  
SQ Sequence 466 AA;  
Query Match 74.9%; Score 2599; DB 7; Length 466;  
Best Local Similarity 79.6%; Pred. No. 3,866-221;  
Matches 379; Conservative 33; Mismatches 54; Indels 10; Gaps 7;  
DB 1 mdwlwnllfmaaaqsigqlqvsggpeklkpggetvkiskcaagtyftnmg-nwvka 59  
QY 1 MKHLFFLLVAPRWVLSQVKLQOQWEGCLLPQSETLSRTCWVSGSISGYIYTWIR 60  
DB 60 qgklkwmgwintgptyteefkgrfafaletantayllimlnknedatyfcarg- 118  
QY 61 PRGLEWIGHYNGATTNYPNSLKSRVTISKDTSKNQFFLNLSVTDADTAVYCARP 120  
DB 119 --e-gha-wg-fa-ywgggtlvtvsaastkpgsvflapssktsaggttaalgcivkdyfp 172  
QY 121 RPDCITTCYGGWDMVGPDLVTVSSASTKGPVFLAPSSKTSAGTAAALGCIVKDYFP 180  
DB 173 eptvsvwnsagtsagvhtfpavlgagsglylsavvtvpssslgtctyicnvnhkpsntk 232

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> Qy 181 EPVTVSNHGALTSVHTFRAVLQSSGLYSLSSVTVFSSSLGTQYICNVNHPKSNTKV 240
Db 233 dkkvepkscdkthtccppopapellggpavflfppkpkdtlmiartpevtcvvvdvshedp 292
Qy 241 DKKAEPKSCDKTHTCPPCPAPELLGPPSVFLFPPKPKDTLMISRPETVCVVVDVSHEDP 300
Db 293 evkfnyvdvqvevhnaaktppreeqynatyravltvlhgdwlngkeyckvkenkalpap 352
Qy 301 EYKFNWYDGVVHNAKTPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
Db 353 iektisk--qgpreqyvtlpsrdelctknqvaltcclvkgyfypsdiaweengqpenny 410
Qy 361 IEKTIKRAKQCPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAWESNGQPENNY 420
Db 411 ktppvldsgdofflyskltvdkrrwqgnvfscsvmhhealhhhytqkslslspgk 466
Qy 421 KTTTPVLDSDGFFLYSKLTVDKSRWQGNVFSCSVMHHEALHHHYTQKSLSLSPGK 476
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RESULT 15

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ID R30774 standard; protein; 454 AA.
AC R30774;
DT 12-MAY-1993 (first entry)
DE H52H4-160 murine anti-CD18 antibody heavy chain.
KW Humanization; rapid; monoclonal antibody.
OS Mus musculus.
PN W09222653-A.
PD 23-DEC-1992.
PF 15-JUN-1992; 005126.
PR 14-JUN-1991; US-715272.
PA (GETH ) GENENTECH INC.
PI Carter PJ, Presta LG.
DR WPI; 93-018139/02.
PT Humanisation of antibodies - by molecular modelling of the variable
PT domains and alteration by gene conversion mutagenesis
PS Disclosure; Fig 6A; 126pp; English.
CC The sequence is that of the heavy chain of murine anti-CD18
CC antibody H52H4-160.
SQ Sequence 454 AA;
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Query Match 74.7%; Score 2594; DB 6; Length 454;
Best Local Similarity 80.8%; Pred. No. 1.10e-220;
Matches 370; Conservative 36; Mismatches 47; Indels 5; Gaps 4;

Db 1 qvqlqsggpeylvkqasvkiacktytftym-hwmkqshgkslewigfnpknngss 59
Qy 20 QVKLQWQGEGLQPSFSLRFTCVWSGSGISGYIYTWIRQTPGRGLEWIGHIYNGCATN 79
Db 60 hmqrfmdkatlavdketstaymelzrltsedgiyyicarwrglnygfdivy--f-dwaga 116
Qy 80 YNPSLKSRVTISKDTSKNQFFINLNSVTDADTAVYYCARGRPDCT-TICYGQWVDVWGP 138
Db 117 gttvtvasaatkpavfplapaskatagtaalgclvkdypfpvptvwnmagaltsgvht 176
Qy 139 GDLVTVSSASTKGP SVFP LAPSKSTSGTAAALGCLVRDYFPEPVTVSNWSCALTSGVHT 198
Db 177 fpavllqsgglylsavtvpsseigtqyicnvnhkpentkvdkkvepkscdkthtccpc 236
Qy 199 FPAVLQSSGLYSLSSVTVFSSSLGTQYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 258
Db 237 papellggpavflfppkpkdtlmiartpevtcvvvdvshedpevkfnwyvdgvevhna 296
Qy 259 PAPELLGPPSVFLFPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYDGVCEVHNAKT 318
```

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```

Db 297 kpreeqynsttrvavltvlhgdwlngkeyckvkenkalpaplektiekakgprepqvy 356
Qy 319 KPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTIKRAKQCPREPQY 378
Db 357 tlppreemtknqvaltcclvkgyfypsdiaweengqpennyktppvldsgdofflyek 416
Qy 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAWESNGQPENNYKTTPPVLDSDGFFLYSK 438
Db 417 ltvdksrwqgnvfscsvmhhealhhhytqkslslspgk 454
Qy 439 LTVDKSRWQGNVFSCSVMHHEALHHHYTQKSLSLSPGK 476
```

Search completed: Tue Dec 17 15:19:00 1996  
Job time : 49 secs.

(TM)

MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated.

Sequence: 1 MSLPAQLGLLLCPGSSG.....EVTHOGLSSPVTKSFNRGEC 239

Searched: 82130 seqs, 25426960 residues

Database: pir47

Statistics: Mean 44.330: Variance 149.331: scale 0.297

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	1132	67.9	215	11	A3746			Ig kappa chain V-III	7.14e-120
2	1119	67.2	219	12	S52028			Ig kappa light chain	2.94e-118
3	1099	66.0	219	12	S16112			Ig kappa chain V reg	8.96e-116
4	1090	65.4	219	12	S38865			Ig kappa chain - mou	1.17e-114
5	1082	64.9	217	12	S42772			Ig kappa chain - mou	1.15e-113
6	1058	63.5	240	12	S62084			Ig kappa chain precu	1.09e-110
7	1057	63.4	225	12	J00029			Ig kappa chain precu	1.45e-110
8	1000	60.0	220	12	A31790			Ig kappa chain V reg	1.66e-103
9	964	57.9	225	12	S37484			Ig kappa chain - mou	4.65e-99
10	930	55.8	230	12	S33161			Ig kappa chain - she	7.27e-95
11	930	55.8	234	12	S01320			Ig kappa chain precu	7.27e-95
12	911	54.7	197	12	S29593			Ig kappa chain (NM65	1.59e-92

```

RESULT      1
ENTRY       A23746      #type complete
TITLE       Iq kappa chain V-III (KAU cold agglutinin) - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change
              23-Mar-1993
ACCESSIONS  A23746
REFERENCE   A23746
            Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
            J. Biol. Chem. (1991) 266:2836-2842
            The primary structure of the Fab fragment of protein KAU, a
            monoclonal immunoglobulin M cold agglutinin

```

**cross-references** MUID:91131575

```

#accession A23746
##status preliminary
##molecule_type protein
##residues 1-215 ##label LEO
SUMMARY length 215 #molecular-weight 23050 #checksum 116

```

Query Match	67.9%;	Score 1132;	DB 11;	Length 215;
Best Local Similarity	79.4%;	Pred. No. 7.14e-120;		
Matches 173:	Conservative	22: Mismatches 19;	Indels 4;	Gaps 2;

```

Db 1 eivltaspatlslsperatlsaggasvs-n---ylawyaqkpgqaprllydassra 56
   1:||||| :::||| 1::| :||| :| :|||||||:||||| 1:|
Ov 21 EVAMTSPISPIITPGEPASTSCRSOSIKUNGDTTISWQOKPGPPRLLYKYVSND 80

```

21 EVVMTQSPISIPITPGEPAISCBSOSIKHSNGDTFISWYOOKPGOPPRILLYKVSNRD 80



```

Qy. 81  SGVPDRFSGSGAGTDTFTIKISAVFEADVGVYFCGGCGGTRTPPTFGGGTKVEIKRTVAAPSV 140

Db 121  siippeseqtelsgaavcflnnfypkldinvkwkldgserqmgvlnsvtdqdsdktetym 180
      ||||| ||| || |||||:|||||::: |||: : ||:|||||||:
Qy 141  FIIPPSEQLSGTASVGLNLFNFPREAKVQMKYDNALQSNQSESVTQDSKDSYSL 200

Db 181  sstltitkdeverhnsytcethktstetpivksfnrec 219
      |||||: ||||: |||| || |||: |||||
Qy 201  SSTLTLSKADYEHKHVYACEVTHQLSPVTKSFNRGEC 239

RESULT 5
ENTRY 542772 #type complete
TITLE Ig kappa chain - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
      06-Jan-1995
ACCESSIONS 542772
REFERENCE 542771
      Schellekens, G.A.
      submitted to the EMBL Data Library, November 1993
#accession 542772
      preliminary
      #status
      #molecule_type mRNA
      #residues 1-217 #label SCH
      #cross-references EMBL:X75536
      #length 217 #molecular-weight 23895 #checksum 8895
SUMMARY

```

	Query Match	64.9%	Score 1082;	DB 12;	Length 217;
	Best Local Similarity	68.7%;	Pred. No. 1.1lse-1l3;		
	Matches	149;	Conservative 35;	Mismatches 33;	Indels 0; Caps 0;
Dbb	1 vmtcpslpplvsldqdasicsrsgslvntngtylhwyldkpggspkvliykvstrfag	60	:   :           :   :           :		
Qy	23 VMTQSPSLPITPGEPASICSRSSQLKHSNGDTFLSMYQQKFQPAPRLLIKYVNRDSG	82	:   :           :           :		
Dbb	61 vpdrfaggagtcdftfkierveaedlywfcgaqstyvpffggatkleikradaaptvai	120	:   :           :           :		
Qy	83 VPDRFSGSAGGTDLTKIISAVEAEDEVFCQGGRTRTPFTGGTKEIKRTVAAPSVEFI	142	:   :           :           :		
Dbb	121 fpssseqiltsagaavvcflnnfykdlnvwkidserangvlinswtddskdstysmas	180	:   :           :           :		
Qy	143 FPPSDQLKSQTASVCCLNNFPREAKVQMVDNALQSNGSQESVTQEODSKDSTYSLS	202	:   :           :           :		
Dbb	181 tlltldeyerhnmytceathktstpsivksfnrgcc	217	:   :           :           :		
Qy	203 TLTLSRADYEKKHYACCEVTHOGLSSSPVKTSFNRGEC	239	:   :           :           :		

RESULT	6
ENTRY	S06084
TITLE	Ig kappa chain precursor - rat
ORGANISM	#formal_name Rattus norvegicus #common_name Norway rat
DATE	28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Mar-1993
ACCESSIONS	S06084
REFERENCE	S06084
#authors	Crowe, J.S.; Smith, M.A.; Cooper, H.J.
#journal	Nucleic Acids Res. (1989) 17:7992
#title	Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.
#cross-references	WUID:90016888
#accession	S06084
#molecule	type mRNA

[illegible]

```

RESULT 7
ENTRY
TITLE      Ig light chain precursor (RP93) - mouse (fragment)
ORGANISM   Mus musculus {common_name house mouse}
DATE       31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
           27-Jan-1995
ACCESSIONS JLO029 #type fragment
REFERENCE   JLO029
AUTHORS     Chien, N.C.; Pollock, R.R.; Desaynard, C.; Scharff, M.D.
JOURNAL     J. Exp. Med. (1988) 167:954-973
#note       Point mutations cause the somatic diversification of IgM and
           IgG2a antiphosphorylcholine antibodies.
#cross-references MUID:88171315
#accession JLO029
#molecule_type mRNA
#residues   1-225 ##label CHI
#experimental_source strain BALB/c, cell line RP93 hybridoma cell
#note       the authors translated the codon CCG for residue 106 as
           Pro, ACC for residue 132 as Ser, AAA for residue 153
           as His, and AAC for residue 210 as Lys
#note       the nucleotide sequence shown is inconsistent with

```

COMMENT	FEATURE
The protein is an anti-phosphorylcholine antibody.	#product Ig light chain #label ILC\
	#domain V region #label VAR\
	#domain hypervariable region 1 #label HR1\
	#domain hypervariable region 2 #label HR2\
	#domain J region #label JIR\
	#domain C region #label COR
SUMMARY	#length 225 #checksum 419
Query Match	63.4% Score 1057; DB 12; Length 225;

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```
Best Local Similarity 64.7%; Pred. No. 1.45e-110;
Matches 143; Conservative 40; Mismatches 38; Indels 0; Gaps 0;

Db 5 esdvlnatqlpvlvqldqasiescsnplvshatgntylewlylqpgqepnlliykian 64
:|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 19 SGVWMTQSPLSLPIITPGEPASISCRSSQSLKHSNGDTFLSWYQKRPQGPRLLIYKVS 78
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 65 rfsgvdrfsgsgsgtdfclseisrveaedlgyvycfsgshvrtwfgggtkleikrdaap 124
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 79 RDSGVDRFSGSGAGDTFLIKISAVEADGVYFCQGQTRTPPTFGGTVKVEIKRTVAAP 138
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 125 twaifpptsseqtksgasvvcflnnfypkdnvkwidserqngvlnawtdqdkdsty 184
:|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 139 SVTFIPPSDEQLKSGTASVVCCLNLFYPREAKVQWKVDNALQSGNSQESVTEQDSKDY 198
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 185 smestliltkdeyerhnsytceathntstspivksfnrnc 225
:|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 199 SLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 239
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:

RESULT 8 A31790 #type complete
ENTRY Ig kappa chain V region (17/9) - mouse
TITLE #formal_name Mus musculus #common_name house mouse
ORGANISM 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
DATE 23-Mar-1993

ACCESSIONS A31790
REFERENCE A92686
#authors Kenten, J.H.; Wilson, I.A.
#journal J. Biol. Chem. (1988) 263:17100-17105
#title Preliminary crystallographic data, primary sequence, and
binding data for an anti-peptide fab and its complex with a
synthetic peptide from influenza virus hemagglutinin.
#cross-references M0ID:89034213
#accession A31790
#molecule_type mRNA
#residues 1-220 ##label SCH
SUMMARY #length 220 #molecular-weight 24236 #checksum 1239

Query Match 60.0%; Score 1000; DB 12; Length 220;
Best Local Similarity 60.9%; Pred. No. 1.66e-103;
Matches 134; Conservative 42; Mismatches 43; Indels 1; Gaps 1;

Db 1 divmtgspssltvtagekvmtascsqslfnsgkqknyltwyqqkpgqpkkvliywastr 60
:|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 21 EVWMTQSPLSLPIITPGEPASISCRSSQSL-KHSNGDTFLSWYQKRPQGPRLLIYKVS 79
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 61 esgvdrftgsgtdftcltlesvqaedlavycqndysnpltfgggtkleikrdaapt 120
:|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 80 DSGVDRFSGSGAGDTFLIKISAVEADGVYFCQGQTRTPPTFGGTVKVEIKRTVAAP 139
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 121 vsfippsseqtksgasvvcflnnfypkdnvkwidserqngvlnawtdqdkdstys 180
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 140 VFIFPPSDEQLKSGTASVVCCLNLFYPREAKVQWKVDNALQSGNSQESVTEQDSKDY 199
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 181 msatliltkdeyerhnsytceathntstspivksfnrnc 220
:|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 200 LSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 239
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:

RESULT 9 S37484 #type fragment
ENTRY Ig kappa chain - mouse (fragment)
TITLE
```

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```
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
06-Jan-1995

ACCESSIONS S37484
REFERENCE S37483
#authors Duncanson, F.F.D.
#submission submitted to the EMBL Data Library, February 1993
#accession S37484
#status preliminary
#molecule_type mRNA
#residues 1-225 ##label DUC
#cross-references EMBL:X70424
SUMMARY #length 225 #checksum 9545

Query Match 57.9%; Score 964; DB 12; Length 225;
Best Local Similarity 59.6%; Pred. No. 4.65e-99;
Matches 137; Conservative 48; Mismatches 39; Indels 6; Gaps 4;

Db 2 fillcvsgahgsivmtqtqtkfillsagdrvtitckasqv--sn-d--vawyqqkpgqp 56
:|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 10 LLLLCVPGSSGEVMTQSPLSLPIITPGEPASISCRSSQSLKHSNGDTFLSWYQKRPQGP 69
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 57 kllyvaasrytgvpdrftgsgtdftftistvqaedlavycqgdy-asytfgggtkl 115
:||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 70 RLLIYKVSNRDSGVDRFSGSGAGDTFLIKISAVEADGVYFCQGQTRTPPTFGGQTKV 129
||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 116 eikrdaaptvsifppsseqltsgasvvcflnnfypkdnvkwidserqngvlnawt 175
||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 130 EIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNLFYPREAKVQWKVDNALQSGNSQESVT 189
||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 176 dqdkdstysmsltlktdeyerhnsytceathntstspivksfnrnc 225
:|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 190 EQDSKDYTSLSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 239
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:

RESULT 10 S33161 #type complete
ENTRY Ig kappa chain - sheep
TITLE #formal_name Ovis orientalis aries, Ovis ammon aries
ORGANISM #common_name domestic sheep
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
06-Jan-1995

ACCESSIONS S33161
REFERENCE S33161
#authors Foley, R.C.; Beh, K.J.
#submission submitted to the EMBL Data Library, July 1990
#description Isolation and characterization of sheep kappa light chain
cDNA.
#accession S33161
#status preliminary
#molecule_type mRNA
#residues 1-230 ##label FOL
#cross-references EMBL:X54110
SUMMARY #length 230 #molecular-weight 25362 #checksum 8015

Query Match 55.8%; Score 930; DB 12; Length 230;
Best Local Similarity 57.4%; Pred. No. 7.27e-95;
Matches 135; Conservative 49; Mismatches 45; Indels 6; Gaps 3;

Db 1 qlqlllllwlpgardicvtqspsslsaaltervsitcrteqsv--sn---ynlwqqk 55
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Qy 6 QLQLGLLLL-CYPGSSGEVMTQSPLSLPIITPGEPASISCRSSQSLKHSNGDTFLSWYQK 64
|||||:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 56 pqqpkllyvatrlhtdvpafsgsgtdytltienleandtatyyclqvsestplafg 115
```





```

Db 120 sifppsaqltsggaavcflnnfyphkdvlnkwidserqngvlnewtdqdkdstysm 179
      ||||| || |||||:|||||: |||||: |||||: |||||: |||||: |||||:
Qy 141 FIEPPSDEQIKSGTASVWCLLNNEYPRYKQVQWKNALQSGNSQESVTEQDSKDSVSL 200
      ||||| |||||:|||||: |||||: |||||: |||||: |||||: |||||:
Db 180 esltlttdyverhnaytceathktstapi 209
      |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Qy 201 SSTLTLSKADYERHKVYACEVTHQGLSSPV 230
      |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:

```

```

RESULT 14
ENTRY
TITLE      Iq kappa chain precursor (15c5) - mouse
ORGANISM   Mus musculus #common_name house mouse
DATE        25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
            10-Nov-1995
ACCESSIONS S14237 #type complete
REFERENCE   S14237
            Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Li-jnen,
            R.H.; Collen, D.
            Eur. J. Biochem. (1990) 192:767-775
            Construction and characterization of a recombinant murine
            monoclonal antibody directed against human fibrin
            fragment-D dimer.
            #cross-references M01D:91006173.
            #accession S14237
            #molecule_type mRNA
            #residues 1-234 ##label VAN
            #cross-references EMBL:X56394
            #length 234 #molecular-weight 26087 #checksum 6000
SUMMARY

```

Query Match	53.0%	Score 898	DB 12	Length 234
Best Local Similarity	55.8%	Pred. No. 6.36e-91		
Matches	134	Conservative 47	Mismatches 52	Indels 7
				Gaps 4
Db	1	mrtpaqlgilllwfpgikcdikmtqpsmsyaslgervtvtckasqdl----	n--syaw 55	
	1	:	:	:
	1	MSLPAQLLGLLLVCPGSSGEVMTQPSLRLTPPEFASISCRSSQSLKHSNGDFTLSW	60	
Qy	56	iqqpkpseptliyr--gnrlvagvpsrfsgsgqgdheltisleyedvqvvyvclrydef	114	
	1	:	:	:
	61	YQQKQGPPLRLIYKVSNR--DSGVPDFRFGSGAGDTFTLXISAVEADVGVFYCGQTRT	119	
Db	115	ptffgsqtkleikradaptvsi fppssqel tgasvvcflnmfykdlnvkwkldgse	174	
	1	:	:	:
	120	PPTFGGCTKVEIKRTVAAPSVFIFPPSDEQILSGTASVCLLANNFYPREAKVQWKVDNAL	179	
Qy	175	rqngvlnswtdqdkedctysmestlltkdkdeyhrhnsytcceathktstetpivkfeirnc	234	
	1	:	:	:
	180	QSGNDSQSEVTQDSKDSYLSLSTLTKADYEKKHVYACEVTHQGLSPGYSFNRGEC	239	

RESULT	15
ENTRY	PT0219 #type fragment
TITLE	Ig kappa chain V-C region (PIC18) - pig (fragment)
ORGANISM	#formal_name Sus scrofa domestica #common_name domestic pig
DATE	31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 03-Mar-1995
ACCESSIONS	PT0219
REFERENCE	PT0219
#authors	Lammers, B.M.; Beaman, K.D.; Kim, Y.B.
#journal	Mol. Immunol. (1991) 28:877-880
#title	Sequence analysis of porcine immunoglobulin light chain cDNAs.

```

#cross-references WUID:91342694
#accession PT0219
#molecule_type mRNA
#residues 1-178 ##label LAM
#experimental_source spleen, strain Minnesota Miniature
#note the authors translated the codon CTC for residue 141 as
Ser

```

```

FEATURE
1-70      #domain V region (fragment) #label VRG\
12-18     #region complementarity-determining 1\
19-51     #region framework 1\
52-60     #region complementarity-determining 2\
61-70     #region framework 2\
71-178    #domain C region #label CRG\
96-156    #disulfide_bonds #status predicted\
176       #disulfide_bonds_in_chain #status predicted
          #length 178 #checksum 4948

SUMMARY
Query Match              50.6%; Score 843; DB 12; Length 178;
Best Local Similarity   66.5%; Pred. No. 3,64e-84;
Matches 117; Conservative 25; Mismatches 34; Indels 0; Gaps

Db      1 kpgsqplllveasdragsvdprfsgsgqdfcltkineaseadagvyvychafkpftrf 60
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy      64 KPGQPRLLLIKVNSRDSQVDRESGSAGTDFTLKLSAVEAEDVGVFCCGGGTPTPTF 123
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||

Db      61 gggqtklelkradakpsvfifppskteqlatptsvvvclinnffpreieavkwkdgvvasg 120
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy      124 GGGTKVEIKRTVAAPSVFIFFPDEQLKSCTASVVCLLNFFPREAKVKMKYDNALQSGN 183
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||

Db      121 hpdsvreqdskdstylsalstlsipteqylshnllyscvethktlasplvtcfmrnc 176
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy      184 SOESVTQDSDSTYSLSLTSLTSKADYEKHKVAAEVEFHOGISSPVTFKSNRGEC 239

```

Search completed: Tue Dec 17 15:24:37 1996  
Job time : 28 secs.



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FT DISULFID 43 113 BY SIMILARITY.
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 102175 CN;

Query Match 45.4%; Score 756; DB 5; Length 133;
Best Local Similarity 80.5%; Pred. No. 1.62e-147;
Matches 107; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

Db      1 mr.lpaqlgllmlwpyssgdvmtqglelptvlqqpasiscrsqslvydsdntylnw 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      1 MSPAQLGLGLLLCVPGSSGEVVMTQTSLPTTPGPASISCRSQQSLKUSNGDFTLSW 60

Db      61 fqrpqgsprtllykvnrdsgvdnrfagsgsdctftlkierveaedvgvyvmcqhws 120
        ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Qy      61 YQKPQGPPRLLYKYNSRDSCVPDRFGSGAGTDTLKISAVEAEADVGVYFCQGGTRP 120

Db      121 wtfgggtkeivr 133
        ||| |||||||
Qy      121 PTEGGGTKEIKR 133

RESULT 2
ID KAC HUMAN STANDARD; PRT; 106 AA.
AC P01834;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN C REGION.
GN IGRK.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE; 71064023.
RA GOTTLIEB P.D., CUNNINGHAM B.A., RUTISHAUSER U., EDELMAN G.M.;
RA BIOCHEMISTRY 9:3155-3161(1970).
RN [2]
RX EU. DISULFIDE BONDS.
RX MEDLINE; 72188439.
RA SUPFER L., BARNIKOL H.U., WATANABE S., HILSCHMANN N.;
RA GALL W.E., EDELMAN G.M.;
RA BIOCHEMISTRY 9:3188-3196(1970).
RN [3]
RX SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE; 72188439.
RA SUPFER L., BARNIKOL H.U., WATANABE S., HILSCHMANN N.;
RA HOPPE-SEYLER S Z. PHYSIOL. CHEM. 353:189-208(1972).
RN [4]
RX SEQUENCE FROM N.A.
RX MEDLINE; 81042304.
RA HIETER P.A., MAX E.E., SEIDMAN J.G., MATZEL J.V. JR., LEDER P.;
RA CELL 22:197-207(1980).
RN [5]
RX SEQUENCE (BENCE-JONES PROTEIN ROY).
RA HILSCHMANN N., BARNIKOL H.U., HESS M., LANGER B., PONSTINGL H.,
RA STEINMETZ-KAYNE M., SUPFER L., WATANABE S.;
RA (IN) GAMMA GLOBULINS: STRUCTURE AND FUNCTION, FRANEK F., SHUGAR D.,
RA ED.S., PP. 57-74, ACADEMIC PRESS, NEW YORK, (1969).
RN [6]
RX SEQUENCE (BENCE-JONES PROTEIN CUM).
RA MEDLINE; 68242259.
RA HILSCHMANN N.;
RA HOPPE-SEYLER S Z. PHYSIOL. CHEM. 348:1718-1722(1967).
RN [7]
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RP	SEQUENCE (BENCE-JONES PROTEIN AG).
RX	MEDLINE; 69234734.
RA	TITANI K., SHINODA T., PUTNAM F.W.;
RL	J. BIOL. CHEM. 244:3550-3560(1969).
[8]	
RN	SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX	MEDLINE; 70201507.
RA	KOHLER H., SHIMIZU A., PAUL C., PUTNAM F.W.;
RL	SCIENCE 169:56-59(1970).
CC	-!- THE EU SEQUENCE HAS THE INV (3) ALLOTYPEIC MARKER, 45-ALA & 83-VAL.
CC	-!- THE EU SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER, 45-ALA AND
CC	83-LEU.
DR	PIR; A02116; K3HU.
DR	HSP; P01842; IDFB.
DR	MM; 147200; 11TH EDITION.
DR	PROSITE; PS00290; IG MHC.
KW	IMMUNOGLOBULIN C REGION.
FT	NON TER 1 1
FT	DISULFID 26 86
FT	SULFID 106 106
FT	VARIANT 83 83
FT	CONFLICT 14 14
FT	CONFLICT 57 57
SQ	SEQUENCE 106 AA; 11609 MM; 64333 CN;
	Query Match 43.3%; Score 721; DB 4; Length 106;
	Best Local Similarity 100.0%; Pred.No. 4.13e-139;
	Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps
Db	1 tvaapsvfippsdeqlsgtsavcclnnfyprkakvqvkdnlqsgnsqsavtqds 60
Qy	134 TVAAPSVFI PPDSQLSGTASVWCCLNNFYPRKAVQKVNDALQSGNSQSVEQDS 193
Db	61 kdetsylstltiskadyekhkvyacethglspsvtksfnrgec 106
Qy	194 KDTSYLSSTLTISKADYEKHKYACEVTHGLSSPVTKSFNRGEC 239
RESULT 3	
ID	KVZG_MOUSE STANDARD; PRT; 113 AA.
AC	P01631;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN V-II REGION (26-10).
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE.
RC	STRAIN=A/J;
RC	MEDLINE; 83178921.
RA	NOVOTNY J., MARGOLIES M.N.;
RL	BIOCHEMISTRY 22:1153-1158(1983).
CC	-!- THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT
CC	BINDS DIGOXIN.
DR	PIR; A01914; KWMS26.
DR	HSP; P01607; IIGI.
KW	IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY; HYBRIDOMA.
FT	DOMAIN 1 23 FRAMEWORK 1.
FT	DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 40 54 FRAMEWORK 2.
FT	DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 62 93 FRAMEWORK 3.



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7

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[1]
RN SEQUENCE.
RA DREYER W.J., GRAY W.R., HOOD L.E.;
RL COLD SPRING HARB. SYMP. QUANT. BIOL. 32:353-367(1967).
CC -I- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- THIS IS A BENGE-JONES PROTEIN.
DR PIR; A01887; K2HUM1.
DR HSSP; P01679; ICBV.
KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; 77514 CN;

Query Match 37.3%; Score 621; DB 5; Length 112;
Best Local Similarity 69.9%; Pred. No. 3.05e-115;
Matches 79; Conservative 23; Mismatches 10; Indels 1; Gaps 1;

Db 1 divltqslslptpgpasiscrsqnlzabdb-yldwylzkgzspzllilylgenra 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 EVMWTSPLSLPTPGPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSND 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 60 sqvnmfsgsgtbfklklsrvzabvgyvcmqalqptlfgggtvneikr 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 SGVPDRFSGSGAGDTFLKLSAVEADVGVYFCGGGTRTPPTFGGKVEIKR 133

RESULT 7
ID KV4B HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-IV REGION (JI).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86041853.
RA KLOBECK H.G., BORNKAMM G.W., COMBRIATO G., MOCIKAT R., POHLENZ H.D.,
RA ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 13:6515-6529(1985).
DR PIR; A01904; K4HUTJ.
DR HSSP; P01607; IMCP.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-III REGION (JI).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 61 75 FRAMEWORK 2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 83 114 FRAMEWORK 3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 123 132 FRAMEWORK 4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 101063 CN;
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Query Match 36.1%; Score 602; DB 5; Length 133;
Best Local Similarity 64.2%; Pred. No. 9.75e-111;
Matches 86; Conservative 24; Mismatches 22; Indels 2; Gaps 2;

Db 1 mvlqtqvfiisllwiegaygdvmtqpsdlavslgeratlnckesqsvlysnknyla 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 MSLPAAQLGLLLLVCGSSGEVMTQSPSLPTPGPASISCRSSQSLKHSNGDTFLS 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 wyqdkgqgpkliiywastrfsgsgtdftitisslqaedvavvyccq-ydt 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 60 WYQKPGQPPRLIIYKVSNDGVPDRFSGSGAGDTFLKLSAVEADVGVYFCGGGTRT 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 120 jptfgggtkveikr 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 120 PPTFGGKVEIKR 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
ID KV2B HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-II REGION (FR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 76253627.
RA RIESEN W.F., JATON J.-C.;
RL BIOCHEMISTRY 15:3829-3833(1976).
CC -I- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUER.
DR HSSP; P01607; IJEL.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 77707 CN;

Query Match 35.7%; Score 594; DB 5; Length 113;
Best Local Similarity 71.7%; Pred. No. 7.64e-109;
Matches 81; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Db 1 dvmtqslfipvtlgepasicrseslvyrbqbtlylbwylqkpgspelliylasyrd 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 EVMWTSPLSLPTPGPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSND 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 sqvpdfsgsgtdftlklitrvqaedvgyvcmqatzapytfgggtklzkr 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 SGVPDRFSGSGAGDTFLKLSAVEADVGVYFCGGGTRTPPTFGGKVEIKR 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
ID KV3F_MOUSE STANDARD; PRT; 132 AA.
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AC	P01658;
AD	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 321).
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; NETAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RC	(1)
RN	SEQUENCE OF 1-37.
RP	MEDLINE; 78235887.
RX	BURSTEIN Y., SCHECHTER I.;
RL	BIOCHEMISTRY 17:2392-2400(1978).
[2]	
RN	SEQUENCE OF 21-132.
RP	MEDLINE; 73140224.
RA	MCKEAN D.J., POTTER M., HOOD L.E.;
RL	BIOCHEMISTRY 12:749-759(1973).
-I-	THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN WAS ALREADY DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.
CC	PIR; A01933; KYMS32.
DR	HSP; P01679; IGGB.
KW	IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; SIGNAL.
FT	SIGNAL 1 20
FT	CHAIN 21 132
FT	DOMAIN 21 43
FT	DOMAIN 44 58
FT	DOMAIN 59 73
FT	DOMAIN 74 80
FT	DOMAIN 81 112
FT	DOMAIN 113 121
FT	DOMAIN 122 131
FT	DISULFID 43 112
FT	NON TER 132 132
SQ	SEQUENCE 132 AA; 14523 MW; 114870 CN;
Query Match	35.7%; Score 594; DB 5; Length 132;
Best Local Similarity	54.9%; Pred.No. 7.64e-109;
Matches	73; Conservative 37; Mismatches 22; Indels 1; Gaps
Db	1 metcdllwlllvpgstgdivltpspaslaavlqgratiscraskev-ntygnsmzw 119
Qy	1 MSPLAQLLGLLILLCVPGSGGEVNTOSPISLPITPCEPASISCSSQSLSKHNGDTELFW 60
Db	60 yzskqgzppklllyraasnlszqiparfsgsgsrctbflltbpvzabdvatyfczszbzbp 119
Qy	61 YOQPCQPPLLIIYKVNSRDGVPDRFSGAGTGDFTFIKISAFAEDVGWVFCCGGTRTP 120
Db	120 wtfsggtkleikr 132
Qy	121 PTFGSGTKEIKR 133

RESULT	10
ID	KVZA HUMAN
AC	P01614;
IC	STANDARD;
PRT;	115 AA.
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN V-II REGION (CUM).
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC	EUTHERIA; PRIMATES.

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RN [1]
RP SEQUENCE.
RX MEDLINE; 68242259.
RA HILSCHMANN N.;
RL HOPPE-SEYLER S Z. PHYSIOL. CHEM. 348:1718-1722(1967) .
[2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE; 70063440.
RA HILSCHMANN N.;
RL NATURWISSENSCHAFTEN 56:195-205 (1969) .
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01885; K2HUCM.
DR HSP; P01607; IIGI.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DISULFID 24 95 BY SIMILARITY.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 72301 CN;

Query Match 35.4%; Score 589; DB 5; Length 115;
Best Local Similarity 71.9%; Pred. No. 1.16e-107;
Matches 82; Conservative 17; Mismatches 14; Indels 1; Gaps 1;

Db 2 diymtqtplsipvtppgepasiscrsasgslldsgdntcyinwylqkagsgqllyltleyr 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Qy 21 EVMVQTQSPLSLIPITPGEPASISCRSSQLKHS-NGDTFFLSWTQQKPQPDPRLLIYKVSNR 79

Db 62 asgvprdfsgsgtgtftklksrvqaeedvvyvmcqrlepytfgqgtkleirr 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Qv 80 DSGVPDRSGSGAGTDFTLKLSAVEAEADVGVFCGQTRTPPTFGGTKEIKR 133

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[illegible]







RESULT	1	
ID	R03554	standard; Protein; 238 AA.
AC	R03554;	
DT	20-AUG-1996	(first entry)
DE	Monoclonal antibody DNA light chain against 65 kD hCMV antigen.	
KW	Polymerase chain reaction; primer; amplify; PCR; light chain; WAB;	
KW	65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.	
OS	Synthetic.	
	Key	Location/Qualifiers
FT	Peptide	1..20
FT	/note= "Signal peptide"	
FT	Protein	21..238
FT	/note= "Mature light chain"	
PN	J08038178-A.	
PD	13-FEB-1996.	
PF	20-FEB-1995; 030742.	
PR	18-FEB-1994; JP-021628.	
PA	(N1S ) NISSHINO IND INC.	
PA	(TANA/) TANAKA H.	
DR	WP1; 96-154852/16.	
DR	N-PSDB; T18060.	
PT	Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -	
PT	produced by primer amplification, used in the diagnosis of hCMV	
PT	infection	
PS	Claim 5; Page 19; 22pp; Japanese.	
CC	The sequences given in R03553-54 represent the heavy and light chain	
CC	respectively of a monoclonal antibody against a 65 kD antigen of hu	

CC cytomegalovirus (hCMV). The DNA's encoding these sequences were  
 CC amplified using the sequences given in T18040-58. The monoclonal  
 CC antibody may be used in the diagnosis of hCMV.  
 SQ Sequence 238 AA;

Query Match 84.1%; Score 1401; DB 16; Length 238;  
 Best Local Similarity 84.1%; Pred. No. 7.72e-104;  
 Matches 201; Conservative 22; Mismatches 15; Indels 1; Gaps 1;

Db 1 mrvpallgllmlwipgsadivmtqtplelsvtpgpaasickesgllhddgktylyw 60

Qy 1 MSPAQLGLLLLCVPGSSGEVWMTQSLIPITPGEPASISCRSSQSLKHSNGDTLSW 60

Db 61 ylkpqqgqqllyevsnrfsgvdfsgsgtdftlkisrveaedvgvycmrslqfa 120

Qy 61 YQKQGPQPRLLIKVSNRSDGVPDRFSGGAGTFTLKISAVEAEDVGVPFGQGRTP 120

Db 121 -tfgggtklelrvtaapsvfippsdeqlksgtasvcllnmfypreakvkvdnalq 179

Qy 121 PTEGGTKVEIKRTVAAPSVTIFPPSDEQLKSGTASVCLLNMFYPREAKVQKVDNALQ 180

Db 180 sgnsqvteqskdetylsstltlskadyekhykvyacevthqglspvtskfnrgec 238

Qy 181 SGNSQSVTEQSKDSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTSEFNREGC 239

#### RESULT 2

ID R86323 standard; Protein; 242 AA.

AC R86323;

DT 12-MAR-1996 (first entry)

DE Chimeric 604.2.5 light chain.

KW Monoclonal antibody 604.2.5; Mab; interleukin-8; IL-8;

KW chimeric antibody; Fab; antibody engineering; inflammation;

KW inflammatory bowel disease; ulcerative colitis; bacterial pneumonia.

OS Chimeric Mus sp.;

OS Chimeric Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..23

FT /label= Sig\_peptide

FT /note= "STII signal peptide"

FT Region 24..137

FT /label= VL region

FT /note= "murine light chain variable region"

FT Region 47..63

FT /label= CDR-1

FT /note= "CDR-1 location determined by Kabat

FT sequence comparison; amino acids 49-59

FT constitute CDR-1 determined by X-ray

FT crystallography"

FT Region 78..84

FT /label= CDR-2

FT /note= "CDR-2 location determined by Kabat

FT sequence comparison; amino acids 78-80

FT constitute CDR-2 determined by X-ray

FT crystallography"

FT Region 117..125

FT /label= CDR-3

FT /note= "CDR-3 location determined by Kabat

FT sequence comparison; amino acids 119-124

FT constitute CDR-3 determined by X-ray

FT crystallography"

FT Region 138..242

FT /label= Constant region

FT /note= "Human IgG1 light chain constant region"

PN W09523865-A1.  
 PD 08-SEP-1995.  
 PF 01-MAR-1995; U02589.  
 PR 03-MAR-1994; US-205864.  
 PA (GETH) GENENTECH INC.  
 PA (INDV) UNIV INDIANA FOUND.  
 PI Doerschuk CM, Fong S, Herbert CA, Kim KJ, Leong SR;  
 DR WPI, 95-320580/41.  
 DR N-PSDB; T03380.

PT New anti-interleukin-8 monoclonal antibodies - useful for treating  
 PT inflammatory disorders, partic. ulcerative colitis, and bacterial  
 PT pneumonia  
 PS Example G; Fig 27A-B; 114pp; English.

CC A chimeric Fab light chain (R86323) consists of the light chain  
 CC variable region of anti-interleukin-8 mouse Mab 604.2.5 and  
 CC the light chain constant region of human IgG1. The chimeric  
 CC Fab light chain is obt'd. by expression of a cDNA construct  
 CC (T03380) in vector pchImFab. A chimeric Fab vector, pG425chim2  
 CC (ATCC 97055), encoding the murine-human variable/constant  
 CC regions of both the light and heavy (see R86324) chains of 604.2.5  
 CC was constructed.

SQ Sequence 242 AA;

Query Match 80.4%; Score 1339; DB 15; Length 242;  
 Best Local Similarity 79.5%; Pred. No. 1.08e-98;  
 Matches 186; Conservative 33; Mismatches 14; Indels 1; Gaps 1;

Db 9 laemfvfsiatnayadvlmtqtplelpslvdqasiecrssqslvhgigtlylhwylqkp 68

Qy 7 LLGLLLLCVPGSS-GEVWMTQSLIPITPGEPASISCRSSQSLKHSNGDTLSWYQK 65

Db 69 gqepklllykvsnrfsqgvdffsgsgtdftlkisrveaedgllyfcsgthvpltfga 128

Qy 66 QQPRLLIKVSNRSDGVPDRFSGGAGTFTLKISAVEAEDVGVPFGQGRTPPTFG 125

Db 129 gtlklelkravaptvfippsdeqlksgtasvcllnmfypreakvkvdnalqsgnsq 188

Qy 126 GTKVEIKRTVAAPSVTIFPPSDEQLKSGTASVCLLNMFYPREAKVQKVDNALQSGNSQ 185

Db 189 esvteqskdetylsstltlskadyekhykvyacevthqglspvtskfnrgec 242

Qy 186 ESVTEQSKDSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTSEFNREGC 239

#### RESULT 3

ID R28809 standard; Protein; 241 AA.

AC R28809;

DT 02-APR-1993 (first entry)

DE Vector pMDR1007.

KW Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;

KW pMDR986; BglII; pMDR1003; JA221(Ig); E. coli; ampicillin resistance;

KW NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;

KW melting agarose; immunoglobulin; kappa chain; signal peptide; LC;

KW humanised; 5A8; light chain; variable region; IV; genomic; constant

KW antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+;

KW lymphocyte; helper; inducer; HIV; syncytia; formation.

OS Synthetic.

FH Key Location/Qualifiers

FT Peptide 1..22

FT /note= "Immunoglobulin kappa chain signal peptide"

FT Region 23..134

FT /note= "Humanised 5A8 IV"

FT Region 135..241

FT /note= "Human kappa chain LC"

J09209305-A.  
 11-JUN-1992.  
 27-NOV-1991; U08843.  
 27-NOV-1990; US-618542.  
 (BIOL J BIOGEN INC.  
 Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;  
 WPI; 92-398399/48.  
 N-PSDB; Q30920.  
 New anti-CD4 antibody homologues - which bind CD4, do not block  
 binding of HIV gp120 to CD4 but block HIV-induced syncytia  
 formation between CD4+ cells  
 Disclosure; Page 166-7; 205pp; English.  
 The sequence given is encoded by the insert of the vector pMDR1007.  
 pMDR1006 (see Q30919) and pSAB132 (see Q30906) were used in the  
 construction of this vector. Three fragments were ligated together  
 to generate pMDR1006; a 572 bp fragment of pMDR985 (see Q30913), a  
 3442bp AatII/EcoRV fragment of pMDR986 (see Q30918) and a 326 bp  
 EcoRV/BglII fragment of pMDR1003 (see Q30900). The ligation mixture  
 was used to transform E. coli JAZ21(Iq) to ampicillin resistance.  
 pMDR1006 was cleaved with NotI and the 1693 bp fragment isolated was  
 ligated into NotI linearised pSAB132 which had been dephosphorylated  
 by calf alkaline phosphatase. This generates the plasmid pMDR1007.  
 The dephosphorylated mixture was fractionated through low temperature  
 melting agarose and used to transform E. coli JAZ21(Iq) to ampicillin  
 resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3'  
 order, the immunoglobulin kappa chain signal peptide, amino acid (AA)  
 1-AA112 of the humanised 5A8 light chain variable region (LV) followed  
 by genomic DNA encoding AA108-AA214 of the human kappa light chain,  
 ie. the light chain constant region (LC). This polypeptide is an  
 antibody homolog which was shown to bind to CD4 but did not block the  
 binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+  
 lymphocytes (helper/inducer cells). The homolog blocked HIV-induced  
 syncytia formation. This homolog can be used in the detection,  
 prophylaxis and treatment of diseases caused by infective agents whose  
 primary targets are CD4+ cells.  
 Sequence 241 AA;

Query Match	79.7%;	Score 1327;	DB 5;	Length 241;
Best Local Similarity	80.0%;	Pred. No. 1.07e-97;		
Matches 192;	Conservative 23;	Mismatches 23;	Indels 2;	Gaps 2;

[illegible]

## RESULT 4

ID B24811 standard: Protein: 239 AA.

AC R24811:  
REF ID: A66907

DT 28-DEC-1992 (first entry)

DE Sequence encoded by the chimeric kappa chain cDNA (Iqkv) contained

DE in pTB1427

KW	Chimeric monoclonal antibody; anti-fibrin antibody; primer;
KW	antithrombotic agent; myocardial infarction therapy.
FS	Synthetic.
QH	Key
FT	Location/Qualifiers
FT	Peptide
FT	1..20
FT	/label= leader
FT	21..133
FT	Region
FT	/label= V-kappa
FT	Region
FT	134..239
FT	/label= C-kappa
FT	Misc difference 130
FT	/note= "Alternatively = Glu"
PN	EP-491351-A.
PD	24-JUN-1992.
PF	17-DEC-1991; 121591.
PR	18-DEC-1990; JP-413829.
PR	11-NOV-1991; JP-294464.
PA	(TAKE ) TAKEDA CHEM IND LTD.
PI	Iwasa S, Taka H, Watanabe T, Tada H;
DR	WPI; 92-209528/26.
DR	N-PSDB; 025691.
PT	Chimeric monoclonal antibodies - contain anti-human fibrin
PT	antibody light and heavy chain variable and constant for treating
PT	thrombotic conditions e.g. myocardial infarction
PS	Example; Figure 9; 87pp; English.
CC	Poly(A) + RNA was prep. from the anti-fibrin chimeric Ab-producing
CC	transformant FIB1-H01/X63 and used as a template to clone human
CC	C-kappa cDNA, using the oligo-dT (Pharmacia) primer as a primer for
CC	first strand cDNA synthesis and the 3'E-kappa and 5'C-kappa primers
CC	for the PCR. An amplified DNA fragment of about 0.33kb was isolated
CC	and used to create a C-kappa cDNA contg. vector, pTBI394. Using the
CC	same technique, with the 3'E-kappa primer as a primer for first
CC	strand synthesis and the 5'L-kappa and 3'C-kappa primers for the
CC	PCR, an anti-fibrin V-kappa (V-kappa-v) cDNA was amplified.
CC	Furthermore, using the 3'E-kappa primer for first stand synthesis
CC	and the 5'mv-kappa and 3'mv-kappa primers for the PCR, an
CC	anti-fibrin V-kappa cDNA (V-kappa-FIB) was amplified. In addition,
CC	a leader sequence cDNA (L-kappa) was amplified using the 3'C-kappa
CC	as a primer for first strand synthesis and the 5'S-kappa and 3'L-
CC	kappa primers for the PCR. The amplified gene fragments (L-kappa:
CC	V-kappa-v; V-kappa-FIB) were isolated and used to construct
CC	respectively plasmids pTBI391, pTBI392, and pTBI393. L-kappa, V-
CC	kappa and C-kappa were joined together to give a plasmid, pTBI427,
CC	contg. the whole length of the chimeric kappa chain cDNA.
SQ	Sequence 239 AA;

Query Match	75.38	Score 1254	DB 5	Length 239
Best Local Similarity	77.08	Pred. No. 1.21e-91		
Matches 184	Conservative	29	Mismatches 25	Indels 1
				Gaps 1

[illegible]

Qy , 181 SGNQESVTEQDSKDYSLSTLTLSKADYEKHKVACEVTHQGLSSPIVTKSFNRGEC 239

RESULT	5	
AD	R52951 standard; Protein; 234 AA.	
IC	R52951;	
DT	27-OCT-1994 (first entry)	
DE	Human anti-IgE MAB light chain.	
KW	Human IgE; CH4 region; triggers mediator release;	
KW	Mast cells; Monoclonal antibody; allergy.	
OS	Homo sapiens.	
FFH	Key	Location/Qualifiers
FT	Region	21..128
FT	/label= light chain variable region	
PPN	EP-592230-A.	
PD	13-APR-1994.	
PP	07-OCT-1993; 308006.	
PPR	07-OCT-1992; JP-293800.	
PA	(SNOW ) SNOW BRAND MILK PROD CO LTD.	
PI	Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;	
PI	Yoshida T;	
DR	WPI; 94-120330/15.	
DR	N-PSDB; Q1872.	
PT	Human monoclonal anti-IgE peptide antibody - inhibits histamine	
PPT	release from mast cells by allergen stimulation, useful for	
PT	preventing allergies	
PS	Claim 3; Page 12; 21pp; English.	
CC	R52951 shows the light chain of a human type anti-IgE peptide	
CC	monoclonal antibody which inhibits the signal transmission for	
CC	the release of chemical mediator from mast cells and basophils	
CC	stimulated with allergen. The antibody can be used for the	
CC	prophylaxis and the therapy of allergy.	
SQ	Sequence 234 AA;	

[illegible]

OS Homo sapiens. Location/Qualifiers  
 FH Key 1..17  
 FT Peptide /label= leader peptide  
 FT Region 18..130  
 FT /label= variable region  
 FT /note= "L'V 1"  
 FT Region 131...243  
 FT /label= variable region  
 FT /note= "L'V 2"  
 FT Region 244..345  
 FT /label= constant region  
 PN W09106305-A.  
 PD 16-MAY-1991.  
 PF 06-NOV-1990; U06426.  
 PR 07-NOV-1989; US-432700.  
 PA (BRIM ) BRISTOL-MYERS SQUIB.  
 PI Shuford WM, Harris LJ, Raff HV;  
 DR WPI; 91-163947/22.  
 DR N-PSDB; Q11878.  
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -  
 PT formed by duplicating esp. variable region of light chain of IgG  
 PT class  
 PS Example 5; Fig 16; 104pp; English.  
 CC This sequence is deduced from the cDNA clone 4B9-Vk15 and includes  
 CC the amino acid sequence beyond the first stop codon ("x" in the  
 CC sequence represents a nonsense codon). The clone is incomplete,  
 CC starting from the G of the ATG initiator codon, but the initial Met  
 CC is given. Antibody molecules of the invention can include one or two  
 CC aberrant light chains containing a duplicated variable region, to  
 CC produce heavier antibodies. These heavier antibodies were found to  
 CC have higher avidity than antibodies with just a single copy of the  
 CC L'V region. The antibodies can be used to treat disease, e.g.  
 CC infection by Streptococcus agalactiae. They are able to pass across  
 CC the placenta.  
 CC See also Q11879 and Q11880.  
 SQ Sequence 414 AA;

Query Match 73.0%; Score 1217; DB 2; Length 414;  
 Best Local Similarity 79.0%; Pred. No. 1.41e-88;  
 Matches 177; Conservative 27; Mismatches 13; Indels 7; Gaps 4;  
 Db 131 ttgeivltgspatlsispgeratlsacraagsv----g-sylawqqkpgaprpiliydas 185  
 Qy 18 SSGEVWMTQSPLSLPTPCEPASISCRSSQSLKSHNGDTFLSWYQKPGQPPRLIYKVS 77  
 Db 186 nratgiparfegsgsgtdftltislepdafavvyqchrdnwpqgafgggtkveikrtv 245  
 Qy 78 NRDSGVPDRFSGSGAGTFTLKISAVEAEDVGVFYFCGQ-GTRTP-PTFGGKTKVEIKRTV 135  
 Db 246 aapsvfifppadeqlkqgtsavvcllnmfypreakvqkvkvdnalsqsgnesvteqdsd 305  
 Qy 136 AAPSVFIFPPDSDEQLKSGTASVWCLINNFYPREAKVQKVDNALQSGNSQESVTEQDSK 195  
 Db 306 styselastltlskadyekhkvyacevthglsasptkksfnrgcc 349  
 Qy 196 STYSLSTLTLSKADYKHKVYACEVTHGSLSSPVTKSENRGEC 239  
 RESULT 8  
 ID R13018 standard; Protein; 414 AA.  
 AC R13018;  
 DT 01-AUG-1991 (first entry)  
 DE 181 IgG aberrant light chain with duplicated variable region.

KW immunoglobulin G; light chain; variable region; duplication;  
 KW passive immunity; group B streptococci.  
 OS Homo sapiens. Location/Qualifiers  
 FH Key 1..17  
 FT Peptide /label= leader peptide  
 FT Region 18..130  
 FT /label= variable region  
 FT /note= "L'V 1"  
 FT Region 131..243  
 FT /label= variable region  
 FT /note= "L'V 2"  
 FT Region 244..345  
 FT /label= constant region  
 PN W09106305-A.  
 PD 16-MAY-1991.  
 PF 06-NOV-1990; U06426.  
 PR 07-NOV-1989; US-432700.  
 PA (BRIM ) BRISTOL-MYERS SQUIB.  
 PI Shuford WM, Harris LJ, Raff HV;  
 DR WPI; 91-163947/22.  
 DR N-PSDB; Q11878.  
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -  
 PT formed by duplicating esp. variable region of light chain of IgG  
 PT class  
 PS Example 5; Fig 16; 104pp; English.  
 CC This sequence is deduced from the cDNA clone 4B9-Vk15 and includes  
 CC the amino acid sequence beyond the first stop codon ("x" in the  
 CC sequence represents a nonsense codon). The clone is incomplete,  
 CC starting from the G of the ATG initiator codon, but the initial Met  
 CC is given. Antibody molecules of the invention can include one or two  
 CC aberrant light chains containing a duplicated variable region, to  
 CC produce heavier antibodies. These heavier antibodies were found to  
 CC have higher avidity than antibodies with just a single copy of the  
 CC L'V region. The antibodies can be used to treat disease, e.g.  
 CC infection by Streptococcus agalactiae. They are able to pass across  
 CC the placenta.  
 CC See also Q11879 and Q11880.  
 SQ Sequence 414 AA;

Query Match 73.0%; Score 1217; DB 2; Length 414;  
 Best Local Similarity 79.0%; Pred. No. 1.41e-88;  
 Matches 177; Conservative 27; Mismatches 13; Indels 7; Gaps 4;  
 Db 131 ttgeivltgspatlsispgeratlsacraagsv----g-sylawqqkpgaprpiliydas 185  
 Qy 18 SSGEVWMTQSPLSLPTPCEPASISCRSSQSLKSHNGDTFLSWYQKPGQPPRLIYKVS 77  
 Db 186 nratgiparfegsgsgtdftltislepdafavvyqchrdnwpqgafgggtkveikrtv 245  
 Qy 78 NRDSGVPDRFSGSGAGTFTLKISAVEAEDVGVFYFCGQ-GTRTP-PTFGGKTKVEIKRTV 135  
 Db 246 aapsvfifppadeqlkqgtsavvcllnmfypreakvqkvkvdnalsqsgnesvteqdsd 305  
 Qy 136 AAPSVFIFPPDSDEQLKSGTASVWCLINNFYPREAKVQKVDNALQSGNSQESVTEQDSK 195  
 Db 306 styselastltlskadyekhkvyacevthglsasptkksfnrgcc 349  
 Qy 196 STYSLSTLTLSKADYKHKVYACEVTHGSLSSPVTKSENRGEC 239  
 RESULT 9  
 ID R20058 standard; Protein; 234 AA.  
 AC R20058;

DT 25-MAR-1992 (first entry)  
DE Light chain of 3D6 anti-HIV antibody.  
KW Plasmid pUC3D6LC; human immunodeficiency virus; AIDS;  
KW complementarity determining region.  
OS Homo sapiens.

PH Key Location/Qualifiers

FT Peptide 1..22

FT /label= signal

FT Protein 23..234

FT Region 23..45

FT /label= Framework\_1

FT Region 46..56

FT /label= CDR\_1

FT Region 57..71

FT /label= Framework\_2

FT Region 72..78

FT /label= CDR\_2

FT Region 79..110

FT /label= Framework\_3

FT Region 111..117

FT /label= CDR\_3

FT Region 118..127

FT /label= Framework\_4

FT Region 128..234

FT /label= Constant\_region

PN W09118983-A.

PD 12-DEC-1991.

PF 28-MAY-1991; 100067.

PR 29-MAY-1990; AT-001178.

PA (JUNG/) JUNGBAUER A.

PI Felgenhauer M, Himmel G, Kohl J, Steindl F;

DR WPI; 92-007468/01.

DR N-PSDB; Q20067.

PT Recombinant protein which binds to complex viral antigen and

PT HIV-1 - contains variable region of antibody derived from 3D6

PT cell line, used for detecting HIV-1 antigen

PS Claim 3; Page 28; 52pp; German.

CC The variable region of the light chain is used in a recombinant

CC protein with the variable region from the heavy chain of 3D6,

CC the two V regions being joined by a linker. The recombinant

CC protein binds to HIV gp160.

CC See also Q20066 and Q20068.

SQ Sequence 234 AA;

Query Match 72.5%; Score 1208; DB 3; Length 234;

Best Local Similarity 74.5%; Pred. No. 7,84e-88;

Matches 178; Conservative 29; Mismatches 25; Indels 7; Gaps 4;

Db 3 mrvpaqlqllllwlbgakcdlqmtqspstleasvgrvrtitctcasqi--ar---wlaw 57

Qy 1 MSIPAQLGLLLLCVPGSSGEVWMTQSPISLPITPGEPASISCRSSQSIKHSNGDTFLSW 60

Db 58 yqkpkpvpklllykassleagvpsrfsgsgtgteftltisslqdddfatyccq-yvnsy 116

Qy 61 YQKPKQPPELLLYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEAEDVGVPYCGQGRTP 120

Db 117 -sfqgptkvdlkrtvaapsvfifpsdeqlkgatavvcllnmfypreakvqkvhdnqlq 175

Qy 121 PTFGGGTKEIKRTVAAPSVFIFPPSPDEQIKSGTASVVCILNNFYPREAKVQWKVDNALQ 180

Db 176 agnsqesvteqgskdstyelsstltlekadyekkhvacevthqglspvtskfnrgec 234

Qy 181 SGNSESQSVTEQDQSDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSPVTSKFNRGEC 239

RESULT 10

ID R77614 standard; Protein; 236 AA.

AC R77614;

DT 15-MAR-1996 (first entry)

DE Humanised 5G1.1 VL + 012.

KW Complement C5; haemolysis; kidney; glomerulonephritis;

KW monoclonal antibody; antiinflammatory; antibody engineering;

KW humanised antibody; complementarity determining region; CDR;

KW ds.

OS Synthetic.

PH Key Location/Qualifiers

FT Peptide 1..23

FT /label= sig\_peptide

FT Peptide 23..236

FT /label= mat\_peptide

FT Region 47..57

FT /label= CDR-L1

FT Region 73..79

FT /label= CDR-L2

FT Region 112..120

FT /label= CDR-L3

PN W09529697-A1.

PD 09-NOV-1995.

PF 01-MAY-1995; U05688.

PR 02-MAY-1994; US-236208.

PA (ALEX-) ALEXION PHARM INC.

PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;

PI Wang Y, Wilkins JA;

DR WPI; 95-392923/50.

DR N-PSDB; T08486.

PT Treating glomerulonephritis with antibody against complement C5

PT component - to inhibit complement induced cell lysis

PS Claim 40; Page 132-34; 181pp; English.

CC A humanised CDR-grafted light chain, designated 5G1.1 VL + 012

CC (R77614), includes CDRs derived from mouse anti-C5 monoclonal

CC antibody 5G1.1. DNA (T08486) coding for the light chain can be

CC subcloned together with DNA (T08484) coding for a humanised Fd

CC (R77611) into vector APEX-3P (T08476) for expression of humanised

CC antibody in human 293 EBNA cells. Such recombinant antibodies retain

CC the ability of mAb 5G1.1 to block human complement C5a generation and

CC thus to reduce glomerular inflammation and kidney dysfunction

CC associated with glomerulonephritis.

SQ Sequence 236 AA;

Query Match 72.3%; Score 1204; DB 15; Length 236;

Best Local Similarity 74.5%; Pred. No. 1.68e-87;

Matches 178; Conservative 26; Mismatches 30; Indels 5; Gaps 4;

Db 3 mrvpaqlqllllwlrgarcdlqmtqspstleasvgrvrtitctcaseni--g-a-lnw 57

Qy 1 MSIPAQLGLLLLCVPGSSGEVWMTQSPISLPITPGEPASISCRSSQSIKHSNGDTFLSW 60

Db 58 yqkpkpvpklllykatnldgvpvrsfsgsgtgtdftltisslqdddfatyccqvnlnp 117

Qy 61 YQKPKQPPELLLYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEAEDVGVPYCGQGRTP 120

Db 118 lfqggtkveikrtvaapsvfifpsdeqlkgatavvcllnmfypreakvqkvhdnqlq 177

Qy 121 PTFGGGTKEIKRTVAAPSVFIFPPSPDEQIKSGTASVVCILNNFYPREAKVQWKVDNALQ 180

Db 178 agnsqesvteqgskdstyelsstltlekadyekkhvacevthqglspvtskfnrgec 236



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Qy 181 SGNQSEVTEQDSKDSYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 11

ID R42065 standard; Protein; 236 AA.  
AC R42065;  
DT 29-APR-1994 (first entry)  
DE Human anti-HBs light chain.  
KW Antibody; Ab; light; heavy; chain; hepatitis B;  
KW HB; surface antigen.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..22  
FT /label= sig\_peptide  
FT Protein 23..236  
FT /label= mat\_protein  
PN W09320205-A.  
PD 14-OCT-1993.  
PF 30-MAR-1993; J00396.  
PR 30-MAR-1992; JP-074678.  
PA (SUNR) SUNTORY LTD.  
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;  
DR WPI; 93-336913/42.  
DR N-FSD8; Q49943.  
PT Human anti-hepatitis B surface antigen antibody gene - can be  
PT used to produce L and H chains of the antibody in large quantity  
PS Disclosure; Fig 4-5; 46pp; Japanese.  
CC Polynucleotides encoding the L and H chains of human anti-HBs  
CC Ab are given in Q49943-Q49944. The Ab can be easily produced in  
CC large quantities for therapeutic use.  
SQ Sequence 236 AA;

Query Match 72.1%; Score 1202; DB 8; Length 236;

Best Local Similarity 73.6%; Pred. No. 2.46e-87;

Matches 176; Conservative 29; Mismatches 29; Indels 5; Gaps 2;

Db 3 mrpvaqlglillwfgarcdqmtqpsamaasvdrvtitcrasqgi----gn-ylvw 57

Qy 1 MSLPALQLGLLLCVPGSGSEVWWTQSLPITPGEPAISICRSQSILKHSNGDTFLSW 60

Db 58 fqqkpkvpxrliyaaslsqgvpsfsgsgstefltlsrlqpedfatyylchhny 117

Qy 61 YQKPKGQPPRLLIYKVSNDGVPDRFSGSGAGTDTLIKISAVEAEDVGVEGCGTRTP 120

Db 118 lsfgggtkveikrtvaapsvfifpsdeqlkegtasvcllnmfypreakvqkvdnalq 177

Qy 121 PTFGGTKVEIKRTVAAPSVFIFPDSDEQLKSGTASVCLLNMFYPREAKVQKVQV 180

Db 178 agnqesvteqdkdstyslslstltlsekadyekhkvyacevthqglspvtksf 236

Qy 181 SGNQSEVTEQDSKDSYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 12

ID R33312 standard; Protein; 218 AA.  
AC R33312;  
DT 05-JUL-1993 (first entry)  
DE Humanised MaEl1 Version 1 (intact IgG) light chain.  
KW Antibody; high affinity; FcE<sub>H</sub>; low affinity; FcE<sub>L</sub>;  
KW IgE receptor; histamine; mast cell; basophil; Kabat;  
KW CDR; murine; MAE11; Fab; humaelliv1.  
OS Synthetic.  
PN W09304173-A.  
PD 04-MAR-1993.

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PF 14-AUG-1992; U06860.  
PR 14-AUG-1991; US-744768.  
PR 07-MAY-1992; US-879495.  
PA (GETH) GENENTECH INC.  
PI Jardieu PM, Presta LG;  
DR WPI; 93-094004/11.  
PT Polypeptide(s) binding to specific Fc epsilon receptors - act as  
PT IgE antagonists; useful for treating and preventing IgE-mediated  
PT disorders e.g. allergies  
PS Example 4; Fig 3; 113pp; English.  
CC Residues were selected from MaEl1 and inserted or substituted into  
CC a human Fab antibody background (Vh region Kabat subgroup III and Vh  
CC region kappa subgroup I). A first version, humaelliv1 or version 1 is  
CC given below. The affinity of version 1 was assayed and found to be  
CC ca. 100 times lower than that of the donor antibody MaEl1.  
CC Therefore, further modifications in the sequence of version 1  
CC were made.  
SQ Sequence 218 AA;

Query Match 71.4%; Score 1190; DB 6; Length 218;

Best Local Similarity 76.7%; Pred. No. 2.42e-86;

Matches 168; Conservative 26; Mismatches 24; Indels 1; Gaps 1;

Db 1 diqltqspssisaavdrvtitcrasqsvdy-dqsyvmwyqgkpkapkllyaaayle 59

Qy 21 EWMVTQSLPLITPGEPAISICRSQSILKHSNGDTFLSWYQKPGQPPRLLIYKVSNRD 80

Db 60 egypsfsgsgstefltlsrlqpedfatyycqshedyfsggtkveikrtvaapsv 119

Qy 81 SGVPDRFSGSGAGTDTLIKISAVEAEDVGVEGCGTRTPPTFGGKVEIKRTVAAPSV 140

Db 120 fifpsdeqlkegtasvcllnmfypreakvqkvdnalqsgnsgesvteqdkdstysl 179

Qy 141 FIFPDSDEQLKSGTASVCLLNMFYPREAKVQKVQVQVQVQVQVQVQVQVQV 200

Db 180 sstltlsekadyekhkvyacevthqglspvtksfntgqc 218

Qy 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 13

ID R38162 standard; Protein; 234 AA.  
AC R38162;  
DT 01-OCT-1993 (first entry)  
DE Sequence of the kappa light chain variable region (VK) of human  
DE immunoglobulin G3 (IgG3) produced by transformed human B-cell line  
DE 88BV59, ATCC CRL 10624.  
KW B-cell; immunoglobulin g; cancer; tumour.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Region 1..214  
FT /tag= a  
FT /label= 1st AA denoted AA#1  
FT Region 24..49  
FT /tag= b  
FT /label= CDR 1  
FT Region 50..88  
FT /tag= c  
FT /label= CDR 2  
FT Region 89..108  
FT /tag= d  
FT /label= CDR 3  
FT Region 109..214  
FT /tag= e

FT	./label= CON
PN	EP-546634-A.
PN	16-JUN-1993.
PD	09-DEC-1992; 203827.
PF	13-DEC-1991; US-807300.
PP	(ALKU ) AKZO NV.
PA	Crichton VZ, Haspel MV, Kobrin BJ;
PI	WPI: 93-190019/24.
PI	N-PSDB; Q43773.
DR	Transformed human B-cell line for monoclonal antibody prodn. for
PT	cancer diagnosis - prepd from peripheral blood B-cells of cancer
PT	patients actively immunised with autologous tumour antigen, for
PT	treating cancers
PT	Claim 9; Fig 3; 18pp; English.
PS	The 88BV59 kappa light chain sequence is indicated by the posns.
CC	of the CD5a and the constant region exon. 88BV59 utilises VxI and
CC	Jk5. The first NH2 terminal 22 residues were confirmed by AA
CC	sequencing.
CC	Sequence 234 AA;
CC	5Q

Query Match 71.4%; Score 1190; DB 7; Length 234;  
Best Local Similarity 74.3%; Pred. No. 2.42e-86;  
Matches 176; Conservative 30; Mismatches 25; Indels 6; Gaps 3;

[illegible]

RESULT	14	
ID	R30777	standard; protein; 233 AA.
AC	R30777;	
DT	12-MAY-1993	(first entry)
DE	ph52-9.0	humanised murine anti-CD18 antibody light chain.
DE	Humanisation; rapid;	monoclonal antibody.
OS	Mus musculus.	
PN	W09222453-A.	
PD	23-DEC-1992.	
PF	15-JUN-1992;	U05126.
PR	14-JUN-1991;	US-715272.
PA	(GETH ) GENENTECH INC.	
PI	Carter PJ, Presta LG.	
DR	WPI; 93-018139/02.	
PT	Humanisation of antibodies -	by molecular modelling of the variable
PT	domains and alteration by	gene conversion mutagenesis
PS	Disclosure; Fig 68;	126pp; English.
CC	The sequence is that of	the humanised light chain sequence of
CC	murine anti-CD18 antibody	ph52-9.0.
SQ	Sequence	233 AA;

Query Match 70.5%; Score 1174; DB 6; Length 233;  
Best Local Similarity 74.9%; Pred. No. 5.11e-85;

Matches	173;	Conservative	26;	Mismatches	26;	Indels	6;	Gaps	4;
Db	8	lfivatatgvdhsdgmqtgspeelaavgdvrttctaaqdi---	n-vlnwqagkoka	62					
		l:l: : l : :::: llll ll: : l : : ::lll : l : : ::lllll : :							
Qy	10	LLLLCP--GSSGEVMTQSPILSIPITPGEPASISCRSSOSIKHNGDTFLSWYQQKQP	QGP	68					
Db	63	pkllyivstlhagvsrfsfsgsgidvltltselqefatvyccqgnl	lpptfgqtk	122					
		l:llll :lllll :lllll :lllll :lllll :lllll :lllll :lllll :lllll :lllll							
Qy	69	PRLIIKYNNRNDGVDRPFGSGAGTDFTLISAVEAEVDGYFCGGTRTPPTFGGTK	128						
Db	123	veikrtvaapsvfiippsdenlkgtavaevcllnfyprkaqvkvhdnalsqsaeav	182						
Qy	129	VEIKRTVAAPSVFIIPPDSDEJQKSGTASVCLLNFFYPREAKVMKDNALQSGNSQESV	188						
Db	183	teqdskdstyelstsltlakadyekkhyyacevthqglasprtkefnrgec	233						
Qy	189	TEQDSDKSTYSLSSTLTLSKADYEKHKVYAACEVTHGLGSPPVTKSFNRGEC	239						

RESULT 15  
ID R22754 standard; Protein; 233 AA.

AC	R22754;
DE	20-OCT-1992 (first entry)
DE	Reshaped CAMPATH-1 antibody light chain.
KW	Antigen; CDR; complementarity determining region; graft rejection;
KW	autoimmune diseases; rheumatoid arthritis; allergy.

OS	Key	Location/Qualifiers
FT	Region	43..53
FT	/note=	"Complementarity determining region 1"
FT	Region	69..75
FT	/note=	"Complementarity determining region 2"
FT	Region	109..117
FT	/note=	"Complementarity determining region 3"
FT	Peptide	1..19
FT	/note=	"signal peptide"
FT	Peptide	20..214
FT	/note=	"mature peptide"
PN	W09205274-A.	
PD	02-APR-1992.	

02-ARX-1992.  
16-SEP-1991; G01578.  
PR 17-SEP-1990; GB-020282.  
PA (GORM/) GORMAN S D.  
PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.  
DR WPI; 92-132139/16.  
DR N-PSDB; Q23567.  
PT Humanisation of antibodies binding to human CD40  
PT mutation of framework-encoding regions of DNA e  
PT domain of rat or mouse antibody chain  
PS Disclosure; Fig 2; 74pp; English.  
CC The sequence is that of the reshaped CAMPATH-1  
CC Reshaped CD4 antibody can be used to induce tol  
CC antigen. It can also be used to alleviate autoi  
CC as rheumatoid arthritis, and to prevent graft r  
CC to a graft, e.g. an organ graft or a bone mar  
CC also be useful to alleviate allergies. Toleranc  
CC also be achieved. See also R22754-R22763.  
SQ Sequence 233 AA;

Query Match 69.7%; Score 1161; DB 4; Length 233;  
Best Local Similarity 73.2%; Pred. No. 6.08e-84;  
Matches 169; Conservative 3; Mismatches 21; Indels 6; Gaps 2;

Db 8 lflvatatgvhsdiqmtqspsslsasvqdrvtitckasqni-----dkylnwyqqkpgka 62

Dec 17 15:09

US-08-487-550-6.rag

17

```
Qy 10 LLLLCP-GSSGEVWVWQSPISLIPGEPASISCRSSQSLKHSNGDTFLSWYQKPCQP 68
    . 1:1: : 1 ::: 1111 11: : 1: :1:11: : 1:1:1111: :
Db 63 pklllyntnllqtgvpsrfegsggtdfttleslqpediatyvcqlchierprtfgggk 122
    1:111: : 1 :::11 1111:1111: 11:111: 11:111: 11:111: 11:111:
Qy 69 PRLLYKVSNRDSCVPDRFSGSGAGTDFTLKISAVEAEDVGVFCCGGCTRTPTFGGGTK 128
    1:111: : 1 :::11 1111:1111: 11:111: 11:111: 11:111: 11:111:
Db 123 veikrtvaapavfiippedeqlkagtaervcllnnfyppreakvqkvdnalqgnsqesv 182
    1:111: : 1 :::11 1111:1111: 11:111: 11:111: 11:111: 11:111:
Qy 129 VEIKRTVAAPSVFIIPPDSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESV 188
    1:111: : 1 :::11 1111:1111: 11:111: 11:111: 11:111: 11:111:
Db 183 tegdskdstylsstltlekadyekkhvyacevthqglespvtksfnrgec 233
    1:111: : 1 :::11 1111:1111: 11:111: 11:111: 11:111: 11:111:
Qy 189 TEQDSKDSYSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
    1:111: : 1 :::11 1111:1111: 11:111: 11:111: 11:111: 11:111:
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Search completed: Tue Dec 17 15:23:52 1996  
Job time : 34 secs.

Result	Query			Description	Pred. No.
	No.	Score	Match Length		
1	2339	67.5	330	Ig gamma-1 chain C r	1.18e-243
2	2335	67.4	329	Ig gamma-1 chain C r	3.38e-243
3	2133	61.5	326	Ig gamma-2 chain C r	4.04e-220
4	2133	61.5	327	Ig gamma-4 chain C r	4.04e-220
5	2043	58.9	470	Ig heavy chain precu	7.47e-210
6	2017	58.2	472	Ig gamma-1 chain - s	6.88e-207
7	1999	57.7	469	Ig gamma-2a chain -	7.75e-205
8	1878	54.2	446	Ig gamma-2a chain (m	4.68e-191
9	1871	54.0	474	Ig gamma-2b chain -	2.93e-190
10	1814	52.3	475	Ig gamma-2b chain pr	8.93e-184
11	1747	50.4	377	Ig gamma-3 chain C r	3.68e-176
12	1747	50.4	377	Ig gamma-3 chain C r	3.68e-176

```

#accession   A93433
##molecule_type  DNA
##residues    1-330  #label ELL
##note       this sequence has the G1m(17) allotypic marker, 97-Lys,
              and the G1m(1) markers, 239-App and 241-Leu
              Lys-330 is removed after translation
##note       A90563
REFERENCE
#authors     Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb,
              P.D.; Waxdal, M.J.; Edelman, G.M.
#journal     Biochemistry (1970) 9:3161-3170
#title       The covalent structure of a human gamma-globulin. VII
              Amino acid sequence of heavy-chain cyanogen bromide
              fragments H-1-H-4.
#cross-references  MUID:71064024

```

```

#contents      myeloma protein Eu
#accession     B90563
#molecule_type protein
#residues      1-96,'R',98-135 ##label CUN
#note          this sequence has the Gln(3) marker, 97-Arg
REFERENCE
#authors       Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg,
                W.H.; Edelman, G.M.
#journal       Biochemistry (1970) 9:3171-3181
#title         The covalent structure of a human gammaG-immunoglobulin.
                VIII. Amino acid sequence of heavy-chain cyanogen bromide
                fragments H-5-H-7.
#cross-references MUID:71064025
#contents      Eu
#accession     A90564
#molecule_type protein
#residues      136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,
                'D',199-238,'E',240,'M',242-267,'DGEPE',273-329
                ##label RUT
#note          this sequence has the Gln(non-1) markers, 239-Glu and
                241-Met
REFERENCE
#authors       Ponstingl, H.; Hilschmann, N.
#journal       Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1571-1604
#title         Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins
                (Myelomprotein Nie), III. Die chymotryptischen Peptide der
                H-Kette, Anordnung der tryptischen Peptide und Diskussion
                der vollstaendigen Primaerstruktur.
#cross-references MUID:77070269
#contents      myeloma protein Nie
#accession     B91668
#molecule_type protein
#residues      1-34,'Q',36-96,'R',98-115,'Q',117-197,'D',199-238,'D',
                240,'L',242-268,'E',270-271,'D',273-330 ##label PON
#note          this sequence has the Gln(17) and Gln(1) markers
REFERENCE
#authors       Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
#journal       Hoppe-Seyler's Z. Physiol. Chem. (1983) 364:713-747
#title         Die Primaerstruktur des kristallisierbaren monoklonalen
                Immunglobulins IgG1 KOL, I.
#cross-references MUID:83289131
#contents      myeloma protein KOL; disulfide bonds
#accession     A91723
#molecule_type protein
#residues      1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',
                268-271,'D',273-330 ##label SCH
#note          this sequence has the Gln(3) and Gln(non-1) markers
REFERENCE
#authors       Gall, W.E.; Edelman, G.M.
#journal       Biochemistry (1970) 9:3188-3196
#title         The covalent structure of a human gammaG-immunoglobulin. X.
                Intrachain disulfide bonds.
#cross-references MUID:71064027
#contents      annotation; disulfide bonds
#accession     A91667
#authors       Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
#journal       Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1515-1540
#title         Rule of antibody structure. The primary structure of
                monoclonal IgG1 immunoglobulin (myeloma protein Nie), I:
                purification and characterization of the protein, the L-
                and H-chains the cyanogenbromide cleavage products, and the
                disulfide bridges.
#cross-references MUID:77070267
#contents      annotation; disulfide bonds

```

```

GENETICS
#gene          GDB:IGHG1
#map_position  14q32.33
#introns       99/1; 114/1; 224/1
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
                glycoprotein
KEYWORDS
FEATURE
20-85          #domain immunoglobulin homology #label IGG1\
137-206        #domain immunoglobulin homology #label IGG2\
243-310        #domain immunoglobulin homology #label IGG3\
27-83,144-204, #disulfide_bonds #status experimental\
250-308        #disulfide_bonds interchain (to light chain) #status
103            experimental\
109,112        #disulfide_bonds interchain (to heavy chain) #status
180            #binding_site carbohydrate (Asn) (covalent) #status
                experimental
SUMMARY        #length 330 #molecular-weight 36106 #checksum 8773
Query Match    67.5%; Score 2339; DB 2; Length 330;
Best local Similarity 99.7%; Pred. No. 1.18e-243;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 astkgsvfplapskatsqtaalgclvkdypfpvptvsnsgaltsgvhtfpavlgss 60
|||||
Qy 149 ASKGSVFPLAPSSKTSGGTALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVLQSS 208
|||||
Db 61 glylasvvtvpsslqtqylcnvnhkpsntkvdkkvepkcdkthtccpcpapellgg 120
|||||
Qy 209 GLYLSVWTVFSSSLGTOTYICNVNHKPSNTKVKDAEPKSCDKTHTCPPCPAPELGG 268
|||||
Db 121 pavflfpkpkdttlmisrtpevtcvvvdvshedpevkfowvdygvevhnaktkpreeqyn 180
|||||
Qy 269 PSVLEFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 328
|||||
Db 181 styrvsvltvlhqdwlngkeyckvsnkalpapiektiskakgpreqvytlppsrde 240
|||||
Qy 329 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGPREQVYTLPPSRDE 388
|||||
Db 241 itknqvsitclvkgyfypsdiaveeengqpennykttppvldsdgdsfflyskltvdkerw 300
|||||
Qy 389 ITRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSGSEFFLYSKLTVDKSRW 448
|||||
Db 301 qggnvfscsvmhleahnhvhtqkelaelpgk 330
|||||
Qy 449 QGGNVFSCSVMHLEAHNHVHTQKSLSLSPGK 478
|||||
RESULT 2
ENTRY     S36861 #type fragment
TITLE     Ig gamma-1 chain C region - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE      31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change
                02-Aug-1994
ACCESSIONS S36861; S33887
REFERENCE   S33904
#authors    Harris, L.J.
#submission submitted to the EMBL Data Library, October 1992
#accession  S36861
#molecule_type DNA
##residues 1-329 ##label HAR
#cross-references EMBL:Z17370
REFERENCE   S33887

```

```
#authors      Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.;
#journal      Honjo, T.
#title        Cell (1982) 29:671-679
#accession    S33887
#molecule_type DNA
#residues     87-112:234-329 ##label TAK
#cross-references EMBL:217370

GENETICS
#introns      98/1; 113/1; 223/1
#superfamily  #superfamily immunoglobulin C region; immunoglobulin homology
#length 329 #checksum 6336

Query Match      67.4%; Score 2335; DB 5; Length 329;
Best local Similarity 99.7%; Pred. No. 3.38e-243;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1  atgpgvflapssaketsgtaalqclvkdyfpepvtvsmagaltqgvtfpavlgsg 60
      |||
Qy 150 STKCPVFLAPSSKSTSGTAALCLLVKDYFPEPVTVSMNSGALTSGVITFPVAVLSSG 209
      |||

Db 61 lysaevvtvpssalgtqyicnvnhkpkvdkvpektscdkthccpcapellggp 120
      |||
Qy 210 LYSLSWVTPVSSSLGTQYICNVNHKPKVNTKVDKAEKPCDKTHTCPCPAPELGGP 269
      |||

Db 121 evflfpkpkdtkimistrpevtcvvdshedpevkfnwydvgrvnhaktpreeqyns 180
      |||
Qy 270 SVFLFPKPKDTLMSRTEVTCVVDVSHEDPEVKFNWYDVGVNHAKTPREEQYNS 329
      |||

Db 181 tyrvsvltvhqdwlngkyekykvsnkalpapietkiskagqprepyvltppsrdel 240
      |||
Qy 330 TYRWSVLTVLHQDLWLNKYEKCKVSNKALPAPTEKTSKAGQPREPYVLTTPSRDEL 389
      |||

Db 241 tknqvslclvkgyfspdlaevwsngqpennyyktpvldsdgsefflyskltvdksrwq 300
      |||
Qy 390 TRNQVSLCLVKGYFSPDLAEVWSNGQPENNYKTPVLDSDGSEFFLYSKLTVDKSRWQ 449
      |||

Db 301 qgnvfscsvmbealhhbhtqkelsispk 329
      |||
Qy 450 QGNVFCVSMHEALHHYTKRSLSPGK 478
      |||

RESULT 3
ENTRY   GZHU      #type complete
TITLE   Ig gamma-2 chain C region - human
ORGANISM
DATE    30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change
        08-Dec-1994
ACCESSIONS A93906; A92809; A90752; A93132; A02148
REFERENCE   A93906
#authors    Ellison, J.; Hood, L.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1982) 79:1984-1988
#title      Linkage and sequence homology of two human immunoglobulin
            gamma heavy chain constant region genes.
#cross-references MUID:82197621
#accession  A93906
#molecule_type DNA
#residues   1-326 ##label ELL
#note       Lys-326 is probably removed posttranslationally
REFERENCE   A92809
#authors    Wang, A.C.; Tung, E.; Fudenberg, H.H.
#journal    J. Immunol. (1980) 125:1048-1054
#title      The primary structure of a human IgG2 heavy chain: genetic,
```

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evolutionary, and functional implications.
#cross-references MUID:81007873
#contents     myeloma protein T11
#accession    A92809
#molecule_type protein
#residues     1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 ##label WAN
#note         Trp-156 is at or near the complement-binding site
REFERENCE     A90752
#authors      Connell, G.E.; Parr, D.M.; Hofmann, T.
#journal      Can. J. Biochem. (1979) 57:758-767
#title        The amino acid sequences of the three heavy chain constant
            region domains of a human IgG2 myeloma protein.
#cross-references MUID:80001357
#contents     myeloma protein Zie
#accession    A90752
#molecule_type protein
#residues     1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,
            'D',195-196,'Q',198-234,'Z',236-263,'BCEPZ',269-325
            ##label CON
#note         this sequence has since been revised
REFERENCE     A93132
#authors      Hofmann, T.; Parr, D.M.
#journal      Mol. Immunol. (1979) 16:923-925
#title        A note on the amino acid sequence of residues 381-391 of
            human immunoglobulin gamma chains.
#cross-references MUID:80114419
#contents     Zie
#accession    A93132
#molecule_type protein
#residues     238-275 ##label HOF
REFERENCE     A94591
#authors      Hofmann, T.; Parr, D.M.
#submission   submitted to the Atlas, March 1980
#contents     annotation; Zie, revisions to residues 25, 59, 60, and
            264-268
#note         the revised sequence differs from that shown in having 60-Ala
            and in the amidation states of residues 58, 194, and 197;
            the amidation states of residues 172-174, 176, and 235 were
            not determined
REFERENCE     A90253
#authors      Milstien, C.; Frangione, B.
#journal      Biochem. J. (1971) 121:217-225
#title        Disulphide bridges of the heavy chain of human immunoglobulin
            G2.
#cross-references MUID:72033500
#contents     annotation; myeloma protein Sa, disulfide bonds
REFERENCE     A93157
#authors      Frangione, B.; Milstien, C.; Pink, J.R.L.
#journal      Nature (1969) 221:145-148
#title        Structural studies of immunoglobulin G.
#cross-references MUID:69064124
#contents     annotation; Sa, disulfide bonds
GENETICS
#gene        GDB:IGHG2
#map position 14q32.33
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-85        #domain immunoglobulin homology #label IGG1\
133-202      #domain immunoglobulin homology #label IGG2\
239-306      #domain immunoglobulin homology #label IGG3\
14           #disulfide bonds interchain (to light chain) #status
            experimental\
27-83,140-200,
246-304      #disulfide_bonds #status experimental\
```

102,103,106,109 #disulfide_bonds interchange (to heavy chain) #status									
SUMMARY #length 326 #molecule-weight 35884 #checksum 7982 experimental									
Query Match 61.5%; Score 2133; DB 2; Length 326;									
Best Local Similarity 90.9%; Pred. No. 4.04e-220;									
Matches 300; Conservative 15; Mismatches 11; Indels 4; Gaps 3;									
Db	1	aetkpsvfplapcstetseestaalgclvkdypcpvvtvsmnsgaltsgvhtfpavlgss	60						
QY	149	ASTKGSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS	208						
Db	61	glylesvvtvpssenfgtqtcvndhkpstkvdtkvtkerck--ve-cppepappv-ag	116						
QY	209	GLYSLSSVVTVPSSSLGTQTICNWHKPSNTYKDKAEKPSCKDKTHTCTCPAPELLGG	268						
Db	117	psvifppkpkdtdlmisrtpevtcvvvvshdpevfqfnwywdgvevhnaktkpreeqfn	176						
QY	269	PSVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYN	328						
Db	177	stfrvsvltvthqdwlngkeyckvsnkglpaplektisktkgqprepqvvtlpsree	236						
QY	329	STRVSVSLTVLHQDWLNGKEYCKVSNKALPAPLEKTIISKAKGQPREPQVYTLPPSRDE	388						
Db	237	mtknqsvltclvkgfypsdiavewesngpennyktptpmlsdsgsflysklitvdksrw	296						
QY	389	LTKNQSVLTCLVKGFPSDIAVESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW	448						
Db	297	qgnvfscsvmhcalhnhvtgklsalspgk	326						
QY	449	QGNVFSCSVMHCALENHVTQKSLSPGK	478						
RESULT	4								
ENTRY	G4HU #type complete								
TITLE	Ig gamma-4 chain C region - human								
ORGANISM	#formal_name Homo sapiens #common_name man								
DATE	02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 23-Mar-1995								
ACCESSIONS	A90933; A90249; A02150								
REFERENCE	A90933								
#author	Ellison, J.; Ruxbaum, J.; Hood, L.								
#journal	DNA (1981) 1:11-18								
#title	Nucleotide sequence of a human immunoglobulin C-gamma4 gene.								
#cross-references	MUID:83157104								
#accession	A90933								
#molecule_type	DNA								
#residues	1-327 #label ELL								
#note	the sequence was determined from the germline gene								
REFERENCE	A90249								
#author	Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.								
#journal	Biochem. J. (1970) 117:33-47								
#title	Human immunoglobulin subclases. Partial amino acid sequencing of the constant region of A gamma4 chain.								
#cross-references	MUID:70207560								
#accession	A90249								
#molecule_type	protein								
#residues	1-30;81-326 #label PIN								
GENETICS									
#gene	GDB:IGHG4								
#map_position	14q32.33								
#introns	99/1; 111/1; 221/1								
CLASSIFICATION	#superfamily immunoglobulin C region; immunoglobulin homolog								
FEATURE									

[illegible]



```
##molecule_type DNA
##residues 142-470 ##label_SYM
##cross-references ENRLE:16701
##note the sequence was determined from the germline gene
```

GENETICS  
#gene  
#exons  
#introns  
CLASSIFICATION  
#superfamily immunoglobulin C region; immunoglobulin homology  
KEYWORDS  
antibody; complement; immunoglobulin; membrane protein  
FEATURE  
318  
#binding site carbohydrate (asn) (covalent) #status

SUMMARY

#length 470 #molecular-weight 50625 #checksum 2181

Query Match 58.9%; Score 2043; DB 5; Length 470;  
Best Local Similarity 61.2%; Pred. No. 7,476-210;  
Matches 290; Conservative 83; Mismatches 89; Indels 12; Gaps 8;

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Db      7 llfvaaplylscvqlresgplvkpsqtlstctcsvgfsissyvaltwrvgpqkalew 66  
       |||::: : ||| ||| ::||: |:::||::|:~::~|||::|:  
  
QY     7 LLFVAVATRVCEVLVESGGGLGVCGSLKVSICVGSGTTFSDHYMVFWRAPKGPEW 66
```

```

Db      67  vggi---tsggttynpalkarlsitkensksgvslsvasvtpedtatyycars--ty-- 119
      |||  :||||  :|||  :|||::|||  |:|||  |||  |||  |  :
Qv      67  VGEIRKPNGGTTEYAAVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTYSIHC 126

```

Db 120 gevvdgaiadawggllvtvasastapkyvplsccgdkssstvtlglvsympcpvt 179  
 { } | : : ||| ||||| : : ||| : : ||| : : ||| : : |||  
 Qv 127 GVCYGGYEFGGALVTVSSATKSPSYFPLAPSSKSTSGGAALGLVRDYEPPEVT 186

Db 180 vtwnsgalksgvhtfpavllqsglyslssmrvtpgstsg-qtftcnvnhpassctkvdkav 238  
 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
 Qv 187 vwnsgal:tsgvhtfpaavlosgglxslssvvtvpssslctotyticnnvnhkpsntkvdkka 246

Db 239 dp-tc-kpspcdcpppelpgagsvifipkpkdltligstpevtcvvvvgdhdpvkf 296  
: | : | - |||:|||||:||||| || |||||:|||||:  
Qv 247 EPKSCDTHTCPPELLGPSEVLEFPKKPKDTIMISRTPEVTCVVVDVSHEDPEVKF 306

```

Db      297 swfvddvemtattkpreeqfnstyrwvsalrihqdwggkefckvhneglpapivrt 356
       :||| ||| : |||||||:||||| | : ||| |||: ||| : ||| :|
Qv     307 NWYVDGVGVHNAKTKPREEOYNSTYRWVSIVTLHDWDWNGCKEYKCKVSNKAIPAPTEKT 366

```

```
Db      357 isttkgarepqvyvlappqeelsksta|lcmvtstfydyiaevwqrngqpesdkygt 416
       ||||| :||||| :::|||: ||||| :||| ||||| :||| :|||
Qv      367 ISKAKGAPREPQVYTLPPSRPELTKNQVSITCLVKGFYPSDIAFWFENSGQPEN-N-YKT 424
```

```

Db 417 tpgqladasylvsklrvdrnswgeqdytvcvmhealhnhyctsktsak 470
||| ||| :|: ||| ||| :|: ||| :|: ||| ||| ||| ||| :|: |||
Ov 475 tppurldsgsfvskltnkspsdncvntscvsmfcalhnyvtokststsdck 478

```

RESULT	ENTRY	STATUS	Fragment
6	S31450		

FILE	ORGANISM	DATE
lg gamma-1 chain - sheep (fragment)		
#formal name Ovis orientalis aries		
#common name domestic sheep		
12 Jan 1995	12 Jan 1995	12 Jan 1995

	ACCESSIONS	S31459	13-Jan-1995
	REFERENCE	S31459	

```
##submission submitted to the EMBL Data Library, December 1992
##accession S31459
##status preliminary
```

```
##molecule type mRNA
##residues 1-472 ##label PAT
##cross-references EMBL:X69797
SUMMARY #length 472 #checksum 9485
```

Query Match	58.2%;	Score 2017;	DB 12;	Length 472;
Best Local Similarity	58.6%;	Pred. No. 6.88e-207;		
Matches	279;	Conservative 91;	Mismatches 94;	Indels 12;
				Gaps 10;

```

Db      5 llfvlsaprgvlsqvr lqesgpslatllqt lvstctlsigfslnnvgvdwvrqapgkalew 64
        |||::: | :||: ||| :| :||: |||::: | :||: |||: ||
Qy      7 llflvavatrqqevqlvesggclvpggslrvscavsgftfSDHYMYWTFRQAPGKGPEN 66

```

**D**b      65 lg---gsgydedidynpvklsrlsitkdtsqsvltlstvttedtavycarvdyds-s  
:  
:  
**Q**y      67 VGFTRNKPGGTTEYAASVKDRFRTISRDDSKSIAYLQMSSLKIEDTAVYCT-TSYISHC

Db 121 hafa-yasy-dfwgpgllisvlaasttpkvypltaaccgdtsstvtlgclvssympcpv 17  
:: :||: ||| |:||: |||| |:||: ||: :||| | |||  
Qy 126 RGGVYGGVFEEFGOGALVTVSASTKGPSVEPLAPSSKTSGGTAALGCLVKQYFPEPV 18

Db	179	tvtwnsgaltsgvhtfpailqasglylssvvtvpastsgaqtfcienvahpæstkvdkr	238
		:     :     :     :     :     :     :     :     :     :     :	
Ov	186	tvtwnsgaltsgvhtfævioxsgglyslssvvtvpæsslgrottytçnnhkpstnkvdkk	241

Db 239 vep-gcpdckhcr-cpppelggpsvfi fppkpkdtltisgtpevtcvvvdvgddpev 299  
||:| | ||:|||||:||||| || |||||:|||||:|||||  
Ov 246 AEPKSC-DKTHTCPPCPAPELIGGSPVFLFPPKPKDTIMISRTPEVTCVVVDVSHEDPEV 306  
||:| | ||:|||||:||||| || |||||:|||||:|||||

Db 297 qfswfdvnevrtartkpreeqfnstfrvsalpihqdwtggekfcckvhnealpapi 35  
| : | | | : | | | | | : | | | : | | | | |  
Ov 305 KENWYDGEVHNHAKTPREFOVNSTVRVWSVTIHDWDINGCKEYKCVSNKALPAPIF 36

Db 417 gtttqladgsgfyflsrlrvdknswgdegdyacvwmhealhhvhtqtslskppgx 472  
 || : |||||:||||: |||: |||: :| :|||||:|||||: :|||  
 Qv 423 kttppvldsgsfeflysklrvdkrrwoognvfcscvwmhealhhvhtokstslspgk 478

RESULT	7
ENTRY	S37483
	status complete

TITLE	Iq gamma-2a chain - mouse
ORGANISM	<i>Mus musculus</i> #common name house mouse
DATE	06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 06-Jan-1995

#authors  
#submission  
#accessions  
#reference  
#submitted to the EMD Data Library  
#February 1993

```
##accession S37483
##status preliminary
##molecule_type mRNA
##sequencing 1,450,000,000 bp
```

```

SUMMARY
  ##cross-references EMBL:X70423
    #length 469 #molecular-weight 51549 #checksum 7833
  
```

Best Local Similarity 57.7%; Pred. No. 7.75e-205;  
Matches 277; Conservative 89; Mismatches 102; Indels 13; Gaps 8;



```
##cross-references EMBL:X13188
##note this sequence was determined from the differentiated
gene
```

```
##accession A23511
##molecule_type DNA
##residues 1-377 ##label HUC
```

## GENETICS

#gene GDB:IGHG3  
#map\_position 14q32.33  
#introns 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology  
SUMMARY #length 377 #molecular-weight 41287 #checksum 8588

Query Match 50.4%; Score 1747; DB 5; Length 377;  
Best Local Similarity 82.8%; Pred. No. 3.68e-176;  
Matches 312; Conservative 15; Mismatches 3; Indels 47; Gaps 9;

Db 1 asktqpsvfplapcsatstggtaalcgclvkdypfpvptvsmnsgaltsgvhtfpavlqss 60  
|||||  
Qy 149 ASTKGPSVFPLAPSSKTSSTGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 208  
|||||  
Db 61 glyslesvvtvpasaelgtqctytcnvnkhpsntkvdkrvelktplgdtthtcrpepksc 120  
|||||  
Qy 209 GLYSLSVVTVPSSSLGTQTYICNVNHRKSNVKYD-----KA-----EPKSC 251  
|||||  
Db 121 dtpppcrpepkscdtpppcprpepkscdtpppcprpapellgppsvflfppkpkdt 180  
|||||  
Qy 252 D-----K---T-----H-----TC-----P-CPAPELLGGPSVFLFPPKPKDT 281  
|||||  
Db 181 lmiartpevtcvvvdshedpevgfkwyvdgvevhnaktkpreeqynstfrvsvltvlh 240  
|||||  
Qy 282 LMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNACTKPREEQYNSTYRVSVLTVLH 341  
|||||  
Db 241 qdwlngkeyckvankalpapietkstkqgpreqvvtlppareemknqvaltclvk 300  
|||||  
Qy 342 QDWLNGKEYCKVSNKALPAPIETKISKAKQPREPVYTLPPSRDELTKNQVSLTCLVK 401  
|||||  
Db 301 gfypsdiaveesgqpnnynttppmlsdsgsflyskltvdksrwwqgnvfacsymhe 360  
|||||  
Qy 402 GFYPDSIAVESNGQPNNYKTTTPVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHE 461  
|||||  
Db 361 alhnrtqkslslepk 377  
|||||  
Qy 462 ALHNHYTQKSLSLSPGK 478

RESULT 12  
ENTRY A60764 #type complete  
TITLE Ig gamma-3 chain C region, form LAT - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 12-Apr-1995  
ACCESSIONS A60764  
REFERENCE A60764  
#authors Huck, S.; Lefranc, G.; Lefranc, M.P.  
#journal Immunogenetics (1989) 30:250-257  
#title A human immunoglobulin IGHG3 allele (Gmb0, bi, c3, c5, u) with an IGHG4 converted region and three hinge exons.

#accession A60764  
#status preliminary  
#molecule\_type DNA  
#residues 1-377 #label HUC  
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology  
SUMMARY #length 377 #molecular-weight 41270 #checksum 9390

Query Match 50.4%; Score 1747; DB 5; Length 377;  
Best Local Similarity 82.8%; Pred. No. 3.68e-176;  
Matches 312; Conservative 15; Mismatches 3; Indels 47; Gaps 9;

Db 1 asktqpsvfplapcsatstggtaalcgclvkdypfpvptvsmnsgaltsgvhtfpavlqss 60

Qy 149 ASTKGPSVFPLAPSSKTSSTGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 208  
|||||  
Db 61 glyslesvvtvpasaelgtqctytcnvnkhpsntkvdkrvelktplgdtthtcrpepksc 120  
|||||  
Qy 209 GLYSLSVVTVPSSSLGTQTYICNVNHRKSNVKYD-----KA-----EPKSC 251  
|||||  
Db 121 dtpppcrpepkscdtpppcprpepkscdtpppcprpapellgppsvflfppkpkdt 180  
|||||  
Qy 252 D-----K---T-----H-----TC-----P-CPAPELLGGPSVFLFPPKPKDT 281  
|||||  
Db 181 lmiartpevtcvvvdshedpevgfkwyvdgvevhnaktkpreeqynstfrvsvltvlh 240  
|||||  
Qy 282 LMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNACTKPREEQYNSTYRVSVLTVLH 341  
|||||  
Db 241 qdwlngkeyckvankalpapietkstkqgpreqvvtlppareemknqvaltclvk 300  
|||||  
Qy 342 QDWLNGKEYCKVSNKALPAPIETKISKAKQPREPVYTLPPSRDELTKNQVSLTCLVK 401  
|||||  
Db 301 gfypsdiaveesgqpnnynttppmlsdsgsflyskltvdksrwwqgnvfacsymhe 360  
|||||  
Qy 402 GFYPDSIAVESNGQPNNYKTTTPVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHE 461  
|||||  
Db 361 alhnrtqkslslepk 377  
|||||  
Qy 462 ALHNHYTQKSLSLSPGK 478

RESULT 13  
ENTRY S31866 #type complete  
TITLE Ig gamma-G4 chain C region - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
ACCESSIONS S31866  
REFERENCE S31866  
#authors Filipula, D.  
#submission submitted to the EMBL Data Library, February 1993  
#description Screening method for protein-protein interactions of cloned gene products.

#accession S31866  
#status preliminary  
#molecule\_type mRNA  
#residues 1-255 #label FIL  
#cross-references EMBL:X70421  
SUMMARY #length 255 #molecular-weight 28325 #checksum 2783

Query Match 48.6%; Score 1686; DB 11; Length 255;  
Best Local Similarity 99.6%; Pred. No. 3.10e-169;  
Matches 231; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 eskacdkthtccpapellgppsvflfppkpkdtlmiartpevtcvvvdshedpavkf 83  
|||||  
Qy 247 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 306  
|||||  
Db 84 nwyvdgvevhnaktkpreeqynstyrsvsvltvlhqdwlngkeyckvankalpapietk 143  
|||||  
Qy 307 NWYVDGVEVHNACTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETK 366  
|||||  
Db 144 iskakqpreqvvtlppsrdeltnqvsltclvkgyfypsdiaveesngqpennktt 203  
|||||  
Qy 367 ISKAKQPREQVYTLPPSRDELTKNQVSLTCLVKGYFYPSDIAVESNGQPNNYKTT 426  
|||||  
Db 204 pvlsdsgsflyskltvdksrwwqgnvfacsymhealhnhytqkslslepk 255

```
|||||
Qy 427 PVLDSGSEFFLYSLVDSKRWQGNVFCSCVMHEALHNHYTKSLSPGK 478
|||||

RESULT 14
ENTRY PT0207 #type complete
TITLE Ig gamma chain C region - chimpanzee
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 12-Apr-1995
ACCESSIONS PT0207
REFERENCE PT0207
#authors Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
#journal Mol. Immunol. (1991) 28:319-322
#title Nucleotide sequence of chimpanzee Fc and hinge regions.
#cross-references M01D:91287716
#accession PT0207
#molecule_type mRNA
#residues 1-234 ##label EHR
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY #length 234 #molecular-weight 26330 #checksum 6128

Query Match 48.4%; Score 1677; DB 5; Length 234;
Best Local Similarity 98.3%; Pred. No. 3.26e-168;
Matches 230; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 antkvdkvpeksdctthcpcaapellggsvfifppkpkdtlmisrtpevtcvvvdv 60
|||||
Qy 238 SNTKVDKKAEPKSCDKTHTCPCPAPELLGGSVFLFPPKPKDTLMISRTPEVTCVVVDV 297
|||||

Db 61 shedpevfnyvdgvevhnaktpreeqnystyrsvvsvltvldqdwlngkeyckvsnk 120
|||||
Qy 298 SHEDPEVFNVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNK 357
|||||

Db 121 alpakietskakgprepyqlppsrdeitknqvaitclvkgfypsdiavewessgq 180
|||||
Qy 358 ALPAPKTSKAKGPREPYQLPPSRDELTKNQVSLTCLVKGFYPSDIAVEFESNQ 417
|||||

Db 181 pennyktpvldsgsflyskltdkwrqgnvfscsvmhealhnhytqks 234
|||||
Qy 418 PENNYKTPPVLDSDGSFFLYSKLTVDKRWQGNVFCSCVMHEALHNHYTKS 471
|||||
```

```
RESULT 15
ENTRY GHRB #type complete
TITLE Ig gamma chain C region - rabbit
ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic rabbit
DATE #sequence_revision 15-Nov-1984 #text_change 04-Nov-1994
ACCESSIONS A91749; A90290; A93928; A90245; A94416; A02161
REFERENCE A91749
#authors Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
#journal Immunogenetics (1983) 18:387-397
#title Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplotype.
#cross-references M01D:84030930
#accession A91749
#molecule_type mRNA
#residues 1-323 ##label BER
#note this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr

REFERENCE A90290
#authors Pratt, D.M.; Mole, L.E.
#journal Biochem. J. (1975) 151:337-349
```

```
#title Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.
#cross-references M01D:76135469
#accession A90290
#molecule_type protein
#residues 1-47,'E',49-71,'PV',72-128 ##label PRA
REFERENCE A93928
#authors Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
#journal Proc. Natl. Acad. Sci. U.S.A. (1982) 79:6018-6022
#title Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain and identification of two genomic C-gamma genes.
#cross-references M01D:83299917
#accession A93928
#molecule_type mRNA
#residues 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 ##label MAR
#note this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker, 185-Ala

REFERENCE A90245
#authors Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
#journal Biochem. J. (1970) 116:249-259
#title Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.
#cross-references M01D:70110015
#accession A90245
#molecule_type protein
#residues 132-143,'E',145-161 ##label FRU
REFERENCE A94416
#authors Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
#book In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, Stockholm, 1967
#accession A94416
#molecule_type protein
#residues 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',234-245,'D',247-255,'G',257-259,'D',261-265,'D',267-279,'W',281-283,'S',285-322 ##label HIL
#note this has the e15 allotypic marker, 185-Ala
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-82 #domain immunoglobulin homology #label ICG1\
130-199 #domain immunoglobulin homology #label ICG2\
236-303 #domain immunoglobulin homology #label ICG3
SUMMARY #length 323 #molecular-weight 35404 #checksum 1467
```

```
Query Match 48.2%; Score 1669; DB 2; Length 323;
Best Local Similarity 70.0%; Pred. No. 2.64e-167;
Matches 229; Conservative 46; Mismatches 45; Indels 7; Gaps 3;

Db 4 kapsvfplapccgdtosvtlglclvkgylepvtvtnsgtltnvgvtfpvgsqsgly 63
|||||
Qy 152 KGPSVFLAPSSKTSGGTAALGLVKDYFPEPVTVMNSGALTSVHTFPAVQLSSGLY 211
|||||

Db 64 elssvsvtsas---qprtcnvahpatntkvdkvapstscskp-tcpp---pellggpsv 116
|||||

Qy 212 SLSSVTPVPSLSLGTQTYICNVNHPKSPNTKVDKAEPKSCDKTHTCPCPAPELLGGSV 271
|||||

Db 117 fifppkpkdtlmisrtpevtcvvvdsgddpevftwyinneqvrtarplreqfnsti 176
|||||
Qy 272 FIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATPKREEYNSTY 331
|||||

Db 177 rvwtlptlthqdwlrgekfkckvhnkalpapietkiskarggqplepkvymgppreles 236
|||||
```

Search completed: Tue Dec 17 15:30:15 1996  
Job time : 52 secs.

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	2339	67.5	330	3	GC1_HUMAN	IG GAMMA-1 CHAIN C RE	0.00e+00
2	2133	61.5	326	3	GC2_HUMAN	IG GAMMA-2 CHAIN C RE	0.00e+00
3	2133	61.5	327	3	GC4_HUMAN	IG GAMMA-4 CHAIN C RE	0.00e+00
4	1669	48.2	323	3	GC_RABIT	IG GAMMA CHAIN C REGI	0.00e+00
5	1616	46.6	329	3	GC2_CAVPO	IG GAMMA-2 CHAIN C RE	0.00e+00
6	1590	45.9	290	3	GC3_HUMAN	IG GAMMA-3 CHAIN C RE	0.00e+00
7	1584	45.7	329	3	GC3_MOUSE	IG GAMMA-3 CHAIN C RE	0.00e+00
8	1582	45.6	326	3	GC1_RAT	IG GAMMA-1 CHAIN C RE	0.00e+00
9	1570	45.3	398	3	GC3M_MOUSE	IG GAMMA-3 CHAIN C RE	0.00e+00
10	1566	45.2	324	3	GC1_MOUSE	IG GAMMA-1 CHAIN C RE	0.00e+00
11	1559	45.0	329	3	GC2_RAT	IG GAMMA-2C CHAIN C R	0.00e+00
12	1559	45.0	393	3	GC1M_MOUSE	IG GAMMA-1 CHAIN C R	0.00e+00
13	1549	44.7	330	3	GC4A_MOUSE	IG GAMMA-2A CHAIN C R	0.00e+00

RESULT	1
ID	GC1 HUMAN STANDARD; PRT; 330 AA.
AC	P01857;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, SEQUENCE UPDATE)
DT	01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE	IG GAMMA-1 CHAIN C REGION.
GN	IGHG1.
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
[1]	
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 82274238.
RA	ELLISON J.W., BERSON B.J., HOOD L.E.;
RL	NUCLEIC ACIDS RES. 10:4071-4079(1982).
[2]	
RP	SEQUENCE OF I-135 (MYELOMA PROTEIN EU).
RX	MEDLINE; 71064024.
RA	CUNNINGHAM B.A., RUTISHAUSER U., GALL W.E., GOTTLIEB P.D.,
RA	MAXDAL M.J., EDELMAN G.M.;
RL	BIOCHEMISTRY 9:3161-3170(1970).
[3]	
RP	SEQUENCE OF 136-329 (EU).
RX	MEDLINE; 71064025.
RA	RUTISHAUSER U., CUNNINGHAM B.A., BENNETT C., KONIGSBERG W.H.,
RA	EDELMAN G.M.;
RL	BIOCHEMISTRY 9:3171-3181(1970).



RN [4]  
 RP SEQUENCE (MYELOMA PROTEIN NIE).  
 RX MEDLINE; 77070269.  
 RA PONTING L H., HILSCHMANN N.;  
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1571-1604 (1976).  
 RN [5]  
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
 RX MEDLINE; 83289131.  
 RA SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N.;  
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 364:713-747 (1983).  
 RN [6]  
 RP DISULFIDE BONDS.  
 RX MEDLINE; 71064027.  
 RA CALL W.E., EDELMAN G.M.;  
 RL BIOCHEMISTRY 9:3188-3196 (1970).  
 RN [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE; 77070267.  
 RA DREKER L., SCHWARZ J., REICHEL W., HILSCHMANN N.;  
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1515-1540 (1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE; 81208100.  
 RA DEISENHOFER J.;  
 RL BIOCHEMISTRY 20:2361-2370 (1981).  
 CC -!- NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS,  
 CC 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM  
 CC (NON-1) MARKERS.  
 CC -!- NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.  
 CC -!- EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177,  
 CC 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.  
 CC -!- KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198,267&272.  
 DR EMBL; J00228; J00228.  
 DR PIR; A02146; GHU.  
 DR PDB; 1FC1; 15-JUL-92.  
 DR PDB; 1FC2; 15-JUL-92.  
 DR MIM; 147100; 11TH EDITION.  
 DR PROSITE; PS00290; IG MHC.  
 KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; 3D-STRUCTURE.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 223 CH2.  
 FT DOMAIN 224 330 CH3.  
 FT DISULFID 27 83  
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 144 204  
 FT DISULFID 250 308  
 FT CARBOHYD 180 180  
 FT VARIANT 97 97 K -> R (IN GIM(3) MARKER).  
 FT VARIANT 239 239 D -> E (IN GIM(NON-1) MARKER).  
 FT VARIANT 241 241 L -> M (IN GIM(NON-1) MARKER).  
 FT MOD\_RES 330 330 REMOVED POST-TRANSLATIONALLY.  
 FT STRAND 123 126  
 FT TURN 130 134  
 FT TURN 136 137  
 FT STRAND 141 148  
 FT STRAND 158 162  
 FT TURN 163 164  
 FT STRAND 165 166  
 FT STRAND 175 178  
 FT STRAND 183 190

FT HELIX 193 197  
 FT TURN 198 199  
 FT STRAND 202 206  
 FT STRAND 215 219  
 FT STRAND 227 227  
 FT STRAND 230 234  
 FT HELIX 238 240  
 FT TURN 241 242  
 FT STRAND 245 256  
 FT STRAND 260 266  
 FT TURN 267 268  
 FT STRAND 269 270  
 FT STRAND 274 276  
 FT STRAND 280 281  
 FT TURN 283 284  
 FT STRAND 287 296  
 FT HELIX 297 301  
 FT TURN 302 303  
 FT STRAND 306 312  
 FT TURN 313 314  
 FT TURN 316 317  
 FT STRAND 320 324  
 SQ SEQUENCE 330 AA; 36106 MM; 642285 CN;  
 Query Match 67.5%; Score 2339; DB 3; Length 330;  
 Best Local Similarity 99.7%; Pred. No. 0.00e+00;  
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 1 astkqpsvflapssktsqgtaalgcLvkdyfpepytvswngaltsgvhtfpavlgss 60  
 Qy 149 ASTKGSVFELAPSSKTSGGTAALGCLVKDYFPEPYTVSWNSGALTSGVHTFPVAVLGSS 208  
 Db 61 glyslasvvtvpsslgtctyicnvnhkpsntkvdkkvepkcdkthtcpcpapellgg 120  
 Qy 209 GLYSLSVVTVPPSSLGTTQYICNVNHPKSNKYDKRAEPKSCDKTHTCPCPAPPELLGG 268  
 Db 121 psvflfpkpkdtlmirtpevtcvvvdsvedpevkfnwydvgevhnaktkpreecyn 180  
 Qy 269 PSVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVKFNWYDVGEVHNATKPREQYN 328  
 Db 181 atyrwsvltvlhqdwlngkeyckvsnkalpapietklskagqprepytllpperde 240  
 Qy 329 STYRWVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGPREPVYTLPPSRDE 388  
 Db 241 ltknqvslctlvkfypsdiaewesngqpennkttppvldsdgsfflyskltvdkerw 300  
 Qy 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 448  
 Db 301 qqgnvfscsvmhcalhnyhtqklsLspak 330  
 Qy 449 QQGNVFCSVMHCAHNYHTQKLSLSPGK 478  
 RESULT 2  
 ID GC2 HUMAN STANDARD; PRT; 326 AA.  
 AC P01859;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE IG GAMMA-2 CHAIN C REGION.  
 GNIGHG2.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82197621.
RA ELLISON J.W., HOOD L.E.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE; 81007873.
RA WANG A.-C., TUNG E., FUDENBERG H.H.;
RL J. IMMUNOL. 125:1048-1054(1980).
RN [3]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE; 80001357.
RA CONNELL G.E., PARR D.M., HOFMANN T.;
RL CAN. J. BIOCHEM. 57:758-767(1979).
RN [4]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE; 80114419.
RA HOFMANN T., PARR D.M.;
RL MOL. IMMUNOL. 16:923-925(1979).
RN [5]
RP ZIE, REVISIONS TO 25; 59; 60 AND 264-268.
RA HOFMANN T., PARR D.M.;
RL SUBMITTED (MAR-1980) TO THE PIR DATA BANK.
RN [6]
RP SEQUENCE OF 1-121 (DOT).
RA STOPPINI M., BELLOTTI V., NEGRI A., MERLINI G., GARVER F., FERRI G.;
RL EUR. J. BIOCHEM. 0:0-0(1995).
RN [7]
RP MYELOMA PROTEIN SA, DISULFIDE BONDS.
RX MEDLINE; 72033500.
RA MILSTEIN C., FRANGIONE B.;
RL BIOCHEM. J. 121:217-225(1971).
RN [8]
RP SA, DISULFIDE BONDS.
RX MEDLINE; 69064124.
RA FRANGIONE B., MILSTEIN C., PINK J.R.L.;
RL NATURE 221:145-148(1969).
DR EMBL; V00554; V00554.
DR PIR; A02148; G2RU.
DR HSP; P01857; IBBJ.
DR MIM; 147110; 11TH EDITION.
DR PROSITE; PS00290; IG_MHC.
KW IMMUNOGLOBULIN C REGION.
FT NON TER 1 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 219
FT DOMAIN 220 326
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 102 102
FT DISULFID 103 103
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 140 200
FT DISULFID 246 304
FT VARIANT 60 60
FT SITE 156 156
FT MOD RES 326 326
SQ SEQUENCE 326 AA; 35884 MW; 629390 CN;
S -> A (IN MYELOMA PROTEINS TIL & ZIE).
AT OR NEAR THE COMPLEMENT-BINDING SITE.
REMOVED POST-TRANSLATIONALLY (PROBABLE).

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Query Match 61.5%; Score 2133; DB 3; Length 326;  
Best Local Similarity 90.9%; Pred. No. 0.00e+00;

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Matches 300; Conservative 15; Mismatches 11; Indels 4; Gaps 3;
Db 1 aatkgpavfplapcstrsteaalgclvkdypvptvawnsagaltgvtftfavlqes 60
Qy 149 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 208
Db 61 gylasavvtvpsenfgtqtvcnvdhkpentkvdktkverkcc--ve-cppcpappv-ag 116
Qy 209 GLYLSLSSWVTPESSSLGTQTYICNNVHKGNTKDKAEKPCDKTHTCPCPAPELLGG 268
Db 117 psvfifppkpkdtlmisrtpetvctvvdvshedpevfqfnwydvgevhnaktktpreedfn 176
Qy 269 PSVFLFPKPKDITLMSRTPETVCTVVDVSHEDPEVFNWYDVGVEVHNKTKPREEDYN 328
Db 177 stfrvsvltvvhqdwlnqkeyckvknkglpapietkietkkgqprepqvvtlpsree 236
Qy 329 STYRWVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388
Db 237 mtknqvslclvkgfypsdiavewsnsgpennnykttppmldsdgsfflyskltvdkerw 296
Qy 389 LTRKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 448
Db 297 qggnvfscavmhealhhvhtqkelaelpgk 326
Qy 449 QGQNVFSCVMHEALHHVHTQKLSLSLSPGK 478
RESULT 3
ID GC4 HUMAN STANDARD; PRT; 327 AA.
AC P01861.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG GAMMA-4 CHAIN C REGION.
GN IGHG4.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83157104.
RA ELLISON J.W., BUXBAUM J.N., HOOD L.E.;
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE; 70207560.
RA PINK J.R.L., BUTTERY S.H., DE VRIES G.M., MILSTEIN C.;
RL BIOCHEM. J. 117:33-47(1970).
DR PIR; A02150; G4HU.
DR HSP; P01857; IBBJ.
DR MIM; 147130; 11TH EDITION.
DR PROSITE; PS00290; IG_MHC.
KW IMMUNOGLOBULIN C REGION.
FT NON TER 1 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 220
FT DOMAIN 221 327
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 141 201
FT DISULFID 247 305
INTERCHAIN (WITH A LIGHT CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).

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[illegible]

QY	266	LGCP	SVFLFPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	325
Db	176	qynttfv	esvipiqhqdwlrgkhefckvynkalpapietkiaktkgprmpdvytlpps	235
QY	326	QYNSTYRV	SVLTLVHQLDMLNGEKYCKVSNKALPAPTEKTSKAGQPREPQVYTIPTPS	385
Db	236	rdelsk	svvtcllinffpadihveasrvvsekeykntpiiedadgsyflyekltv	295
QY	386	RDLTKNQVSL	ITCLVKGYFSDIAVENESGQP--ENNKTTPPVLDSDGSFFLYSKLTV	443
Db	296	dksadvg	gtvytcsvmhealnhhvtqkaisrpg	329
QY	444	DKSRMQGN	VFSCSYMHEALHNHYTKLSISPG	477
RESULT 6				
ID	GC3	HUMAN	STANDARD;	PRT; 290 AA.
AC	P01860;			
DT	21-JUL-1986	(REL. 01, CREATED)		
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)		
DT	01-FEB-1991	(REL. 17, LAST ANNOTATION UPDATE)		
DE	IG	GAMMA-3 CHAIN C REGION (HEAVY CHAIN DISEASE PROTEIN) (HDC).		
GN	IGHG3.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RX	SEQUENCE (DISEASE PROTEIN WIS).			
RY	MEDLINE; 81021548.			
RA	FRANGIONE B., ROSENWASSER E., PRELLI F., FRANKLIN E.C.;			
RL	BIOCHEMISTRY 19;4304-4308(1980).			
RN	[2]			
RP	NORMAL GAMMA-3 CHAINS, REVISIONS TO 12-97 OF PROTEIN WIS.			
RX	MEDLINE; 77118561.			
RA	MICHAELSEN T.E., FRANGIONE B., FRANKLIN E.C.;			
RL	J. BIOL. CHEM. 252:983-989(1977).			
RN	[3]			
RP	DISEASE PROTEIN ZUC, REVISIONS TO 59-289 OF PROTEIN WIS.			
RX	MEDLINE; 77021516.			
RA	WOLFSTEIN-TODEL C., FRANGIONE B., PRELLI F., FRANKLIN E.C.;			
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 71:907-914(1976).			
RN	[4]			
RP	SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).			
RX	MEDLINE; 82247835.			
RA	ALEXANDER A., STEINMETZ M., BARRITAU D., FRANGIONE B.,			
RA	FRANKLIN E.C., HOOD L., BOXBAUM J.N.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 79:3260-3264(1982).			
CC	-1- THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.			
CC	-1- THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE REF. 2.			
CC	-1- DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE CH1 REGION.			
CC	-1- DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.			
CC	-1- DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLASS.			
CC	-1- THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).			
CC	-1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.			
DR	EMBL; J00231; J00231.			
DR	PIR; A02149; G3HUW1.			

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DR HSP; P01857; IFC1.  
DR MM; 147120; 11TH EDITION.  
DR PROSITE; PS00290; IG MHC.  
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.  
FT DOMAIN 12 73 HINGE.  
FT DOMAIN 74 183 CH2.  
FT DOMAIN 184 289 CH3.  
FT REPEAT 29 43  
FT REPEAT 44 58  
FT REPEAT 59 73  
FT MOD RES 1 1  
FT CARBOHYD 6 6  
FT DISULFID 7 7  
FT DISULFID 24 24  
FT DISULFID 27 27  
FT DISULFID 33 33  
FT DISULFID 39 39  
FT DISULFID 42 42  
FT DISULFID 48 48  
FT DISULFID 54 54  
FT DISULFID 57 57  
FT DISULFID 63 63  
FT DISULFID 69 69  
FT DISULFID 72 72  
FT CARBOHYD 140 140  
FT MOD RES 290 290  
FT VARIANT 126 127  
FT VARIANT 134 134  
FT VARIANT 139 139  
FT VARIANT 182 182  
FT VARIANT 227 227  
FT VARIANT 227 227  
FT VARIANT 279 279  
SQ SEQUENCE 290 AA; 32331 MW; 485009 CN;

Query Match 45.9%; Score 1590; DB 3; Length 290;  
Best Local Similarity 90.1%; Pred. No. 0.00e+00;  
Matches 210; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 58 pepkscdtpcpncapellggsvflfpkpkdtlmisrtpevtcvvvdshdpevq 117  
:||||| || |||||  
Qy 246 AEPKSGDKTHCPCPAPPELLGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHDPEVK 305  
:||||| || |||||  
Db 118 fkyvdgqvhnaktkpreqqfnatfrvsvltvhlqmwldgkeyckvsnkalpapie 177  
:||||| || |||||  
Qy 306 FNWYDGVGVHNKTPREQYNSTRVSVLTVLHQMGLNGKEYCKVSNKALPAPIEK 365  
:||||| || |||||  
Db 178 tiaktkgpqpvytlpssreemtknqslclvkgfypsdiavewessgppnnyntt 237  
:||||| || |||||  
Qy 366 TISKAKGQRPQVYTLPSRDELTNRQNSLTLVKGFPYSDIAVWESNGQPNNTKTT 425  
:||||| || |||||  
Db 238 ppmldsdgfflyekltvdkerwqgnifescvmealnhrftqklsapok 290  
:||||| || |||||  
Qy 426 PPVLDSDGSFFLYSKLTVDKSRWQGNVFCVMEALHNHYTKLSLSPGK 478  
:||||| || |||||

RESULT 7  
ID GC3 MOUSE STANDARD; PRT; 329 AA.  
AC P22436;  
DT 01-AUG-1991 (REL. 19, CREATED)  
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)  
DT 01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)  
DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.  
OS MUS MUSCULUS (MOUSE).

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 85027161.  
RA WELS J.A., WORD C.J., RIMM D., DER-BALAN G.P., MARTINEZ H.M.,  
RA TUCKER P.W., BLATTNER F.R.;  
RL EMBO J. 3:2041-2046(1984).  
DR EMBL; J00451; J00451.  
DR PIR; B02156; G3MSC.  
DR HSP; P01857; IFC1.  
DR PROSITE; PS00290; IG MHC.  
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; TRANSMEMBRANE;  
KW ALTERNATIVE SPLICING.  
FT NON TER 1 1  
FT DOMAIN 1 97 CHI.  
FT DOMAIN 98 113 HINGE.  
FT DOMAIN 114 223 CH2.  
FT DOMAIN 224 327 CH3.  
SQ SEQUENCE 329 AA; 36228 MW; 617081 CN;

Query Match 45.7%; Score 1584; DB 3; Length 329;  
Best Local Similarity 63.6%; Pred. No. 0.00e+00;  
Matches 210; Conservative 61; Mismatches 57; Indels 2; Gaps 2;

Db 1 ttapavvplvpgsdtsqssvltlqclvkgfpeptvkwnygalssgvtvsvlge-g 59  
:||||| || |||||  
Qy 150 STKGPVFLPAPSKSTSGTAALGCLVKDYPFVTVVSNWGAALTSVHTPPAVLQSSG 209  
:||||| || |||||  
Db 60 fyeiseltvpsstwsqvtvncvnhpaektelkrieipktpstppgscppgnilgg 119  
:||||| || |||||  
Qy 210 LYSLSVWTPVSSSLCTQYICNVNHNKPSNTKVDKAEKPSCD-KTHTCPAPPELLIG 268  
:||||| || |||||  
Db 120 psvfifpkipkdmiseltkptcvvvdshdpevqfvdhkvhtawtqpreaqyn 179  
:||||| || |||||  
Qy 269 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHDPEVKFNWYDGVGVHNKTPREQYN 328  
:||||| || |||||  
Db 180 aftrvsvlqghdwmrgkfkckvsnkalpapiertiskpgradtqvytippreq 239  
:||||| || |||||  
Qy 329 STRVSVLTVLHQMGLNGKEYCKVSNKALPAPIEKTISKAKGPREQVYTLPPSRDE 388  
:||||| || |||||  
Db 240 mskkkvcltvtntffseaisvewerengeqdykntppildsdgtyflyekltvtdsw 299  
:||||| || |||||  
Qy 389 LTRNQVSLTLVKGFPYSDIAVWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRW 448  
:||||| || |||||  
Db 300 lqgeiftcsvhealnhrhtqklsapok 329  
:||||| || |||||  
Qy 449 QQGNVFCVMEALHNHYTKLSLSPGK 478  
:||||| || |||||

RESULT 8  
ID GC1 RAT STANDARD; PRT; 326 AA.  
AC P20759;  
DT 01-FEB-1991 (REL. 17, CREATED)  
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)  
DE IG GAMMA-1 CHAIN C REGION.  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89232738.  
RA BRUEGGEMANN M.;

RL	EMBO J. 3:2041-2046(1984).
[2]	
RN	SEQUENCE OF 328-398 FROM N.A.
RP	MEDLINE; 8401483.
RX	
RA	KOWAROMY M., CLAYTON L., ROGERS J., ROBERTSON S., KETTMAN J.,
RA	
RA	WALL R.;
RA	NUCLEIC ACIDS RES. 11:6775-6785(1983).
DR	EMBL; J00451; J00451.
DR	EMBL; V01526; V01526.
DR	PIR; A02155; G3MSM.
DR	HSSP; P01857; 1FC1.
DR	PROSITE; PS00290; IG_MHC.
KW	IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; TRANSMEMBRANE;
KW	ALTERNATIVE SPLICING.
FT	NON TER 1 1
FT	DOWAIN 1 FT CH1.
FT	DOWAIN 98 113 HINGE.
FT	DOWAIN 114 223 CH2.
FT	DOWAIN 224 327 CH3.
FT	TRANSMEM 346 362 POTENTIAL.
FT	DOWAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT	CONFLICT 333 333 E -> G (IN REF. 2).
FT	CONFLICT 342 342 E -> Q (IN REF. 2).
FT	CONFLICT 388 388 P -> F (IN REF. 2).
SQ	SEQUENCE 398 AA; 43929 MW; 896835 CN;

[illegible][illegible]

OC	EUTHERIA; RODENTIA.
RN	(1)
RN	SEQUENCE FROM N.A.
RP	MEDLINE; 80045036.
RX	HONJO T., OBATA M., YAMAWAKI-KATAOKA Y., KATAOKA T., KAWAKAMI T., TAKAHASHI N., MANO Y.; CELL 18:559-568(1979).
RL	[2]
RN	SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RP	MEDLINE; 80202559.
RX	OBATA M., YAMAWAKI-KATAOKA Y., TAKAHASHI N., KATAOKA T., SHIMIZU A., MANO Y., SEIDMAN J.G., PETERLIN B.M., LEDER P., HONJO T.; GENE 9:87-97(1980).
RL	[3]
RN	SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RP	MEDLINE; 80012837.
RX	ROGERS J., CLARKE P., SALSBER W.; NUCLEIC ACIDS RES. 6:3305-3321(1979).
RL	[4]
RN	SEQUENCE (MYELOMA PROTEIN MOPC 21).
RP	MEDLINE; 78242288.
RX	ADETUGBO K.; J. BIOL. CHEM. 253:6068-6075(1978).
RL	[5]
RN	DISULFIDE BONDS (MOPC 21).
RP	MEDLINE; 73008889.
RX	SVASTI J., MILSTEIN C.; BIOCHEM. J. 126:837-850(1972).
RA	BIOCHEM. J. 126:837-850(1972).
DR	EMBL; V00793; V00793.
DR	EMBL; V00795; V00795.
DR	PIR; A02159; GIMS.
DR	HSP; P01679; IBAF.
DR	PROSITE; PS00290; IG_MHC.
KW	IMMUNOGLOBULIN C REGION; ALTERNATIVE SPLICING; GLYCOPROTEIN.
FT	NON TER 1 1
FT	DOMAIN 1 97 CHI.
FT	DOMAIN 98 110 HINGE.
FT	DOMAIN 111 217 CH2.
FT	DOMAIN 218 324 CH3.
FT	DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 138 198 INTERCHAIN (WITH A HEAVY CHAIN).
FT	CARBOHYD 174 174 REMOVED POST-TRANSLATIONALLY.
FT	DISULFID 244 302
FT	MOD RES 324 324
SQ	SEQUENCE 324 AA; 35704 MW; 601902 CN;
Query Match	45.2%; Score 1566; DB 3; Length 324;
Best Local Similarity	62.1%; Pred. No. 0.00e+00;
Matches	205; Conservative 63; Mismatches 56; Indels 6; Gaps 4;
Db	1 aktppsyytlapgsaaqntnmvlgclvkgyfpeptvtwnegalsagvhftfpavlgcd 60           : : :             :       :       :       :       :
Qy	149 ASTKGSEVFP LAPSSKSTSGGTAAALGCLVKVDPEPPTVSNWSGALTSGVHTTFAVLQSS 208           : : :             :       :       :       :       :
Db	61 -lytlesavtypsrpsretvtcnvapaeastkvdkkivprdcg-ckpci-ctypdev--- 114   :       : :    :    :       :    :    :    :    :    :
Qy	209 GLYSLSVVTPVPSSLTGITVCYNWNHKSNTKVDAEPKSCDKTHTCPAPPELLGG 268   :       :    :       :    :       :    :       :    :       :
Db	115 ssvfiappkpdkvltiltpkvtcvvvdiiskddbevqsfwvdvvehtactqpreefn 174 :       :       :    :       :    :       :    :       :    :       :

QY	269	PSVFLEPPRPKADTLMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	328
Db	175	stfrsvslpimhqdwlngkcfkcrvnsaafpapietkietkgrkpaqvytipppkeq	234
QY	329	STRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVWITLPSRDE	388
Db	235	makdkvseltcmittfdffeditvewqngqpaenykntcpimntngsfvyvsklnvqkew	294
QY	389	LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYTKTTPVLDSDGSEFFLYSKLTVDKSRW	448
Db	295	eagntftscvlheglhnhhtekslshspk	324
QY	449	QOGNWFSCVMHEALHNHYTKQSLISLSPGK	478
RESULT	11		
ID	GCC RAT	STANDARD;	PRT; 329 AA.
AC	P20762;		
DT	01-FEB-1991 (REL. 17, CREATED)		
DT	01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)		
DT	01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)		
DE	IG GAMMA-2C CHAIN C REGION.		
OS	RATTUS NORVEGICUS (RAT).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
CC	EUTHERIA; RODENTIA.		
RC	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE; 88166903.		
RX	BRUEGGEMANN M., DELMASTRO-GALFRE P., WALDMANN H., CALABI F.;		
RL	EUR. J. IMMUNOL. 18:317-319(1988).		
DR	EMBL; X07189; X07189.		
DR	PIR; S00847; S00847.		
DR	HSSP; P01857; IFC1.		
DR	PROSITE; P500290; IG MHC.		
KW	IMMUNOGLOBULIN C REGION.		
FT	NON TER 1 1		
FT	DOMAIN 1 97		CHI.
FT	DOMAIN 98 113		HINGE.
FT	DOMAIN 114 222		CH2.
FT	DOMAIN 223 329		CH3.
FT	DISULFID 15 15		INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID 27 82		
FT	DISULFID 111 111		INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 113 113		INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 143 203		
FT	DISULFID 249 307		
SQ	SEQUENCE 329 AA; 36571 MW; 626020 CN;		
Query Match	45.0%;	Score 1559;	DB 3; Length 329;
Best Local Similarity	61.8%;	Pred. No. 0.00e+00;	
Matches	204;	Conservative 61;	Mismatches 64; Indels 1; Gaps 1;
Db	1	arttapsvylpvcqscgtselvtlglcvkgyfpepvtvknegalsgvtfpavlgeq	59
QY	149	ASTKGFVFPPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHFFPVLASS	208
Db	60	qlvtlssvtpastwsqvtvcavahpatkenlikriepripkprptdicscdnlg	119
QY	209	GLYSLSSVWVPPSSSIGTQTYICNVNHNKPSNTKVDKRAEPEKSCDKTHTCPPELIGG	268
Db	120	psvfiipkpkdmlitltpkvtcvvdvseeepdvqfwdvnrvtfaqtqphseqln	179
QY	269	PSVFLEPPRPKADTLMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	328



Db	180	gtrfvvslhghqdmagsefkckvnmkdlpsiektisxprgkatpovtippreq	239
Qy	329	stvrsvsvltvltqdwlmngckvksnkaklpadtektiskagqprepovvttppsrde	388
Db	240	msknvsvllcmvtsfypasieavewerngeqdykntlpvldsdesyflysklavtdew	299
Qy	389	ltnkqvstlclvrkgeypsdjavewngcpennyktpptpvldsgsflysklvtvdkswr	448
Db	300	mrqdytcsvvhealnhtknlslrspgk	329
Qy	449	qogwvfscsvmhealnhyvtokslslspgk	478

RESULT	12	GCIM MOUSE	STANDARD;	PRT;	393 AA.
ID	AC				
DT	21-JUL-1986	(REL. 01, CREATED)			
DT	01-AUG-1991	(REL. 19, LAST SEQUENCE UPDATE)			
DT	01-NOV-1995	(REL. 32, LAST ANNOTATION UPDATE)			
DE	IG GAMMA-1	CHAIN C REGION, MEMBRANE-BOUND FORM.			
OS	MUS MUSCULUS	(MOUSE).			
OC	EUKARYOTA;	MEZAOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA;	RODENTIA.			
RN	[1]				
RN	SEQUENCE FROM N.A.				
RX	MEDLINE;	80045036.			
RA	HONJO T.,	OBATA M., YAMAWAKI-KATAOKA Y., KATAOKA T., KAWAKAMI			
RA	TAKAHASHI N.,	MANO Y.;			
RL	CELL 18:559-568	(1979).			
RN	[2]				
RP	SEQUENCE OF 323-393	FROM N.A.			
RX	MEDLINE;	82197626.			
RA	TYLER B.M.,	COWMAN A.F., GERONDAKIS S.D., ADAMS J.M., BERNARD			
RL	PROC. NATL. ACAD. SCI. U.S.A.	79:2008-2012(1982).			
RN	[3]				
RP	SEQUENCE OF 323-366	FROM N.A.			
RX	MEDLINE;	82115295.			
RA	ROGERS J.,	CHOI E., SOUZA L., CARTER C., WORD C.J., KUEHL M.,			
RA	EISENBERG D.,	WALL R.;			
RL	CELL 26:19-27	(1981).			
RN	[4]				
RP	SEQUENCE OF 1-44	FROM N.A.			
RX	MEDLINE;	8222190.			
RA	YAMAWAKI-KATAOKA Y.,	NAKAI S., MIYATA T., HONJO T.;			
RL	PROC. NATL. ACAD. SCI. U.S.A.	79:2623-2627(1982).			
CC	-1-	ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO			
CC	SPECIES FOR IG	GAMMA CHAINS. THE MAJOR SPECIES ENCODES SEC			
CC	GAMMA CHAINS. A	LESS ABUNDANT SPECIES APPEARS TO ENCODE SEC			
CC	BOUND CHAINS IN	THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODE			
CC	IN SEPARATE EXONS,	THAT IS HOMOLOGOUS WITH THE MEMBRANE-BO			
CC	SEGMENT OF WD	CHAINS.			
DR	EMBL;	V00793; V00793.			
DR	PIR;	B02159; GINSM.			
DR	HSSP;	P01857; 1BAF.			
DR	PROSITE;	PS00290; IG MHC.			
KW	IMMUNOGLOBULIN	C REGION; ALTERNATIVE SPLICING; TRANSMEMBRANE;			
KW	GLYCOPROTEIN.				
FT	NON TER	1			
FT	DOMAIN	1			CHI.
FT	DOMAIN	98			HINGE.
FT	DOMAIN	111			CH2.
FT	DOMAIN	218			CH3.
FT	DISULFID	27			82
FT	DISULFID	102			102
FT	INTERCHAIN	(WITH A LIGHT CHAIN).			

[illegible][illegible]







CC tetrapeptide motif GPCR, i.e. the Principal Neutralising  
CC Determinant common to the V3 loop of different HIV isolates.  
CC A recombinant Ab was produced in which the H chain V region was  
CC derived from 447-52D and to which a signal sequence and a H chain  
CC intronic sequence are appended, fused to a fragment contg. a short  
CC intronic segment of the human gamma 1 C region and the human gamma  
CC 1 encoding domain in its genomic form.  
SQ Sequence 461 AA;

Query Match 84.6%; Score 2931; DB 8; Length 461;  
Best Local Similarity 96.3%; Pred. No. 5, 92e-228;  
Matches 417; Conservative 16; Mismatches 25; Indels 4; Gaps 4;  
Db 1 evqlvesggllvkgqslrltcvsgftsdvlnwvraqpdkglewvqrikartdgtt 60  
Qy 20 EVQLVESGGGLVQPGGSLRVSAVSGFTSDHYMYWFRQAPKGPFWGFTIRKNGGTT 79  
Db 61 dyaaavkgrftisrdskstiaqlqmslkiEDTAVYYCTT-SYISHCRG-GVYGGYF-E 136  
Qy 80 EYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTT-SYISHCRG-GVYGGYF-E 136  
Db 120 vwlgkttvvasaetkgspevfplapsketaggtaalglcvkdyfpepvtvsmnegalts 179  
Qy 137 FMGGALVTVSSASTKGPVFPPLAPSSKTSGGTAALGLCVKDYFPEPVTVSMNSGALTS 196  
Db 180 gvhftfavlqasglyslsavvtpssalgtqylcnvnhkpsntkvdskvepscdktht 239  
Qy 197 GVHTFPAVLQSSGLYSLSSVTVSPSSLTQTQYICNVNHKPSNTKVDKAEKPSKDTHT 256  
Db 240 cpcpapelggpsvflfpkpkdtlmsirtpevtcvvwdvshedpevkfmyvqdvveh 299  
Qy 257 CPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSDHEDPEVKFNWYVDGVEVH 316  
Db 300 naktkpreegnystyrsvvltvthqdwlngkeyckvkenkalpepietkiskagpre 359  
Qy 317 NAKTKPREEQYNSTYRWVSVLTVLHQDLNGLNGKEYCKVKNKALPAPTEKTSKARKQPRE 376  
Db 360 pqvvtlpprdeltknqvltclvkgyfypsdiaveesngqpennnykttppvldedgff 419  
Qy 377 PQVYTLPPSRDELTKNQVSLTCLVKGYFSDIAVWESNGQPENNYKTTFPVLDSDGSFF 436  
Db 420 lyskitvdksrwqggnvfscsvmhcalhnhytqkslelepqk 461  
Qy 437 LYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 478  
RESULT 2  
ID R20057 standard; Protein; 475 AA.  
AC R20057;  
DT 25-MAR-1992 (first entry)  
DE Heavy chain of 306 anti-HIV antibody.  
KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;  
KW complementarity determining region.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= signal  
FT Region 20..49  
FT /label= Framework\_1  
FT Region 50..54  
FT /label= CDR-1  
FT Region 55..68  
FT /label= Framework\_2  
FT Region 69..85

FT /label= CDR\_2 86..117  
FT Region  
FT /label= Framework\_3  
FT Region 118..134  
FT /label= CDR\_3 135..145  
FT Region  
FT /label= Framework\_4  
FT Region 146..475  
FT /label= Constant\_region  
PN W09118983-A.  
PD 12-DEC-1991.  
PF 28-MAY-1991; 100067.  
PR 29-MAY-1990; AT-001178.  
PA (JUNG/) JUNGBAUER A.  
PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;  
DR WPI; 92-007468/01.  
DR N-PSDB; Q20066.  
PT Recombinant protein which binds to complex viral antigen and  
PT HIV-1 - contains variable region of antibody derived from 306  
PT cell line, used for detecting HIV-1 antigen  
PS Claim 2; Page 24; 52pp; German.  
CC The variable region of the heavy chain is used in a recombinant  
CC protein with the variable region from the kappa light chain of 306,  
CC the two V regions being joined by a linker. The recombinant protein  
CC binds to HIV gp160.  
CC See also Q20067 and Q20068.  
SQ Sequence 475 AA;

Query Match 84.6%; Score 2931; DB 3; Length 475;  
Best Local Similarity 86.4%; Pred. No. 5, 92e-228;  
Matches 413; Conservative 25; Mismatches 37; Indels 3; Gaps 3;  
Db 1 melglswiflailkvqceqlvesggllvqparlrlecaagftfndyamhwvraqp 60  
Qy 1 MGWSLILFLVAVATRVQCEQLVESGGGLVQPGGSLRVSAVSGFTSDHYMYWFRQAP 60  
Db 61 gkglewvsgl-sw-dassigiyadavkgrftisrdnknaknalyqmnsraedmalyyevkg 118  
Qy 61 CKGPEWVGFTIRKNGGTEYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTS 120  
Db 119 -rdydsdgyftvafdlwgggtmvtvssastkgspevfplapsketaggtaalglcvkdy 177  
Qy 121 YISHCRGCVYGGYFEEWQCALVTVSSASTKGPVFPPLAPSSKTSGGTAALGLCVKDY 180  
Db 178 fpepvtvsmnegaltqevhtfpavlqasglyslsavvtpssalgtqylcnvnhkpsnt 237  
Qy 181 PPEPVTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVSPSSLTQTQYICNVNHKPSNT 240  
Db 238 kvdkkvepscdkthtccpcaapelggpsvflfpkpkdtlmsirtpevtcvvvdvehe 297  
Qy 241 KYDKKAEKPSKDKTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSH 300  
Db 298 dpevkfmyvqdvvevhnaktkpreegnystyrsvvltvthqdwlngkeyckvkenkalp 357  
Qy 301 DPEVKFNWYVDGVEVHNKTPREEQYNSTYRWVSVLTVLHQDLNGLNGKEYCKVKNKALP 360  
Db 358 apiektiskakgprepqvvtlppsrdeitknqvltclvkgyfypsdiaveesngqpenn 417  
Qy 361 APIEKTISKAKGPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSDIAVWESNGQPE 420  
Db 418 nykttppvldsdgsfflyskltvdksrwqggnvfscsvmhcalhnhytqkslelepqk 475  
Qy 421 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 478

RESULT	3	
ID	R24442 standard; Protein; 481 AA.	
AC	R24442;	
DT	02-JAN-1992 (first entry)	
DE	Sequence of antibody molecule IgG1.	
KW	Antibody; immunoglobulin G1.	
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	Misc difference 308	
FT	/label= N	
FT	/note= "Substn. to create glycan addition site"	
FT	Misc difference 310	
FT	/label= S	
FT	/note= "see above"	
FT	Misc difference 321	
FT	/label= N	
FT	/note= "see above"	
FT	Misc difference 329	
FT	/label= N	
FT	/note= "see above"	
FT	Misc difference 331	
FT	/label= S	
FT	/note= "see above"	
FT	Misc difference 356	
FT	/label= N	
FT	/note= "see above"	
FT	Misc difference 369	
FT	/label= N	
FT	/note= "see above"	
FT	/note= "see above"	
PD	11-JUN-1992.	
PE	18-NOV-1991; U08605.	
PR	23-NOV-1990; US-618314.	
PA	(GEO ) GEN HOSPITAL CORP.	
PI	Seed B, Walz G;	
DR	WPI; 92-216789/26.	
DR	N-PSDB: Q25443.	
PT	Inhibition of cell adhesion mediated through ELAM-1 mol. binding	
PT	- used in treating chronic inflammation, rheumatoid arthritis,	
PT	psoriasis, etc.	
PS	Disclosure; Fig 1; 46pp; English.	
CC	The IgG1, in its nascent form, bears no sialyl-Lex side chains. The	
CC	inventors designed a molecule including several such sites for	
CC	attachment of sialyl-Lex side chains (see R24442, FT). The	
CC	additional N-linked glycosylation sites are introduced at locations	
CC	which impair complement fixing and Fc receptor binding ability. They	
CC	are preferably located in the CH2 region of the Ig molecule.	
CC	Antibodies bearing multiple sialyl-Lex determinants are useful for	
CC	disrupting undesirable interactions between cells or proteins.	
CC	Disrupting this interaction has therapeutic applications, for	
CC	example, in minimising inflammation following tissue injury.	
SQ	Sequence 481 AA;	

	Query Match	83.1%	Score 2880;	DB 5;	Length 481;
	Best Local Similarity	85.2%;	Pred. No. 9,99e-224;		
	Matches	408;	Conservative	26;	Mismatches 42;
				Indels	3;
				Gaps	2;
Db	5	mdwtwrlffvvaatgvsqvlvgsgaevkkgpsvkvscasggtfasyaiswvrga	64		
		:   :           :   :   :   :			
Qy	1	MGWSL-ILLFLVAVTRVQCEVQLVSGGGGLVQPGGSLRVSCAVSGFTFSDHYMYFRQA	59		
Db	65	pggglewmggii--plfqtanyaqkfgrvrtitadetstcaymelsslreedtavyycar	122		
		:           :           :           :           :			

Qy	60	PGKGPVWGFIRNKPNGGTTEYAAASVKDRFTISRDDSKSIAYLQMSSEKIEDTAVYCYCTT	119
Db	123	dnqaycsqgcyagwfdpwagdtlvrtvsaatkpqsrvfplapsketsegtaalgclvkd	182
Qy	120	SYISHCRGVCYCYGFYERWQGLVTVSSASTKQSVFPJAPSSKTSGTAAGLCLVKD	179
Db	183	yfpvptvsmnagaltgshvfpavlaqsglylsavvtvpssalgtqyicnnvhkpsn	242
Qy	180	YFPEPTVYWNNSGALTSGVHTEFAVLQSSGLYLSISVWTVPPSSLSLGTQYIYICNNVHKPSN	239
Db	243	tkvdkkvpkscdkthtkppcpapeilggpsvflfppkpkdtlmairstpevtcvvvdvsh	302
Qy	240	TKYDKKAEPKSCDKTHTKPPCPAPELLGGFSVFLEFPKPKDTLMAIRSTPEVTCVVVDVSH	299
Db	303	edevkfwnyvdgvevhnaktkpreeqynstyrvavltvlhqdwlngkeyckvsnkal	362
Qy	300	EDPEVKEWNKYVDGVEVHNAKTKPREQYNSYRVSVLTVLHQDWLNGKEYCKVSNKAL	359
Db	363	papietkiskakgpreqvytippderlctknqvsitclvkqfypsdlaveseangpe	422
Qy	360	PAPIETKSKAKGPREQVYTIPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPE	419
Db	423	nmvktppvldsdqsflylskltvdtkerwqgnvfcsmvhaahmhytqkalslpgk	481
Qv	420	NYVKTTPVLDSDGSFFLYSKLTVDKSRMNOGNEFCSYMHFAAHNYHYTKQSISLSPCK	478

RESULT	4
ID	R22757 standard; Protein; 470 kDa.
AC	R22757;
DT	20-OCT-1992 (first entry)
DE	Reshaped CAMPATH-1 antibody heavy chain.
DE	Antigen; CDR; complementarity determining region; graft rejection;
KW	autoimmune diseases; rheumatoid arthritis; allergy.

## RESULT 4

ID R22757 standard; Protein; 470 AA.

AC	R22757;
DT	20-OCT-1992 (first entry)
DE	Reshaped CAMPATH-1 antibody heavy chain.
KW	Antigen; CDR; complementarity determining region; graft rejection;
KS	autoimmune diseases; rheumatoid arthritis; allergy.
OW	Patting rattage

OS	Access	Access	Key	Location/Qualifiers
----	--------	--------	-----	---------------------

FT	Region	50-54	Production, 1980
1	1	1	1
2	2	2	2
3	3	3	3
4	4	4	4
5	5	5	5
6	6	6	6
7	7	7	7
8	8	8	8
9	9	9	9
10	10	10	10
11	11	11	11
12	12	12	12
13	13	13	13
14	14	14	14
15	15	15	15
16	16	16	16
17	17	17	17
18	18	18	18
19	19	19	19
20	20	20	20
21	21	21	21
22	22	22	22
23	23	23	23
24	24	24	24
25	25	25	25
26	26	26	26
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43	43	43	43
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89	89	89	89
90	90	90	90
91	91	91	91
92	92	92	92
93	93	93	93
94	94	94	94
95	95	95	95
96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

FT /note= "Complementarity determining region 1"

FT Region 69.87

FT /note= "Complementarity determining region 2"

FT. Region 101-110

FT /note= "Complementarity determining region 3"

FT peptide 1-19

```
FT /note= "signal peptide"
```

FT	Peptide	20..470	Peptide
FT	Peptide	20..470	Peptide

FT /note= "mature peptide"

PN W09205274-A.

PD 02-APR-1992.

PF 16-SEP-1991: G01578.

PR 17-SEP-1990: GB-020282.

PA (GORM/) GORMAN S D.

PT Clark M B. Cobbald S P. Gorman S D. Waldmann

DB WPT: 92-132139/16.

DR : N-PSDB: 023570.

PT Humanisation of antibodies binding to human C

PT mutation of framework-encoding regions of DNA

PT domain of rat or mouse antibody chain

PS Disclosure: Fig 5: 74pp: English.

CC The sequence is that of the reshaped CAMPATH-

Reshaped CD4 antibody can be used to induce t

CC antigen. It can also be used to alleviate auto-

as rheumatoid arthritis, and to prevent graft

CC to a graft, e.g. an organ graft or a bone marrow graft.

CC also be useful to alleviate allergies. Toleran





P.I. Arima K, Kurihara T, Matsukura S, Nishihara T, Teuruoka N;  
DR WPI; 93-336913/42.  
DR N-PSDB: Q49944.

PT Human anti-hepatitis B surface antigen antibody gene - can be  
 PS used to produce L and H chains of the antibody in large quantity  
 PT Disclosure; Fig 6-8; 45pp; Japanese.  
 CC Polynucleotides encoding the L and H chains of human anti-HBs  
 CC Ab are given in Q4994-Q4994. The Ab can be easily produced in  
 CC large quantities for therapeutic use.  
 CC Sequence 459 AA;  
 SQ

Query Match	81.5%	Score 2024;	DB 8;	Length 459;
Best Local Similarity	88.6%	Pred. No. 4.37e-219;		
Matches 410;	Conservative 14;	Mismatches 28;	Indels 11;	Gaps 5;

```
7 vqcqvqlvesgggvvqpggrslrlscasagftfsnsmhwvrqpqgkglewvavily--dg 64
   |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
17 VQCEVQLVESGGGLVQP GGS LRVSCAVSGFTFSHYMYWFRQAPGKGPEWVGVSIRNKPNG 76
```

```
Db      65 nhkfyadsvkgrftisrdsnkntlylvkslqltadtgvyyc-----i----rdqt-ygvhrf 116
Qv      77 GTTFYASVKDREFTISRDSSKSIAVIOMSSIKIEDTAVVCTTSYISHRGSGVCYGCV-F 135
```

```

117 dswgqgltvtvssastkgsvfplapsskstsggtaalqclvkdyfpepvtvswngala 176
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
136 fswgcacitvttvssaenwcdvstidpssckscscctaaagcttztvtdvtdvmytvsngacat 195

```

Db 177 sgvhtfpavlqssg,lyslssvvtvpssslqtqtienvnhkpsantkvdkkvpkscdkth 236

Db 237 tcpcpapellggpsvflfpbkpdktlmistrtpvtcvvvdvshdpvkfnhwyvdgvev 296

```
Db      297 hnaktkpreedynstyrvvsvltvlnhqdwlngkeyckvsnkalpapiektsekakagpr 356
```

Db 357 epqvytlppsrde l t knqvs l t clvk g fypsdiavewesngqpnnyk t t p p v l d s d g s f 416

Db 417 flyskltvdksrwqqgnvfscsvmhealhnhytqksls!spgk 459

RESULT 7

DE	Humanised MaEl Version 1 (intact IgG)	heavy chain.
DT	05-JUL-1993 (first entry)	
AC	R3331;	
AC	R3331;	
DT	05-JUL-1993 (first entry)	
DE	Humanised MaEl Version 1 (intact IgG)	heavy chain.

KW Antisbody; mrgn affinity; FCER; low affinity; FcE2;  
KW IgE receptor; histamine; mast cell; basophil; Kabat;  
KW CDR; murine; MAELI; Fab; humae11vl.  
QS Synthetic.

FN W09304173-A.  
PD 04-MAR-1993.  
PF 14-AUG-1992; U06860.  
DD 14-AUG-1991; HS 744759

PR 07-MAY-1992; US-R/9495.  
PA (GETH ) GENENTECH INC.  
PI Jardieu PM, Presta LG;

DR WPI; 93-094004/11.  
PT Polypeptide(s) binding to specific Fc epsilon receptors - act as  
PT IgE antagonists; useful for treating and preventing IgE-mediated  
PT disorders e.g. allergies  
PS Example 4; Fig 3; 113pp; English.  
CC Residues were selected from MaEII and inserted or substituted into  
CC a human Fab antibody background (Vh region Kabat subgroup III and V1  
CC region kappa subgroup I). A first version, humae11v1 or version 1 is  
CC given below. The affinity of version 1 was assayed and found to be  
CC ca. 100 times lower than that of the donor antibody MaEII.  
CC Therefore, further modifications in the sequence of version 1  
CC were made.

Query Match 81.2%; Score 2813; DB 6; Length 453;  
Best Local Similarity 88.7%; Pred. No. 3.56e-218;  
Matches 410; Conservative 18; Mismatches 22; Indels 12; Gaps 8;

**Db** 1 evqlvesggglvqpggslrlscavsgysitsgyswnwlrqpapkglewastiy--dg-s 57  
|||||  
|||||  
**Qv** 20 EVQLVESGGGLVQPGGSLRVSCAVSGFETSDHYNY-WFOAPGKGPKEVGFIANKPNNGT 78  
|||||  
|||||

```
Db      58   tnrvadvkgrfciisrddskntfylqmnsraedhtavyycarg--shyfg-h-w---hfavw    111
          |:| | | | | | | | :| | | | | | | | | | | | | | | | | | | | | | | 
Qv     79   TEVAASUKOREFTSRDSSKSTAYIOWSMSSKTIEDPAVYCTTSVI SHRCGCCVCYCCEFEW    138
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Db 112 gggtlvtvssastkgkpsvfplapsskstsggtaalgclvkdyfpeptvawnsgalts 171  
|||:|||||  
|||:|||||  
O<sup>a</sup> 130 cccacatvmvssasenc--dsytdi ascsksccctaaacttztzvfddvmtvsnscaltts 196  
|||:|||||

[illegible]

Db 232 c p p c p a p e l l g g p s v f l f p p k p k d t l m i s t p e v t c v v d v s h e d p e v k f n w y d g v e v h 291  
=====

Db 292 naktkpreegnystyrvvsvltvlhqdwingkeyckckenkalpapiektiesakgqpre 351

Db 352 ppytlppsreentknqvsltclvkqfypsdiavewesngqpennykttppvldsdasff 411

Db 412 lyskltvdksrwqqgnvfscsmhealhnhytqtslspspgk 453

## RESULT 8

AC R24812;  
DT 28-DEC-1992 (first entry)  
DE Sequence encoded by the chimeric H chain cDNA contained in pTB1373

	Location/Qualifiers
AM	Key
AN	Chimeric monoclonal antibody; anti-fibrin antibody; primer; antithrombotic agent; myocardial infarction therapy.
AW	Synthetic.
OS	Synthetic.
FH	Key

FT	Peptide	13..19
FT	/label= Leader	
FT	Region	20..134
FT	/label= vu	

FT	Region	135..232	
FT	/label= CH1		
FT	Region	233..247	
FT	/label= hinge		
FT	Region	248..357	
FT	/label= CH2		
FT	Region	358..464	
FT	/label= CH3		
FT	Misc difference 465		
FT	/note= "translated stop codon"		
PD	EP-491351-A.		
PD	24-JUN-1992.		
PF	17-DEC-1991; 121591.		
PR	18-DEC-1990; JP-413829.		
PR	11-NOV-1991; JP-294464.		
PI	(TAKE ) TAKEDA CHEM IND LTD.		
PI	Iwasa S, Taka H, Watanabe T, Tada H;		
DR	WPI; 92-209528/26.		
DR	N-PSDB; Q25692.		
PT	Chimeric monoclonal antibodies - contain anti-human fibrin		
PT	antibody light and heavy chain variable and constant for treating		
PT	thrombotic conditions e.g. myocardial infarction		
PS	Example; Figure 11; 87pp; English.		
CC	Plasmid pTB1373 contains the whole length of a mouse-human		
CC	chimeric anti-human fibrin heavy chain cDNA open reading		
CC	frame. It was prepnd. using Poly(A)+ RNA from the anti-fibrin		
CC	chimeric Ab-producing transformant FIB1-H01/X63 as a template		
CC	to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as		
CC	a primer for first strand cDNA synthesis and the 5'C2H and 3'EH		
CC	primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding		
CC	cDNA was amplified. Similarly a human gamma-1 chain CH1 domain		
CC	encoding cDNA and an anti-fibrin antibody VH cDNA and a leader		
CC	peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CH		
CC	respectively as a primer for first strand cDNA synthesis and the		
CC	primer combination of 5'C1H and 3'C2H, of 5'1H and 3'CH and of		
CC	5'SH and 3'1H respectively as primers for PCR. The amplified gene		
CC	products were isolated and used to produce plasmids. After		
CC	confirmation of the cDNA sequence of each plasmid, the cDNA		
CC	encoding LH, VH, CH1 and CH2CH3 were joined together to give		
CC	plasmid pTB1373 contg. the whole length chimeric H chain		
CC	(LH, VH, CH1, CH2CH3), also abbreviated as Igh-F1B,		
QQ	Sequence 466 AA;		
Query Match		81.0%;	Score 2806; DB 5; Length 466;
Best Local Similarity		84.9%;	Pred. No. 1.35e-217;
Matches		406;	Conservative 30; Mismatches 28; Indels 14; Gaps 5;
Db	1	mdsrlnlvllilkgdcvqlvesggglvkgpgsklkscaasgfttfanydmswvrgtp	60
		:   :         :	
Qy	1	MGWSLLILFLVAVATRVCEQVLVESGGGLVPGGSLRVSVCAVSGFTFSRHYMYFRQAP	60
Db	61	errlewaasi---avagttypdcmkqrftierdnarnilylqlslrsedtamycg-n	116
		:       :   :       :   :	
Qy	61	GKGPWVGFIIRNPGNGTTEVAASVKDRFTTISRDSDKSIAYLQMSLKIEDTAVYYCTTS	120
Db	117	f-ad-----dywqgqlrtvessaatkpvpfpapasketsegtaalgclvkd	166
		: : : : :	
Qy	121	YISHCRGGVCGYGFEFWQCALVTVSSASTKGPVFLAPLSKTSKTSGGTAAALGCLWKDY	180
Db	167	fpevtvwmnegalteg rhtfpavlqsglylalsevwtvpsseltgtctyctvnhkpsnt	226
Qy	181	FPEPTVSMNSGALTSC/HTTFAVLQSGGLYSLSSVTVFSSSLGCTQTYICNVNHPKPSNT	240
Db	227	kvdrrvepkscdktktcocpapelllgqpsvflfpkpkpdkdliarietpvtcvvwdvse	286

Qy	241	KVDKAEAPKSCDKTHTCPCPAPELLGGF SVFLFPKPKDPTLMISRTPEVTCVVVDVSH	300
Db	287	dpevkfnwydgvevhnaktkpreegnyrvsvltvlhqdwlngkeyckvknkalp	346
Qy	301	DPEKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP	360
Db	347	apietkiskaggreppqvvtlppsreemtnkqvslctclvkgfypsdiaveesngqpen	406
Qy	361	APIETKISKAGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEESNGQPEN	420
Db	407	nykttppvldsgsflyskltvdkerwqgmvfscsvmhleahnnhtqkalslepqk	464
Qy	421	NYKTTTPVLDSGSFELYSKLTVDKSRHQGNVFCSVMHLEAHNNHTQKSLISLPCK	478
RESULT	9		
ID	R31023	standard; Protein; 476 AA.	
AC	R31023;		
DT	19-MAY-1993	(first entry)	
DE	Antibody D heavy chain.		
KW	Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;		
KW	lymphocyte; hepatitis A virus; HAV; sero; positive; patient;		
KW	murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.		
OS	Synthetic.		
PH	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT	/notes	*Signal peptide*	
FT	Region	20..49	
FT	/label= FR1		
FT	/label= CDR1	50..54	
FT	Region	55..68	
FT	/label= FR2		
FT	/label= CDR2	69..84	
FT	Region	85..113	
FT	/label= FR3		
FT	Region	114..121	
FT	/label= CDR3		
FT	Region	122..132	
FT	/label= FR4		
FT	Domain	133..241	
FT	/label= CH1		
FT	Region	242..262	
FT	/label= HINGE		
FT	Domain	263..379	
FT	/label= CH2		
FT	Domain	380..497	
FT	/label= CH3		
PN	EP-523949-A.		
PD	20-JAN-1993.		
PF	14-JUL-1992; 306420.		
PR	15-JUL-1991; GB-015284.		
PR	01-AUG-1991; GB-016594.		
PR	23-MAR-1992; GB-006284.		
PA	(WELL ) WELLCOME FOUND LTD.		
PI	Crowe JS, Lewis AP;		
DR	WPI; 93-019951/03.		
DR	N-PSDR; Q35099.		
PT	Prodn. of recombinant primate antibodies - useful for treating		
PT	infections caused by hepatitis A, B and C. herpes,		
PT	cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,		
PT	arthritis etc.		

RESULT	10
ID	R80617 standard; Protein; 467 AA.
AC	R80617;
DT	19-APR-1996 (first entry)
DE	Anti-human IL-4 humanised MAb h25D2-9 mature heavy chain.
KW	Anti-human IL-4 humanin-4; II-4; humanised; purification; treatment; IL-4 diseases; immunoassay; heavy chain; h25D2-9; antibody.
OS	Homo sapiens.
FH Key	Location/Qualifiers
FT Peptide	I..19
FT /label= leader_sequence	/label= leader_sequence
FT Peptide	_20..467
FT /label= mat_peptide	/label= mat_peptide
PN	W09524481-A2.
PN	

RESULT	11
ID	R22759 standard; Protein; 467 AA.
AC	R22759;
DT	20-OCT-1992 (first entry)
DE	Reshaped CD4 antibody heavy chain CD4VHNEW-Ser30.
KW	Antigen; CDR; complementarity determining region; graft rejection;
KW	autoimmune diseases; rheumatoid arthritis; allergy.
OS	Rattus rattus.



230	kvdvkvpøkcadtktccpøpapellggsvflfpkpkdltlmisrtpcvtvvvdvshe	289
241	KVDKKAEPKSCDKTHTCPCPAPELLGGSVFLFPKPKDltlmisrtpcvtvvvdvshe	300
290	dpevkfnwydgvevhnaktkpreegynstyrvsvslvhlghdwlndkyckckvankalp	349
301	DPEVKFNWYDGVGVHNAKTKPREEGYNSTRVSVSLVHLGHDLNGCKYCKCNKALP	360
350	aplektiskaggrepgvytlppsrldetknqsalctclkvgypsdiavewesngpen	409
361	APIEKTISKAGGREPGVYTLPPSRDLTKNQVSUtlclkvGYPSDIaVewESNGPEN	420
410	nykttppvldsdgsfflyskitvdkerwaggnvfascvmhealnhytqkslsiapk	467
421	NYKTTTPVLDSDGSFFLYSKITVDKSRWQGNVFSOSVMHEALNHYTKSLSPK	478

RESULT	13	
ID	P70547	standard; protein; 470 AA.
AC	P70547;	
DT	12-FEB-1991	(first entry)
DE	Sequence of novel mouse-human chimeric antibody H chain.	
KW	Leukaemia lymphoma diagnosis; tumour diagnosis;	
KW	novel mouse-human chimeric antibody H chain.	
OS	Homo sapiens and Mus musculus.	
Key	Location/Qualifiers	
ET	Region	1..140
ET	/note="Mouse V region"	
ET	Region	141..480
ET	/note="Human C region"	
PN	J62201598-A.	
PD	05-SEP-1987.	
PF	28-FEB-1986; 041983.	
PR	28-FEB-1986; JP-041983.	
PA	(TEIJ ) TEIJIN KK.	
DR	WPI; 87-288384/41.	
PT	Mouse-human chimera antibody H chain - comprises mouse antibody H	
PT	chain V region aminoacid sequence and human antibody C region	
PT	sequence, to react with leukaemia lymphoma antigen	
PS	Claim 8; Page 3; 21pp; Japanese.	
CC	A human gene library prepd. from isolated human chromosomal DNA, was	
CC	screened for human antibody H chain gene fragment contg. human	
CC	C-gamma-1 gene (see N70844, N70845, N70486 and N70882). A mouse	
CC	NI-1 gene library prepd. from isolated mouse chromosomal DNA, was	
CC	screened for mouse antibody H chain gene; then the DNA sequence of	
CC	the VDJ region of this gene was determined. Using the above human	
CC	and mouse genes, chimeric antibody gene expression vectors	
CC	pMH-1, -2, -3, -4 and -5 were prepd.	
CC	Sequence	470 AA;
SO		

Query Match 79.3%; Score 2748; DB 2; Length 470;  
Best Local Similarity 85.6%; Pred. No. 8.64e-213;  
Matches 404; Conservative 22; Mismatches 31; Indels 15; Gaps 7;

Db	1	dqlv	veegglv	pgggrk	lscsa	gffsf	gmhvr	qapek	lewai	eggy	---tl	58			
Qy	20	EQVLVEGGGLVQPGGSLRVSCAVSGFTSDHYWYFRQAPCKGPEWVGFINRPNKGSTT	79												
Db	59	yvad	tvkgr	ftrier	dnpk	ntlfl	qmts	lrscd	etam	ycass	gnf	wfvdw	dgattv	tlvs	118
Qy	80	EYAA	SVKDTETISRD	DSKSIAYLQMS	TKIEDTAVY	CTTSY---ISH---CRG-G	-----VC	130							
Db	119	svqnf	wfvdw	dgattv	tvesa	astkqps	vfplap	saketsq	taalqxl	lvkdy	fcp	epvt	178		

131	--YGC--	YFEWQGALTVSSASTKGSVFPLAP	SSKSSGGTAAJGCLVKD	YFPEPV	186
Db		vsmnsgaltsgvhtfpav	lseqglylaesvvtvpssalgtcty	lxnmhkpentkvd	238
179					
187		VSNNSGALTSVHTFP	PAVLSSGLYSLGSVVTVPSS	LGCTQTYCNVNHKPSNTK	VDKKA 246
Qy					
239		epksedkthtcpcapael	lggsvsflfpkpkdt	lniertpevt	cuvvdvshedpevkf 298
Db					
247		EPKS	CDKTHTCPPAPELLGCP	SVFLPFPKDTLMISRTPEVT	CWVDVSHEDPEVKF 306
Qy					
299		nwydgvvhnakt	kpreegnaty	rwsvltvlhqdwlngkeyk	ckvsnkalpalekt 358
Db					
307		NWYDGVVHNKTP	PREQYNSTYRWVS	VLTVLHQLDWLNGKEYK	CKVSNKALPALTEKT 366
Qy					
359		iskakgqprepyvtl	lppsreemtknqslctclvk	gfypsd	iaveesngqpenntktp 418
Db					
367		ISKAKGQPREPYVT	LPSPREUETKNQVSLTCLVK	GFYPSDIAVESNGQPENNTKTP	426
Qy					
419		pvlsdsgfflyskltv	dksrwaqgnvfscsmhea	lhnbyrtqslaleap	gk 470
Db					
427		PVLSDSGFFLYSKLT	DKSRWQGNVFCSCVMHEALH	NHYTKSLSLSPGK	478
Qy					

RESULT	14	
ID	P60351	standard; protein; 470 AA.
AC	P60351;	
DT	01-JAN-1980	(first entry)
DE	Chimeric human-mouse immunoglobulin heavy chain.	
KW	Chimeric protein; immunoglobulin heavy chain;	
KW	common acute lymphocytic leukemia antigen; cancer; tumor;	
KW	disease diagnosis; IgG1; ss.	
OS	Homo sapiens, Mus musculus.	
PN	EP-184187-A.	
PD	11-JUN-1986.	
PF	03-DEC-1985; 115311.	
PR	04-DEC-1984; JP-254980.	

PI (1510) 7. ELGIN M.  
FA Akira K, Yushi N, Yataro I, Takeshi W;  
DR WPI; 86-151350/24.  
DR  
PT New chimeric mouse and human immunoglobulin heavy chain -  
PT specific for common acute lymphocytic leukaemia antigen, and  
PT corresp. DNA coding sequences  
PS Claim 8; Page 26; 42pp; English.  
CC Preferably the sequence of mouse Ig heavy chain variable region is  
CC derived from a heavy chain reacting with the antigen specific for  
CC human common acute lymphocytic leukemia and the human Ig heavy chain  
CC constant region is from human IgG7. The 2 fragments are joined via  
CC an En-fragment which contains at least a human enhancer and may  
CC additionally contain a mouse enhancer or other introns derived from a  
CC human or mouse. The chimeric construct is useful in the diagnosis  
CC and therapy of human CALL. See also N60253, N60254-57 and N60263-64.  
SQ Sequence 470 AA;

Query Match 79.3%; Score 2748; DB 3; Length 470;  
Best Local Similarity 85.6%; Pred. No. 8.64e-213;  
Matches 404; Conservative 22; Mismatches 31; Indels 15; Gaps 7;

[illegible]

Qy	•	80	EYAASVORFTLSRDSKSIAYLQMSLKIEDTAVYCTTSY--ISH--CRG-G-----VC	130
Db		119	seygnfwfdvwaagtlvtvsaetkpvafplapeaketsagtaalgkvlvkdyppevvt	178
Qy		131	--YCC--YFEFWCGQGLVTVSSASTKGPVFP LAPSSKSTSGTGAALGCLVADYFPEVVT	186
Db		179	vwnegaltsgvhtfpavlgasgllysaaevtvvpsslgtqtxlnvnhkpsntkvdkkv	238
Qy		187	VSNNSGALTSQVHTFPAVLQSSGLYLSSSVTVPS SSLGTQTYICNVNHKPSNTKVDKKA	246
Db		239	epkscdkthtcppcpapellggpsvflfpkpkdtlmsrtpevtcvvvdshedpevkf	298
Qy		247	EPKSCDKTHTCPPCPAPELLGGSVFLFPKPKDTLMSRTPVTCVVVDVSHEDPEVKF	306
Db		299	nwyvdqvevhnaktkpreeqynstyrvvavltvlhqwdingkyckvsnkalpapiekt	358
Qy		307	NWYVDQVEVHNAKTKPREQYNSTYRWVSVLTVLHQWDLNGKEYCKVSNKALPAPTEKT	366
Db		359	iskakqpreqvytlppseemtknqvaltelvkgfyppediavewesngqpennykttp	418
Qy		367	ISKAKQPREQVYTLPPSRDELTKQVSLTCLVKGYFSDIAVEHESNGQPENNYKTT	426
Db		419	pvlidsqgfflyskltvdtsrkwaqgnvfacsymhealhhnyhtqkalslpgkk	470
Qy		427	PVLDSQDGFFLYSKLTVDKSRMQGNVFCSCVMHEALHHNYHTQKLSLSLPGK	478

RESULT 15

ID	R43339 standard; Protein; 449 AA.
AC	R43339;
DT	29-NOV-1993 (first entry)
DE	DE Completely humanised C4G1 Ig heavy chain.
KW	Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIa/IIb;
KS	monoclonal antibody; platelet agglutination; humanised antibody.
OS	Synthetic.
PN	W0913133-A.
PD	08-JUL-1993.
PF	15-DEC-1992; J01630.
PR	20-DEC-1991; US-812111.
PR	09-JUN-1992; US-895952.
PR	11-SEP-1992; US-944159.
PA	(PROT-) PROTEIN DESIGN LABS INC.
PA	(YAMA ) YAMAOUCHI PHARM CO LTD.
Co	Mo S5; Teo JY;
DR	WPI; 93-227275/28.
PT	Compsn. contg. immunoglobulin specific for the GP-IIB and -IIIA
PT	protein - contg. for treating disorders related to vascular thrombosis
PS	Claim 26; Fig 5C; 54pp; Japanese.
CC	This is the sequence of the humanised C4G1 immunoglobulin heavy
CC	chain fragment. See R43338 for the light chain sequence. The
CC	antibody is specific for the platelet membrane glycoprotein
CC	GPIIa/IIIB and inhibits platelet agglutination. The Ig is thus
CC	useful in the treatment of thrombosis.
SQ	Sequence 449 AA;

```

Query Match      78.9%; Score 2735; DB 7; Length 449;
Best Local Similarity 85.2%; Pred. No. 1.03e-211;
Matches 391; Conservative 28; Mismatches 30; Indels 10; Gaps 6;

Db      1  qvlgvsgaevkvpqgsvkvsckasgafnlyliewrqpqggilewlgvl-y-pqsqgt 58
:|||||:  |||:|||| |::|||:  : ||||| |||: | | : |
Qy      20  EVQLVESGGGLVQPGGSLRVASVSGFTFSDHYMYWFRQAPKGKGFIEWVGFIRNKPNGT 79

Db      59  nynekfkgvtltvdstntatymelsalrseedlavfca-----t-rdgn-ymfwaywg 110

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Qy	80	EYAASVKORFISRDDSKSIAYLQMSLSKIEDTAVYYCTTSYSHCRGGVCYGGYFEFWG	139
Db	111	qgtLvtvasaetkpsvfplapseketsgtgaalgcLvkdyfpepvtvsmegaltqgvh	170
Qy	140	QCALVTVSSASTKGPVSFFPLAPSSKSTSGCTAALGCLUKDYFPEPVTVSNNGALTSGVH	199
Db	171	tfpaavlqsgslgylseavvtvpssslgtqgtcyicnvnhkpsentkvdkvpekcddktctcpp	230
Qy	200	TFPAVLQSSGLYSLSWVTPVSSSLGTQTYICNVNHRKPSNTVKDKAEPRKSDKTHTCPP	259
Db	231	cpaellggpsvflfpbpkdtlmiartpevtcvvwdvbedevkfnwyvdgvevhnak	290
Qy	260	CPAELLGCGPSVFLFPPPKQDTLMSRTEPVTCCVVDVSHEDPEVKENWYVUGVEVHNAK	319
Db	291	tkpreeqynstyrwsvlvtlhqdwlngkeykckvkenalpapiektiskakgqpreqv	350
Qy	320	TKPREEQYNSTYRWVSVLTVLHQDWLNGKEYCKVKCSNKALPAPTEKTSIKAKGQPREQV	379
Db	351	ytlpperdelcknqvslctLvkvgfypsdiavewesngqpennyykttppvldsdgdflyls	410
Qy	380	YTLPPERDELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTTPPVLDSGCSFFLYLS	439
Db	411	kltvdksrwqgnvfvscsvmhEalhnhbtykqslslspgk	449
Qy	440	KLTVDKSRWQGNVFCSCSVMEALHNNHYTKQSLSLSPGK	478

Search completed: Tue Dec 17 15:29:05 1996  
Job time : 47 secs.

Dec 17 15:21

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US-08-487-550-10.mpr

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W P S R E H (TW)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 15:35:29 1996; MasPar time 9.19 Seconds  
Tabular output not generated. 652.835 Million cell updates/sec

Title: >US-08-487-550-10  
Description: (1-236) from US08487550.pep  
Perfect Score: 1635  
Sequence: 1 MRVPAQLGLLLILPARGC.....CQVTHEGSTVEKTVAPTECS 236

Scoring table: PAM 150  
Gap 11

Searched: 82130 seqs, 25426960 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir47  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 44.070; Variance 175.386; scale 0.251  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description Pred. No.
1	1352	82.7	235 5	S05270 Ig lambda chain prec 1.78e-124
2	1339	81.9	215 14	S29558 Ig lambda chain v re 4.23e-123
3	1333	81.5	233 11	S25752 Ig lambda chain - hu 1.83e-122
4	1326	81.1	236 11	S25746 Ig lambda chain - hu 1.01e-121
5	1322	80.9	232 11	S25742 Ig lambda chain - hu 2.67e-121
6	1323	80.9	235 11	S25750 Ig lambda chain - hu 2.09e-121
7	1318	80.6	234 11	S25757 Ig lambda chain - hu 7.07e-121
8	1291	79.0	216 5	A42193 Ig lambda chain (BJP 5.07e-118
9	1291	79.0	233 11	S25744 Ig lambda chain - hu 5.07e-118
10	1286	78.7	213 11	S21066 Ig lambda chain v re 1.71e-117
11	1284	78.5	235 11	S25754 Ig lambda chain - hu 2.79e-117
12	1279	78.2	235 5	S14675 Ig lambda chain - hu 9.42e-117

13	1267	77.5	216 5	S03401 Ig lambda chain (Kol 1.75e-115
14	1261	77.1	235 11	S25759 Ig lambda chain - hu 7.53e-115
15	1242	76.0	235 11	S25758 Ig lambda chain - hu 7.65e-113
16	1187	72.6	208 5	B49444 Ig lambda chain (New 4.88e-107
17	1170	71.6	232 11	S25756 Ig lambda chain - hu 3.02e-105
18	1148	70.2	231 11	S25738 Ig lambda chain - hu 6.29e-103
19	1146	70.1	233 11	S25747 Ig lambda chain - hu 1.02e-102
20	1142	69.8	233 11	S25741 Ig lambda chain - hu 2.70e-102
21	1141	69.8	233 11	S25748 Ig lambda chain - hu 3.44e-102
22	1128	69.0	231 11	S25751 Ig lambda chain - hu 8.03e-101
23	1127	68.9	235 11	S25749 Ig lambda chain - hu 1.02e-100
24	1110	67.9	231 11	S25753 Ig lambda chain - hu 6.29e-99
25	1103	67.5	226 11	S25745 Ig lambda chain - hu 3.43e-98
26	1072	65.6	243 11	S25755 Ig lambda chain - hu 6.22e-95
27	1055	64.5	190 11	S25740 Ig lambda chain - hu 3.80e-93
28	911	55.7	181 5	PT0220 Ig lambda chain V-C 4.51e-78
29	885	54.1	232 12	S17399 Ig lambda chain prec 2.32e-75
30	875	53.5	230 5	S49449 Ig lambda chain - du 2.56e-74
31	866	53.0	213 5	A21177 Ig light chain precu 2.21e-73
32	789	48.3	118 11	S12441 Ig lambda chain (Ke- 2.20e-65
33	784	48.0	118 11	S12442 Ig lambda chain (Ke- 7.24e-65
34	773	47.3	229 12	A20969 Ig kappa chain precu 9.97e-64
35	763	46.7	118 11	S12443 Ig lambda chain (Ke+ 1.08e-62
36	760	46.5	118 11	S12440 Ig lambda chain (MCC 2.21e-62
37	757	46.3	118 5	A39949 Ig lambda chain J-C 4.51e-62
38	743	45.4	149 5	S23626 Ig lambda chain v re 1.26e-60
39	738	45.1	234 5	A39956 Ig lambda chain prec 4.14e-60
40	713	43.6	119 5	S03464 Ig lambda chain J-C 1.57e-57
41	713	43.6	213 5	A33911 Ig lambda chain-rela 1.57e-57
42	711	43.5	145 11	S25743 Ig lambda chain - hu 2.52e-57
43	706	43.2	105 2	L2H0 Ig lambda chain C re 8.24e-57
44	700	42.8	234 12	S14237 Ig kappa chain precu 3.42e-56
45	698	42.7	234 12	S01320 Ig kappa chain precu 5.49e-56

ALIGNMENTS

RESULT 1  
ENTRY S05270 #type complete  
TITLE Ig lambda chain precursor - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 30-Sep-1993

ACCESSIONS S05270; S04601  
REFERENCE S05270  
#authors Kishimoto, T.  
#submission submitted to the EMBL Data Library, March 1989  
#accession S05270  
#molecule\_type mRNA  
#residues 1-235 ##label KIS1  
#cross-references EMBL:X14583 S04601

REFERENCE  
#authors Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.  
#journal Nucleic Acids Res. (1989) 17:4385  
#title Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells.  
#cross-references MUID:89296497  
#accession S04601  
#molecule\_type mRNA  
#residues 1-130 ##label KIS2  
#cross-references EMBL:X14583

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin





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SUMMARY #length 226 #molecular-weight 24783 #checksum 2436

Query Match 81.1%; Score 1326; DB 11; Length 236;  
Best Local Similarity 83.7%; Pred. No. 1.01e-121;  
Matches 195; Conservative 23; Mismatches 14; Indels 1; Gaps 1;

Db 4 ep1lltllhctgwaqsvltppsvagpgkkticagtsnigaghhvhwyqvpqgt 63  
Qy 5 AQLGLLLWLPARGCESVLTQPPSVSGAPGQKVTISCTGTSNIG-CYDLHWYQQLPCT 63  
Db 64 apkllyadmrpgvprdiagskgtaslaigtlaedeadyycgsfdaalsgwfvgg 123  
Qy 64 APKLLIYDINKRPSGISDRSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAAQVFGG 123  
Db 124 atklvtlqgpkaaavtlfppseelqankatlvcclisdfypgavtvawkadspvtgav 183  
Qy 124 CTRLVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 183  
Db 184 ettptkqnnkyaassy1sltpqwkshksyqcvtthegstvektvaptecs 236  
Qy 184 ETTPTKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS 236

## RESULT 5

ENTRY S25742 #type complete  
TITLE Ig lambda chain - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change  
26-May-1995  
ACCESSIONS S25742  
REFERENCE S16439  
#authors Combriato, G.; Klobbeck, H.G.  
#journal Eur. J. Immunol. (1991) 21:1513-1522  
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.  
#cross-references MUID:91257162  
#accession S25742  
#status preliminary  
#molecule\_type mRNA  
#residues 1-232 #label COM  
#cross-references EMBL:X57806  
#note translation of nucleotide sequence is not given  
SUMMARY #length 232 #molecular-weight 24456 #checksum 4011

Query Match 80.9%; Score 1322; DB 11; Length 232;  
Best Local Similarity 83.6%; Pred. No. 2.67e-121;  
Matches 194; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

Db 1 ep1lltllhctgwaqsvltppsvagpgkkticagtsnigaghhvhwyqvpqgr 60  
Qy 5 AQLGLLLWLPARGCESVLTQPPSVSGAPGQKVTISCTGTSNIG-CYDLHWYQQLPCTA 64  
Db 61 pkllifennkrpsaipdrfsagksgtatlgtgdeadyycgtwdsitdvrfggg 120  
Qy 65 PKLLIYDINKRPSGISDRSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAAQVFGG 124  
Db 121 tklvtlqgpkaaavtlfppseelqankatlvcclisdfypgavtvawkadspvkagve 180  
Qy 125 TRLVVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 184  
Db 181 ttptskqnnkyaassy1sltpqwkshksyqcvtthegstvektvaptecs 232  
Qy 185 TTPTSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS 236

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RESULT 6  
ENTRY S25750 #type complete  
TITLE Ig lambda chain - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change  
26-May-1995  
ACCESSIONS S25750  
REFERENCE S16439  
#authors Combriato, G.; Klobbeck, H.G.  
#journal Eur. J. Immunol. (1991) 21:1513-1522  
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.  
#cross-references MUID:91257162  
#accession S25750  
#status preliminary  
#molecule\_type mRNA  
#residues 1-235 #label COM  
#cross-references EMBL:X57815  
#note translation of nucleotide sequence is not given  
SUMMARY #length 235 #molecular-weight 24710 #checksum 4829

Query Match 80.9%; Score 1323; DB 11; Length 235;  
Best Local Similarity 83.5%; Pred. No. 2.09e-121;  
Matches 192; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

Db 6 llltllthcagwaqsvltppsvagpgkkticagtsnigaghhvhwyqvlgtapk 65  
Qy 7 LLGLLLWLPARGCESVLTQPPSVSGAPGQKVTISCTGTSNIG-CYDLHWYQQLPCTAPK 66  
Db 66 lliyrnnrpsgvdprfsgskgsaslaigtgdeadyycawddalagpvgfggk 125  
Qy 67 LLIVDINKRPSGISDRSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAAQVFGGTR 126  
Db 126 ltvlgqpkaaavtlfppseelqankatlvcclisdfypgavtvawkadspvkagvett 185  
Qy 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186  
Db 186 tpskqnnkyaassy1sltpqwkshrsyqcvtthegstvektvaptecs 235  
Qy 187 TPSKQNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS 236

## RESULT 7

ENTRY S25757 #type fragment  
TITLE Ig lambda chain - human (fragment)  
ORGANISM #formal name Homo sapiens #common name man  
DATE 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change  
30-Jun-1995  
ACCESSIONS S25757  
REFERENCE S16439  
#authors Combriato, G.; Klobbeck, H.G.  
#journal Eur. J. Immunol. (1991) 21:1513-1522  
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.  
#cross-references MUID:91257162  
#accession S25757  
#status preliminary  
#molecule\_type mRNA  
#residues 1-234 #label COM  
#cross-references EMBL:X57822



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```
#accession S21066
#status preliminary
#molecule_type protein
#residues 1-213 ##label D10
#note the sequence from Fig. 4 is inconsistent with that from
      Fig. 1 in having 74-Thr and lacking amino acid 111-213
SUMMARY
      #length 213 #molecular-weight 22540 #checksum 4993

Query Match      78.7%; Score 1286; DB 11; Length 213;
Best Local Similarity 88.5%; Pred. No. 1.71e-117;
Matches 192; Conservative 13; Mismatches 7; Indels 5; Gaps 3;

Db 1 qsvltgppvsgagqgtvtictgsenlgarydmwyqqlpgtapklliyngtirpsgv 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 ESULTQPPSVSGAPGQKVTICTGTSNIGG-YDLHWYQQLPGTAPKLLIYDINKRPSGI 79
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 pdrfsgskgtasaelaitqlaedegdyctwd---yv-vfgggtklvlgppkaapsv 116
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAQVFGGSTRLTVLGQPKAAPSV 139
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 117 tlfpsseelqankatlvcilsdyfpgavtvawkadspvkagvettitpskgnkyaas 176
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 140 TLPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTPPSKQSNKYAAS 199
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 177 sylvltpsqkshrsycqvthegstvektvaptacs 213
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 200 SYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTACS 236
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
ENTRY
TITLE      Iq lambda chain - human (fragment)
ORGANISM   #formal name Homo sapiens #common name man
DATE       22-Nov-1993 #sequence_revision 26-May-1995 #text_change
      30-Jun-1995
ACCESSIONS S25754
REFERENCE S16439
#authors Combratio, G.; Klobbeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human
      immunoglobulin lambda light chain locus are separated by 14
      kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession S25754
#status preliminary
#molecule_type mRNA
#residues 1-235 ##label COM
#cross-references EMBL:X57819
#note translation of nucleotide sequence is not given
SUMMARY
      #length 235 #checksum 5196

Query Match      78.5%; Score 1284; DB 11; Length 235;
Best Local Similarity 81.0%; Pred. No. 2.79e-117;
Matches 187; Conservative 22; Mismatches 21; Indels 1; Gaps 1;

Db 5 llltlllthcagwaqevlqppsasgtpqgrvlicscgssnigntvmwyqqlpgtapk 64
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 7 LLGLLLLPARGCESVLTQPPSVSGAPGQKVTICTGTSNIGGYDLHWYQQLPGTAPK 66
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 65 lllhannrpgvdpdrfsgskgtasaelaisqlsedeadeaycaawddlngryvftgt 124
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 67 LLIIYDINKRPSGIDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAQ-VFGCGT 125
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 125 kvtlvgppkaptvtlfpssseelqankatlvcilsdyfpgavtvawkadspvkagvet 184
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Qy 126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVET 185
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 185 lkpskgnnkyaassyldltpeqwkshrsycqvthegstvektvaptacs 235
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 186 TTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTACS 236
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
ENTRY
TITLE      Iq lambda chain - human
ORGANISM   #formal name Homo sapiens #common name man
DATE       19-May-1994 #sequence_revision 19-May-1994 #text_change
      12-Apr-1995
ACCESSIONS S14675; S12445
REFERENCE S14675
#authors Vasicek, T.J.
#submission submitted to the EMBL Data Library, February 1990
#accession S14675
#molecule_type DNA
#residues 1-235 ##label VAS1
#cross-references EMBL:X51754
REFERENCE S12440
#authors Vasicek, T.J.; Leder, P.
#journal J. Exp. Med. (1990) 172:609-620
#title Structure and expression of the human immunoglobulin lambda
      genes.
#cross-references MUID:90324881
#accession S12445
#molecule_type DNA
#residues 1-129 ##label VAS2
#cross-references EMBL:X51754
GENETICS
#introns 16/1; 130/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY
      #length 235 #molecular-weight 24859 #checksum 7937

Query Match      78.2%; Score 1279; DB 5; Length 235;
Best Local Similarity 79.3%; Pred. No. 9.42e-117;
Matches 184; Conservative 26; Mismatches 19; Indels 3; Gaps 3;

Db 5 llltlllthcagwaqevlqppsasgtqgrvlicscgtsedignvnyvwyrbhpgka 64
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 7 LLGLLLLPARGCESVLTQPPSVSGAPGQKVTICTGTSNIGGYD-LHWYQQLPGTAP 64
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 65 pklmivytkrpsvnprrfsgskgtaseltvsglqaedeadeaycysyags-nalifggg 123
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 65 PKLLIYDINKRPSGIDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAQVFGG 124
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 124 trltvlgppkaapsvtlfpssseelqankatlvcilsdyfpgavtvawkadspvkagve 183
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 125 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVE 184
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 184 ttpskgnnkyaassyldltpeqwkshrsycqvthegstvektvaptacs 235
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 185 TTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTACS 236
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
ENTRY
TITLE      S03401
      Iq lambda chain (Kol) - human
ORGANISM   #formal name Homo sapiens #common name man
DATE       07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
      12-Apr-1995
```

```

ACCESSIONS      503401
REFERENCE       503401
#authors        Kratzin, H.D.; Palm, W.; Stangel, M.; Schmidt, W.E.;
#journal        Friedrich, J.; Hillechmann, N.
#title          Biol. Chem. Hoppe-Seyler (1989) 370:263-272
#title          The primary structure of the crystallizable monoclonal
#title          immunoglobulin IgG1 Kol. II. Amino-acid sequence of the
#title          l-chain, lambda-type, subgroup I.
#cross-references MUID:89228564
#accession      503401
#molecule_type #molecule_type protein
#residues       1-216 #label KRA
#note           article in German with English abstract
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS        pyroglutamic acid
FEATURE         #modified_site pyrrolidone carboxylic acid (Gln) #status
                experimental
                #length 216 #molecular-weight 22798 #checknum 5181
SUMMARY
1

```

Query Match	77.5%;	Score 1267;	DB 5;	Length 216;
Best Local Similarity	83.3%;	Pred. No. 1.75e-115;		
Matches	180;	Mismatches 21;	Indels 0;	Gaps 0;
Conservative				
Db	1	qsylvtpqpsasgtpqgrvtiscsgtsnigstvnwyqqlpgmapklllyrdamrpsgvp	60	
		:     :     :     :     :     :     :     :     :     :     :		
Qy	21	ESVLTQPPSPVSGAPGQKVTISCTGSTSNIGGYDQQLHWYQQQLGCTAPKLLIYDINKRPSGIS	80	
Db	61	drfsqsgksgasaaiaigqlqaedetdycaawdsanayvfgtkvtvlgspkanptvt	120	
		:     :     :     :     :     :     :     :     :     :     :		
Qy	81	DRFSGSKSGTAASLAITGLQTEDEADYQCQSYDSSLNAQVFGGTRLTVLGQPKAAPSVT	140	
Db	121	lfppaseelqankatlvcvlledfygsavtvawkadsppkvagvettkpkegnknkyaas	180	
		:     :     :     :     :     :     :     :     :     :     :		
Qy	141	LFPPSSEELQANKATIVCLISDFYPCAVTAVKADSPVKAGVETTPSKQSNKNKYAAS	200	
Db	181	ylsltpcqskhrsyrcqthegstvektvaptcs	216	
Qy	201	YLSLTPQMKSHRSYSCOVTHEGSTVEKTVAPTCS	236	

```

RESULT      14
ENTRY
TITLE      Ig lambda chain - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       22-Nov-1993 #sequence_revision 26-May-1995 #text_change
           26-May-1995
ACCESSIONS S25759
REFERENCE   S16439
            Combiato, G.; Klobbeck, H.G.
            Eur. J. Immunol. (1991) 21:1513-1522
            V(lambda) and J(lambda)-C(lambda) gene segments of the human
            immunoglobulin lambda light chain locus are separated by 14
            kb and rearrange by a deletion mechanism.
            #cross-references M01D:91257162
            #accession      S25759
            #status         preliminary
            #molecule_type mRNA
            #residues       1-235 #label COM
            #cross-references EMBL:X57824
            #note            translation of nucleotide sequence is not given
            #length 235 #molecular-weight 24748 #checksum 5527
SUMMARY

```

Query Match 77.1%; Score 1261; DB 11; Length 235;

[illegible]

```

RESULT 15
ENTRY
TITLE      Ig lambda chain - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       22-Nov-1993 #sequence_revision 26-May-1995 #text_change
           26-May-1995

ACCESSIONS S25758 #type complete
REFERENCE   S16439
AUTHORS    Combrato, G.; Klobbeck, H.G.
JOURNAL     Eur. J. Immunol. (1991) 21:1513-1522
TITLE       V(lambda) and J(lambda)-C(lambda) gene segments of the human
           immunoglobulin lambda light chain locus are separated by 14
           kb and rearrange by a deletion mechanism.

#cross-references MUID:91257162
#accession S25758
           #status preliminary
           #molecule_type mRNA
           #residues 1-235 #label COM
           #cross-references EMBL:X57823
           #note translation of nucleotide sequence is not given
           #length 235 #molecular_weight 24913 #checksum 9784

SUMMARY

```

Query Match	76.0%;	Score 1242;	DB 11;	Length 235;
Best Local Similarity	78.0%;	Pred. No. 7.65e-113;		
Matches	181;	Conservative 26;	Mismatches 22;	Indels 3; Gaps 3;

Db	5	llfltlcqtgawagsaltpcaevsgpgsgitictcgssdvggynyvswyqghpqka	64
Qy	7	LLGLLLML-PCARGESVLTQPPSVSGAPGQKVTISCTGSTNIGYD-LHHYQQLPCTA	64
Db	65	pkmiydvtrpsgvnfgsgkntaalciisglqpededdyctc-ktsssfyvfqtg	123
Qy	65	PKLLIYDINKRPISGIDRFSGSKSGTAASLAITGLQTEADYYCQSYDSSINAQVFGG	124
Db	124	tksvlggqknptvtlfpssaeelqankatlvcuilsdfpygavtvawkdqspvkagve	183
Qy	125	TRTLVGLQKAAAPSVTLFPPSSEELQANKATLVCLISDFYCVAVTAWKADSPVKAGVE	184
Db	184	tkpsqgmnkyaasyisltpcqwkhrsvscqvtheqstvektvaptcs	235
Qy	185	TTTTPKQSNKNKYAASYSLLTPQMKSHRSYSCQVTHEGSTVEKTVPATPCS	236

Search completed: Tue Dec 17 15:36:06 1996

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Job time : 37 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Dec 17 15:36:24 1996; MasPar time 5.94 Seconds  
Tabular output not generated. 690.941 Million cell updates/sec

Title: &gt;US-08-487-550-10

Description: (1-236) from US08487550.pep

Perfect Score: 1635

Sequence: 1 MRVPAQLLGILLMLPGARC.....CQVTHEGSTVEKTVAPTECS 236

Scoring table: PAM 150

Gap 11

Searched: 49340 seqs, 17385503 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot32

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7

8:part8 9:part9

Statistics: Mean 44.128; Variance 75.634; scale 0.583

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description Pred. No.

1 713 43.6 213 4 I141\_HUMAN IMMUNOGLOBULIN-RELATE 1.08e-136

2 706 43.2 105 5 LAC\_HUMAN IG LAMBDA CHAIN C REG 5.05e-135

3 623 38.1 130 5 LV1G\_HUMAN IG LAMBDA CHAIN PRECU 2.47e-115

4 604 36.9 111 5 LV1D\_HUMAN IG LAMBDA CHAIN V-I R 7.51e-111

5 587 35.9 112 5 LV2K\_HUMAN IG LAMBDA CHAIN V-II 7.54e-107

6 579 35.4 105 5 LAC\_PIG IG LAMBDA CHAIN C REG 5.72e-105

7 579 35.4 111 5 LV1C\_HUMAN IG LAMBDA CHAIN V-I R 5.72e-105

8 563 34.4 112 5 LV1H\_HUMAN IG LAMBDA CHAIN V-I R 3.25e-101

9 560 34.3 111 5 LV2B\_HUMAN IG LAMBDA CHAIN V-II 1.64e-100

10 559 34.2 109 5 LV1F\_HUMAN IG LAMBDA CHAIN V-I R 2.81e-100

11 557 34.1 105 5 LAC1\_MOUSE IG LAMBDA-1 CHAIN C R 8.26e-100

12 554 33.9 111 5 LV2I\_HUMAN IG LAMBDA CHAIN V-II 4.16e-99

13 555 33.9 112 5 LV1B\_HUMAN IG LAMBDA CHAIN V-I R 2.43e-99

14 550 33.6 111 5 LV1A\_HUMAN IG LAMBDA CHAIN V-I R 3.59e-98  
15 547 33.5 111 5 LV2F\_HUMAN IG LAMBDA CHAIN V-II 1.81e-97  
16 546 33.4 111 5 LV2H\_HUMAN IG LAMBDA CHAIN V-II 3.09e-97  
17 542 33.1 104 5 LAC2\_RAT IG LAMBDA-2 CHAIN C R 2.66e-96  
18 542 33.1 105 5 LAC\_RABIT IG LAMBDA CHAIN C REG 2.66e-96  
19 541 33.1 111 5 LV2D\_HUMAN IG LAMBDA CHAIN V-II 4.56e-96  
20 537 32.7 109 5 LV1I\_HUMAN IG LAMBDA CHAIN V-I R 3.92e-95  
21 534 32.7 104 5 LAC3\_MOUSE IG LAMBDA-3 CHAIN C R 1.96e-94  
22 534 32.7 105 5 LAC5\_MUSSH IP LAMBDA-5 CHAIN C R 1.96e-94  
23 528 32.3 129 5 KV1W\_HUMAN IG KAPPA CHAIN PRECUR 4.92e-93  
24 527 32.2 104 5 LAC1\_RAT IG LAMBDA-1 CHAIN C R 8.42e-93  
25 523 32.0 111 5 LV2C\_HUMAN IG LAMBDA CHAIN V-II 7.20e-92  
26 520 31.8 104 5 LAC2\_MOUSE IG LAMBDA-2 CHAIN C R 3.60e-91  
27 516 31.6 111 5 LV2A\_HUMAN IG LAMBDA CHAIN V-II 3.07e-90  
28 513 31.4 111 5 LV2G\_HUMAN IG LAMBDA CHAIN V-II 1.53e-89  
29 504 30.8 109 5 LV2E\_HUMAN IG LAMBDA CHAIN V-II 1.89e-87  
30 501 30.6 105 5 LAC5\_MOUSE IG LAMBDA-5 CHAIN C R 9.37e-87  
31 496 30.3 117 5 KV1J\_HUMAN IG KAPPA CHAIN PRECUR 1.35e-85  
32 494 30.2 110 5 LV2J\_HUMAN IG LAMBDA CHAIN V-II 3.93e-85  
33 486 29.7 103 5 LV1E\_HUMAN IG LAMBDA CHAIN V-I R 2.80e-83  
34 468 28.6 111 5 LV6D\_HUMAN IG LAMBDA CHAIN V-VI 4.02e-79  
35 468 28.6 129 5 KV1X\_HUMAN IG KAPPA CHAIN PRECUR 4.02e-79  
36 466 28.5 112 5 LV6A\_HUMAN IG LAMBDA CHAIN V-VI 1.16e-78  
37 465 28.4 111 5 LV6C\_HUMAN IG LAMBDA CHAIN V-VI 1.97e-78  
38 464 28.4 129 5 KV3L\_HUMAN IG KAPPA CHAIN PRECUR 3.35e-78  
39 460 28.1 131 5 LV6E\_HUMAN IG LAMBDA CHAIN PRECU 2.79e-77  
40 458 28.0 103 5 LAC\_CHICK IG LAMBDA CHAIN C REG 8.06e-77  
41 451 27.6 129 5 KV3H\_HUMAN IG KAPPA CHAIN PRECUR 3.28e-75  
42 451 27.6 129 5 KV3M\_HUMAN IG KAPPA CHAIN PRECUR 3.28e-75  
43 443 27.1 116 5 KV3J\_HUMAN IG KAPPA CHAIN PRECUR 2.24e-73  
44 442 27.0 106 5 LV4E\_HUMAN IG LAMBDA CHAIN V-IV 3.80e-73  
45 441 27.0 115 5 KV3I\_HUMAN IG KAPPA CHAIN PRECUR 6.45e-73

## ALIGNMENTS

RESULT 1  
ID I141\_HUMAN STANDARD; PRT; 213 AA.  
AC P15814;  
DT 01-APR-1990 (REL. 14, CREATED)  
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)  
DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)  
DE IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN {}  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89315835.  
RA HOLLIS G.F., EVANS R.J., STAFFORD-HOLLIS J.M., KORSMEYER S.J.,  
RA MCKEARN J.P.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 86:5552-5556(1989).  
CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL  
CC B-CELL LINE (WHICH IS SURFACE IG NEGATIVE).  
CC -!- THIS LAMBDA LIGHT-CHAIN-RELATED PROTEIN MAY BE THE IMMUN-  
CC GLOBULIN OMEGA LIGHT-CHAIN.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY  
CC AND SHOWS SIMILARITY TO LAMBDA LIGHT CHAIN IN C-TERMINAL HALF  
CC (J AND C REGIONS).  
CC EMBL; M27749; M27749.  
DR PTR; A33911; A33911.  
DR HSP; P01842; 8FAB.  
DR PROSITE; PS00290; IG\_MHC.  
DR IMMUNOGLOBULIN FOLD; B-CELL; SIGNAL.





SQ SEQUENCE 105 AA; 11236 MW; 67031 CN;  
 Query Match 43.2%; Score 706; DB 5; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 5.05e-135;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 qpkaapsvtlfpssseelqankatlvlclisdfypgavtvawkadsspvkagvetttskq 60
   |||||
Qv 132 qpkaapsvtlfpssseelqankatlvlclisdfypgavtvawkadsspvkagvetttskq 191

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<b>Db</b>	61 snnkyaassy ls l t p e q w k s h r s y s c q v t h e g s t v e k t v a p t e c s	105
<b>Qv</b>	192 SNNKYAASSYLSITPEQWKSHRSYSQVTHGSGTVEKTVAPTECS	236

RESULT	3	STANDARD;	PRT;	130 AA.
ID	LVIG HUMAN			
AC	P06316;			
DT	01-JAN-1988	(REL. 06, CREATED)		
DT	01-JAN-1988	(REL. 06, LAST SEQUENCE UPDATE)		
DT	01-NOV-1990	(REL. 16, LAST ANNOTATION UPDATE)		
DE	IG LAMBDA CHAIN PRECURSOR V-I REGION (BL2).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; PRIMATES.			
RN	11			

RP	SEQUENCE FROM N.A.
RX	MEDLINE; 85062823.
RA	TSUJIMOTO Y., GROCE C.M.;
RL	NUCLEIC ACIDS RES. 12:8407-8414 (1984).
RR	PIR; A01966; LIHUBL.
RH	HSP; P01703; 1BJL.
KW	IMMUNOGLOBULIN V REGION; SIGNAL.

FT	SIGNAL	1	19	IG LAMBDA CHAIN V-I REGION (BL2).
FT	CHAIN	20	130	V SEGMENT.
FT	DOMAIN	20	115	J SEGMENT.
FT	DOMAIN	116	130	BY SIMILARITY.
FT	DISULFID	41	108	
FT	NON TER	130	130	
SQ	SEQUENCE	130 AA:	13564 MW; 96916 CN;	

Query Match 38.1%; Score 623; DB 5; Length 130;  
Best Local Similarity 70.5%; Pred. No. 2.47e-115;  
Matches 93; Conservative 21; Mismatches 15; Indels 3; Gaps 3;

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Db      1 mtcspllltlllh-ctgswaqsvltqpsvsapqkvlticsgsssnigndy-vswyqq 58
      |::|||:::|||||||:|||||||:|||||:|||||:|||||
Qw      1 MNVPAQILGILILWIDCARCFVITQDPSVCAPCQKVITSCIGSTNIGG-YDLHWQO 59

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Db 59 vpgtapklllydnhnkrpsigipdfsgkskgtsatlgitglqtgdeadvycgtwnnslsqw 118  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
C:: 50 tgcatawii tvntknrdscienbescszctaaai nttci oetfedahvvcasvssennno 110

Db 119 vfgggtkltvlg 130  
 |||||:||||  
 Qw 120 vccctbtvfc 131

RESULT	4
ID	LVID HUMAN STANDARD; PRT; 111 AA.
AC	P01702;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)

DE IG LAMBDA CHAIN V-I REGION (NIG-64).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Tetrapoda; Mammalia;  
OC Eutheria; Primates.

[1]  
RN SEQUENCE.  
RP MEDLINE; 83186114.  
RX KAMETANI F., TAKAYASU T., SUZUKI S., SHINODA T., OKUYAMA T.,  
RA SHIMIZU A.;  
PL J. BIOCHEM. 93:421-429(1983).

DR	PIR; A01965; LIHUNG.
DR	HSP; P01703; BJLJ.
KW	IMMUNOGLOBULIN V REGION.
FT	MOD RES      1
FT	DLSUFD      22
FT	NON TER    111
SQ	SEQUENCE 111 AA; 11454 MW; 70582 CN;

PYRROLIDONE CARBOXYLIC ACID.  
BY SIMILARITY.

Query Match	36.9%;	Score 604;	DB 5;	Length 111;
Best Local Similarity	78.4%;	Pred. No. 7.51e-111;		
Matches	87;	Conservative 13;	Mismatches 11;	Indels 0;
		Gaps 0;		

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Db      1  qsvltqpssvaapqgqvtiscsgssnigdfvswyqqlpgtapklllydnknrpsgip 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Ov     21  FSVLTQPPSVSCAPGOKVTISTGSTNIGGVDLHWYQOLPGTAPKLLIYDINKRPSGIS 80

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61 drfsgskgstsatlgitglqtgdeadycgtwdsslsvgmfgggtrtvlg
      |||||!|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
81 DRSSCSKSTAAATACGLOFEDCADYYCOSVDSSNAOYFGCGTRITVIG
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RESULT	5	
ID	LV2K HUMAN	STANDARD;
		PRT; 112 AA.

AC	P04209;
DT	20-MAR-1987 (REL. 04, CREATED)
DT	20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
DT	20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE	IG LAMHDA CHAIN V-II REGION (NTG-84).

OC NONO SARIEVS (HOREN/).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUETHERIA; PRIMATES.

RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 85204383.  
 RA TONOKI H., KAMETANI F., HOSHI A., SHINODA T., ISOBE T.;  
 RL FEBS LETT. 185:139-141(1985).  
 CC -!- THIS IS A BENGE-JONES PROTEIN ISOLATED FROM AN INDIVIDUAL WITH  
 CC MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.

DR	PIR; A01971; L2HUNG.
DR	HSP; P01842; IBJL.
KW	IMMUNOGLOBULIN V REGION; AMYLOID; BENCE-JONES PROTEIN.
FT	DISULFID 22 90 BY SIMILARITY.
FT	NON TER 112 112
SQ	SEQUENCE 112 AA; 11581 MW; 70872 CN;

Query Match 35.9%; Score 587; DB 5; Length 112;  
Best Local Similarity 70.5%; Pred. No. 7.54e-107;  
Matches 20: Mismatches 12; Indels 1; Gaps 1;  
79: Conservative

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Db      1  qsaltqpasvsgpqqqstisctgttsdvggydfvswyqahpgkapklllydvnrpsgi  60
      :  ||||:||||:|  :||||:|:||||:|:||||:|  :||||:|  :||||:|  :||||
Gv      21  FSVLTQPSVSAGAPGKVTYISCTGCTSNIGGYDI--HWYQOOLPCTAPKLIYDINKRPSGI  79

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61 snrfsgsksnatstttsqlgaedeadvvcssftttnsravfggatk.lsvlg

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(QV      |.|.|.|.|.|.|.|.:|.:|.:|.|.|.|.|.|.:|.::|.|.|.|.:||  
80 SDRFSSKSGTAASLAITGLQTEADYYCQS DYSDSINAQVFGGGTRLTVLG 131
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RESULT	6	STANDARD;	PRT;	105 AA.
ID	LAC PIG			
AC	P01846;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-APR-1988 (REL. 07, LAST ANNOTATION UPDATE)			
DE	IG LAMBDA CHAIN C REGION.			
OS	SUS SCROFA (PIG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; ARTIODACTYLA.			
RN	(1)			
RP	SEQUENCE.			

RA	MEDLINE; 78000294.
KX	NOVOTNY J., FRANEK F., MARGOLIES M.N., HABER E.;
RL	BIOCHEMISTRY 16:3765-3772(1977).
CC	-!- THIS CHAIN WAS OBTAINED FROM A MIXTURE OF NORMAL IMMUNOGLOBULINS.
DR	PIR: A02129; L1PG.
DR	HSP; P01842; 1BJL.
DR	PROSITE; PS00290; IG MHC.
KW	IMMUNOGLOBULIN C REGION.
FT	NON TER 1
FT	DISULFID 27 86
FT	DISULFID 104 104
SQ	SEQUENCE 105 AA; 11003 MW; 66481 CN; INTERCHAIN (WITH HEAVY CHAIN).

Query Match 35.4%; Score 579; DB 5; Length 105;  
Best Local Similarity 74.3%; Pred. No. 5,72e-105;  
Matches 78; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

**Db** 1 qpkaaptvnlfpsssee lgtnkatlvc llsdfypgavtvtvkagttvtvggvettkpskq 60  
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
**Qv** 132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQ 191

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Db 61 snnkyaasylalsasdwkssagftcqvthegtwiVectvtpseca 105
      |||||::: ||| ::|||:: ||||::||:
Qv 192 SNNKYAASYLSTPEONKSHRSYSCVTHGSTVEKTVAPTECS 236

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RESULT	7	STANDARD;	PRT;	111 AA.
ID	LVIC HUMAN			
AC	P01701;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)			
DE	IG LAMBDA CHAIN V-I REGION (NEW) .			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			

RX	MEDLINE; 69060892.
RA	LANGER B., STEINMETZ-KAYNE M., HILSCHMANN N.;
RL	HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 349:945-951(1968).
CC	-!- THIS IS A BENCE-JONES PROTEIN.
DR	PIR; A01964; LIHUNW.
DR	HSP; P01703; 1BJL.
KW	IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT	MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	DISULFID 22 89 BY SIMILARITY.
FT	NON TER 111 111

SQ SEQUENCE 111 AA; 11453 MW; 68748 CN;

Query Match	35.4%;	Score 579;	DB 5;	Length 111;
Best Local Similarity	73.9%;	Pred. No. 5.72e-105;		
Matches	82;	Conservative	19;	Mismatches 10;
			Indels	0;
			Gaps	0;

Db 1 qsvltqpsvsaaaggqkvt.lscsggstnignyvswhqlpgtapklliyednkprpsip 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

61 drisaksqtsatlgitqlrtgdeadvycatwdsslnavvfgagtkvtvlg 111

Qy 81 DRFGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGTRLTVLG 131

RESULT	8								
ID	LVII HUMAN	STANDARD;	PRT;	112 AA.					
AC	P06887;								
DT	01-JAN-1988	(REL. 06, CREATED)							
DT	01-JAN-1988	(REL. 06, LAST SEQUENCE UPDATE)							
DT	01-JAN-1988	(REL. 06, LAST ANNOTATION UPDATE)							
DE	IG LAMEDA CHAIN V-I REGION (MEM).								
OS	HOMO SAPIENS (HUMAN).								
OC	EUKARYOTA; METAZOA;								
OC	EUTHERIA; PRIMATES.								
RN	(1)								
RP	SEQUENCE.								

RX	MEDLINE; 85257662.
RA	MIHAESCO E., ROY J.-P., CONCY N., PERAN-RIVAT L., MIHAESCO C.;
RL	EUR. J. BIOCHEM. 150:349-357 (1985).
CC	-I- RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES WERE
CC	POSITIONED BY HOMOLGY.
CC	-I- THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+ MARKERS.
DR	PIR; A25479; LIHOMM.
DR	HSPG; P01703; 1BJL.
KW	IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY.
FT	MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	DISULFID 22 90 BY SIMILARITY.
FT	NON TER 112 112
SO	SEQUENCE 112 AA; 11789 MW; 68998 CN;

Query Match	34.4%;	Score 563;	DB 5;	Length 112;
Best Local Similarity	69.4%;	Pred. No. 3.25e-101;		
Matches	77;	Conservative	21;	Mismatches 12;
			Indels	1;
			Gaps	1;

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Db 1 qsvltqpsasgtpggrvtscsgssnvgsnzpaywyqqipgtpaklllynyynqrpsgv 60
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61 pdrfsasrgstas|aisqlgsedeadvvcaawdds|dgvyfqtatktvvl 111

[illegible]

RESULT	9	
ID	LV2B HUMAN	STANDARD; PRT; 111 AA.
AC	P01705;	
DT	21-JUL-1986 (REL. 01, CREATED)	
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	
DT	20-MAR-1987 (REL.. 04, LAST ANNOTATION UPDATE)	
DE	IG LAMBDA CHAIN V-II REGION (NEI).	
OS	OS HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	

RP SEQUENCE.  
RX MEDLINE; 72233223.  
RA CARVER F.A., HILSCHMANN N.;  
RL EUR. J. BIOCHEM. 26:10-32(1972).  
CC -!- THIS IS A BENICE-JONES PROTEIN.  
DR PIR; A01970; L2HONI.  
DR HSP; P01703; 1B3L.  
KW IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN; GLYCOPROTEIN.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT CARBOHYD 96 96  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11591 MW; 70802 CN;

Query Match 34.3%; Score 560; DB 5; Length 111;  
Best Local Similarity 67.9%; Pred. No. 1.64e-100;  
Matches 76; Conservative 24; Mismatches 10; Indels 2; Gaps 2;

Db 1 qsaltpaevsgpggqitictgttdvgsynfvswygnpgkapklmyeqnkrpsgv 60

Qy 21 ESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDL-HWYQQLPCTAPKLLIYDINKRPSGI 79

Db 61 anfsagsgktaalslqgvedeadycysagn-strvfgggttrvls 111

Qy 80 SDRFSGSKGTAASLAITGIATGTEADYQCSYDSSINAQVFGGTRTLVLG 131

RESULT 10  
ID LVIF HUMAN STANDARD; PRT; 109 AA.

AC P04208;  
DT 20-MAR-1987 (REL. 04, CREATED)  
DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)  
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)  
DE IG LAMBDA CHAIN V-I REGION (WAH).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.

RP SEQUENCE.  
RX MEDLINE; 83221661.  
RA TAKAHASHI Y., TAKAHASHI N., TETAERT D., PUTNAM F.W.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 80:3686-3690(1983).  
DR PIR; A01967; LIHUMA.  
DR HSP; P01703; 1B3L.  
KW IMMUNOGLOBULIN V REGION.  
FT DOMAIN 1 97 V SEGMENT.  
FT DOMAIN 98 109 J SEGMENT.  
FT DISULFID 22 89 BY SIMILARITY.  
FT NON TER 109 109  
SQ SEQUENCE 109 AA; 11725 MW; 67654 CN;

Query Match 34.2%; Score 559; DB 5; Length 109;  
Best Local Similarity 73.9%; Pred. No. 2.81e-100;  
Matches 82; Conservative 14; Mismatches 13; Indels 2; Gaps 1;

Db 1 qevltgppsaagtpgqrvticfsgseelnigryvyvqqldpttpkllykdnqrpsgv 60

Qy 21 ESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQLPCTAPKLLIYDINKRPSGIS 80

Db 61 drfagskgtaslaelrlsreaddycaawdds1w--vfgggttlvls 109

Qy 81 DRFSGSKGTAASLAITLQTEADYQCSYDSSINAQVFGGTRTLVLG 131

RESULT 11  
ID LACI MOUSE STANDARD; PRT; 105 AA.  
AC P01843;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-APR-1988 (REL. 07, LAST ANNOTATION UPDATE)  
DE IG LAMBDA-1 CHAIN C REGION.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 83014953.  
RA SELSING E., MILLER J., WILSON R., STORB U.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 79:4681-4685(1982).  
RN [2]  
RP SEQUENCE FROM N.A. (MOPC 315).  
RX MEDLINE; 81148806.  
RA BOTHWELL A.L.M., PASKIND M., SCHWARTZ R.C., SONENSHIN G.E.,  
RA GETTER M.L., BALTIMORE D.;  
RL NATURE 290:65-67(1981).  
RN [3]  
RP SEQUENCE FROM N.A. (S43).  
RX MEDLINE; 82220143.  
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,  
RA BALTIMORE D.;  
RL NATURE 298:380-382(1982).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).

RA APPELLA E.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 68:590-594(1971).  
CC -!- THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1 NORMAL LAMBDA-2  
CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING A LARGE PART OF  
THE V REGION. THE C REGION SEQUENCE (SHOWN HERE) APPEARS COMPLETE-  
ELY NORMAL.  
CC PIR; A02126; LIMS.  
DR HSP; P01842; 1MFB.  
DR PROSITE; PS00290; IG MHC.  
KW IMMUNOGLOBULIN C REGION.  
FT NON TER 1 1  
FT DISULFID 27 86 INTERCHAIN (WITH HEAVY CHAIN).  
ET -> TE (IN REF. 4).  
Q -> E (IN REF. 4).  
FT CONFLICT 56 56  
FT CONFLICT 75 75 MISSING (IN REF. 4).  
FT CONFLICT 81 82 HS -> SH (IN REF. 4).  
FT CONFLICT 85 85 S -> SS (IN REF. 4).  
FT CONFLICT 96 96 E -> Q (IN REF. 4).  
SQ SEQUENCE 105 AA; 11575 MW; 63813 CN;

Query Match 34.1%; Score 557; DB 5; Length 105;  
Best Local Similarity 71.4%; Pred. No. 8.26e-100;  
Matches 75; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

Db 1 qpkspsvtlfpaseeetkhtlvtctdfypgvvtvdkvdtgvtqgmattqpskq 60

Qy 132 QPKASVTLFPSPSEELQANKATLVCLISDFYFGAVTVANKADSSPKAGVETTPSKQ 191

Db 61 snkymassytlrtarawerhsyqcvtqhtveksleradcs 105

Qy 192 SNNKYAASSYLSLTPQWKSRSYSQVTHEGSTVKTVAPECS 236

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<< RESULT 12
ID LV21 HUMAN STANDARD; PRT; 111 AA.
AC P01712;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG LAMBDA CHAIN V-II REGION (WIN).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79062503.
RA CHEN B.L., CHIU Y.-Y.H., HUMPHREY R.L., POLJAK R.J.;
RL BIOCHIM. BIOPHYS. ACTA 537:9-21(1978).
CC -!- THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01978; L2HWN.
DR HSP; P01709; IMCB.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11694 MH; 71443 CN;

Query Match 33.9%; Score 554; DB 5; Length 111;
Best Local Similarity 66.1%; Pred. No. 4.16e-99;
Matches 74; Conservative 22; Mismatches 14; Indels 2;

Db 1 qsaltprvsgpgsgvtisctgsyvnvtgnyhvwsgdqgkvkImiydvdkp
:| ||||| ||||| ||||| ||||| ||| :| :| ||| ||| ||||| :|||
Qy 21 ESWLTPPSVSGAPGQKVTISCTGSTNSTGGYD-LHWYQQLPGTAPKLLIYDINKRP
Db 61 pdrfsgekaentaelslglnaaneadvycsyggt-yellifgggkltvlg 111
:||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 80 SDRFSGSGSGLTAASLAITGLQTEADYYCQSDSSLNAAQVFGGGLTVLIG 131

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RESULT	13
ID	LVBH HUMAN STANDARD; PRT; 112 AA.
AC	P01700;
DT	21-JUL-1986 (REL. 01, CREATED)
DC	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DD	20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE	IG LAMBDA CHAIN V-I REGION (HA).
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC	EUETHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE.
RX	MEDLINE; 71103824.
RA	SHINODA T., TITANI K., PUTNAM F.W.;
RJ	J. BIOL. CHEM. 245:4475-4487(1970).
RC	-I- THIS IS A BENCE-JONES PROTEIN.
DR	PIR; A01963; LIHUUA.
KW	HSP; P01703; IBJL.
DW	IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN.
FT	MOD RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT	DISULFID 22 90 BY SIMILARITY.
FT	NON TER 112 112
SQ	SEQUENCE 112 AA; 11896 MW; 66818 CN;
Query Match 33.9%; Score 555; DB 5; Length 112; Best Local Similarity 71.2%; Pred. No. 2.43e-99;	

	Matches	79;	Conservative	18;	Mismatches	13;	Indels	1;	Gaps	1;	
Db	1	qsvltcpsvagtgcgvtiscsggsnsdgnnyvyagqlbgatpklllyrddkrpqav	60	:	:	:		:	:	:	
Qy	21	ESVLTQPPSVGAPQGKVITSGTGSTNIGGYD-LHWYQQLPGETAKLILYIDINKRPSGI	79	:	:	:		:	:	:	
Db	61	pdrfskskgttsaalaglreedeahyhcaawdrylsauvfgggtqltvl	111	:	:	:		:	:	:	
Qy	80	SDFRFSGSKSGTASLATIGTGLTDEADYYCQSYSLSNAOAVFGCGTRTLVT	130	:	:	:		:	:	:	

RESULT	14	
ID	LVIA HUMAN	STANDARD; PRT; 111 AA.
AC	P01639;	
DT	21-JUL-1986 (REL. 01, CREATED)	
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	
DT	20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)	
DE	IG LAMBDA CHAIN V-I REGION (VOR).	
OS	HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	
RN	{1}	
RP	SEQUENCE.	
RX	MEDLINE; 76023790.	
RL	ANGELHARD M., HILSCHMANN N.;	
RL	HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:1413-1444 (1975).	
CC	-!- THE C REGION OF THIS CHAIN HAS THE O2+ MARKER.	
CC	-!- THIS IS A BENCE-JONES PROTEIN.	
DR	PIR; A01962; LIHUVO.	
DR	HSP; P01703; 1BJL.	
KW	IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.	
FT	MOD RES 1 1	PYRROLIDONE CARBOXYLIC ACID.
FT	DISULFID 22 89	BY SIMILARITY.
FT	NON TER 111 111	
SO	SEQUENCE 111 AA; 11514 MW; 68247 CN;	

Query Match 33.6%; Score 550; DB 5; Length 111;  
Best Local Similarity 65.8%; Pred. No. 3.59e-98;  
Matches 73; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

Db	1	qsvitqpsaeagtbgqrvtiscsgnfnfdigrsvvnywvghptaprllyeedrsgvyp	60
		:     :     :     :     :     :     :     :     :     :     :	
Qy	21	ESVLTQPPVSCARQKVTICTGTSNIGCYDLHWYQQLPTAPKLLIYDINKRSGIS	80
		:     :     :     :     :     :     :     :     :     :     :	
Db	61	drfsqgkctaaalaaglgqasneadyfcstwdslldpvyfgggtkrtvlg	111
		:     :     :     :     :     :     :     :     :     :     :	
Qy	81	DRFSGSKSTAASLAITGLQTEDEADYYCYSDYSSINAKVFGGGTRLTVLG	131
		:     :     :     :     :     :     :     :     :     :     :	

RESULT	15
ID	LVZF HUMAN STANDARD; PRT; 111 AA.
AC	P01709;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE	IG LAMBDA CHAIN V-II REGION (MGC).
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE.
RX	MEDLINE; 75013804.
BA	FETT J.W., DEUTSCH H.F.; RA
RL	BIOCHEMISTRY 13:4102-4114 (1974).

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RN * [2]
RP LAMDA CHAIN GENES.
RX MEDLINE; 76093781.
RA FETT J.W., DEUTSCH H.F.;
RL IMMUNOCHEMISTRY 12:643-652(1975).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA EDMUNDSON A.B., ELY K.R., ABOLA E.E., SCHIFFER M.,
RA PANAGIOTOPOULOS N.;
RL BIOCHEMISTRY 14:3953-3961(1975).
RN [4]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE; 90133913.
RA ELY K.R., HERRON J.N., HARKER M., EDMUNDSON A.B.;
RL J. MOL. BIOL. 210:601-615(1989).
CC -!- THIS IS A BENICE-JONES PROTEIN.
CC -!- THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH A VERY
CC UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY, SUGGESTING
CC THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
CC -!- THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+ MARKERS.
DR PIR; A01975; L2HUMC.
DR PDB; ZMCG; 15-JUL-92.
KW IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN; 3D-STRUCTURE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
FT STRAND 5 5
FT STRAND 10 12
FT STRAND 18 23
FT TURN 26 32
FT STRAND 36 40
FT TURN 42 43
FT STRAND 50 51
FT TURN 52 54
FT STRAND 55 55
FT TURN 62 63
FT STRAND 66 68
FT STRAND 72 77
FT HELIX 82 84
FT STRAND 86 93
FT STRAND 99 101
FT STRAND 105 109
SQ SEQUENCE 111 AA; 11558 MW; 72461 CN;
Query Match 33.5%; Score 547; DB 5; Length 111;
Best Local Similarity 65.2%; Pred.No. 1.81e-97;
Matches 73; Conservative 25; Mismatches 12; Indels 2; Gaps 2;
Db 1 qsaltqpsaagelqgsvtisactgtsedvggynyvwyqqhagkapkviievmkrpsgv 60
Qy 21 ESVLTQPPSVSGAPGQKVTISCTGSTNIGCYD-LHWYQQLFETAPKLLIYINKRPSGI 79
Db 61 pdrfsgekgntaaltvsglqsedeadycssyegs-dnfvfgtktvtvlg 111
:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
Qy 80 SDRFSGSKSGTAASLAITGLQTEDEADYQCQSYDSSINAQVEGGTRLTVLG 131

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Search completed: Tue Dec 17 15:36:43 1996  
Job time : 19 secs.





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CC tetrapeptide motif GPGR, i.e. the Principal Neutralising  
 CC Determinant common to the V3 loop of different HIV isolates.  
 CC A recombinant Ab was produced in which the L chain V region was  
 CC derived from 447-520 and to which a signal sequence and a L chain  
 CC intronic sequence are appended, fused to a fragment contg. a short  
 CC intronic segment of the human lambda 2 C region and the human  
 CC lambda 2 constant encoding domain.  
 SQ Sequence 217 AA;

Query Match 79.6%; Score 1302; DB 8; Length 217;  
 Best Local Similarity 88.1%; Pred. No. 1.45e-88;  
 Matches 192; Conservative 16; Mismatches 7; Indels 3; Gaps 3;

Db 1 qsvltppsvaapqkvrticsagssnignnyl-wyqdfgtapkllygnnkrrpsgi 59  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 21 ESVLTQPPSVSGAPGQKVITISCTGSTNTGG-YDLHWYQQLFGTAPKLLIYDINKRPSGI 79  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 60 pdfsfsgskgstatlqitqlgtgdeadyfcatsdwtsglsadwffgggkklvtlsgpkaaps 119  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 80 SDRFSKSGKTAASLAITGLQTEDEADYYCQSYDSSINAA-VFGGGTRLTVLGQPKAAPS 138  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 120 vtlfpssseelqankatlvcclisdfypgavtvawkadspvkagvettptskqsnkyaas 179  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 139 VTLFPSSSEELQANKATLVCCLISDFYPGAVTVAMKADSPVKAGVETTPTSKQSNKYAA 198  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 180 ssylsltpqwkshrsyqcvtthegstvektvaptacs 217  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 199 SSYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTACS 236

## RESULT 2

ID R31024 standard; Protein; 235 AA.  
 AC R31024;  
 DT 19-MAY-1993 (first entry)  
 DE Antibody D light chain.  
 KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;  
 KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;  
 KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "Signal peptide"  
 FT /Region 20..42  
 FT /label= FR1  
 FT /Region 43..53  
 FT /label= CDR1  
 FT /Region 54..68  
 FT /label= FR2  
 FT /Region 69..75  
 FT /label= CDR2  
 FT /Region 76..107  
 FT /label= FR3  
 FT /Region 108..116  
 FT /label= CDR3  
 FT /Region 117..126  
 FT /label= FR4  
 FT /Domain 127..234  
 FT /label= C lambda  
 PN EP-523949-A.  
 PD 20-JAN-1993.  
 PF 14-JUL-1992; 306420.  
 PR 15-JUL-1991; GB-015284.  
 PR 01-AUG-1991; GB-016594.  
 PR 23-MAR-1992; GB-006284.  
 PR

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PA (WELL ) WELLCOME FOUNDT LTD.  
 PI Crowe JS, Lewis AP;  
 DR WPI; 93-019951/03.  
 DR N-PSDB; Q35100.  
 PT Prodn. of recombinant primate antibodies - useful for treating  
 PT infections caused by hepatitis A, B and C, herpes,  
 PT cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,  
 PT arthritis etc.  
 PS Disclosure; Fig 3; 35pp; English.  
 CC The sequences given in R31023-24 represent the heavy and light chains  
 CC of Antibody D respectively. Antibody D is a monoclonal antibody which  
 CC was derived from peripheral blood lymphocytes from a hepatitis A virus  
 CC (HAV) sero positive patient. Antibody D is closely related in nature  
 CC to murine antibody B5B3. Total RNA was isolated from antibody D  
 CC expressing cells and polyadenylated RNA was extracted. These polyA  
 CC RNA's were used to prepare a cDNA library which was screened for human  
 CC kappa light (L) chains and two positive clones were detected.  
 CC Further heavy (H) chain clones were also isolated.  
 SQ Sequence 235 AA;

Query Match 78.8%; Score 1288; DB 6; Length 235;  
 Best Local Similarity 80.2%; Pred. No. 1.74e-87;  
 Matches 186; Conservative 25; Mismatches 18; Indels 3; Gaps 3;

Db 5 lllltlltqdtgswagsaltqpasvsgspgqetisctgtmndvgsynlvswyqchpka 64  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 7 LLGLLLLLWL-FCARCESVLTQPPSVSGAPGQKVITISCTGSTNIGGYDL-HWYQQLPCTA 64  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 65 pklmlyevskrpgqvenrfsgskagntaeltisglqaedeaddyccsyagstv-vfggg 123  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 65 PKLLIYDINKRPSGISDRFSKSGKTAASLAITGLQTEDEADYYCQSYDSSLNAAVFGGG 124  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 124 tkltvlqgpkapavtlfpssseelqankatlvcclisdfypgavtvawkadspvkagve 183  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 125 TRLTVLGQPKAAPSVTLPSPSEELQANKATLVCCLISDFYPGAVTVAMKADSPVKAGVE 184  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 184 ttpskqsnkyaasaylsltpqwkshrsyqcvtthegstvektvaptacs 235  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 185 TTTPSQSNKYAAASYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTACS 236

## RESULT 3

ID P81260 standard; protein; 233 AA.  
 AC P81260;  
 DT 09-NOV-1990 (first entry)  
 DE VDJC regions of human sperm-immobilising monoclonal antibody.  
 KW Anti-human sperm-immobilising monoclonal antibody; leader region;  
 KW variable region; joining region; constant region; sterility;  
 KW vaccine; contraceptive.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Region 21..115  
 FT /label=variable\_region  
 FT /Region 116..127  
 FT /label=joining\_region  
 FT /Region 128..233  
 FT /label=constant\_region  
 PN J63126482-A.  
 PD 30-MAY-1988.  
 PF 15-NOV-1986; 272412.  
 PR 15-NOV-1986; JP-272412.  
 PR (TOFU) TOA NENRYO KOGYO KK.  
 DR WPI; 88-187839/27.  
 DR N-PSDB; N81655.  
 DR



PF	21-DEC-1990; G02015.
PR	21-DEC-1989; GB-028874.
PR	21-DEC-1990; WO-G02017.
PR	21-DEC-1990; WO-G02018.
PR	(ORTH ) ORTHO PHARM CORP.
PI	Jolliffe LK, Zivin RA, Pulito VL, Adair JR, Athwal DS;
DR	WPI; 91-222914/30.
DR	N-PSDB; Q12633.
PT	New CD4 specific recombinant - complementarity determining region
PT	grafted antibody for treating graft rejection and T cell
PT	disorders
PS	Claim 1; Fig 8; 96pp; English.
CCC	This is an example of a CDR-grafted light chain of the invention.
CCC	The constant regions are based on sequences of the human kappa
CCC	constant domain, the signal sequence is derived from murine MAb
CCC	B72.3 and the CDR sequences are based on the murine OKT4A light chain
CCC	CDRs. The recombinant antibody encoded by this sequence has affinity
CCC	for CD4 similar to that of OKT4A.
CCC	See also Q12627-Q12632.
CCC	Sequence 234 AA;
CCC	50

Query Match 46.7%; Score 763; DB 3; Length 234;  
Best Local Similarity 45.6%;  
Pred. No. 2.40e-47;  
Matches 109; Conservative 55; Mismatches 66; Indels 9; Gaps 8;

[illegible]

RESULT	6
ID	R77614 standard; Protein; 236 AA.
AC	R77614;
DT	15-MAR-1996 (first entry)
DE	Humanised 5G1.1 VL + 012.
KW	Complement C5; haemolysis; kidney; glomerulonephritis;
KW	monoclonal antibody; antinflammatory; antibody engineering;
KW	humanised antibody; complementarity determining region; CDR;
KW	ds.

OS	Synthetic.	Key	Location/Qualifiers
FF	Peptide		1..23
FF	/label= sig_peptide		
FF	Peptide		23..236
FF	/label= mat_peptide		
FF	Region		47..57
FF	/label= CDR-L1		
FF	Region		73..79
FF	/label= CDR-L2		
FF	Region		112..120
FF	/label= CDR-L3		
PN	WO9529697-A1.		

PD 09-NOV-1995.  
PF 01-MAY-1995; U05688.  
PR 02-MAY-1994; US-236208.  
PA (ALEX-) ALEXION PHARM INC.  
PI Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;  
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;  
PI Wang Y, Wilkins JA;  
PI WPI: 95-392923/50.  
DR N-PSDB; T08486.  
DR Treating glomerulonephritis with antibody against complement C5  
PT component - to inhibit complement induced cell lysis  
PT Claim 40; Page 132-34; 18pp; English.  
PS A humanised CDR-grafted light chain, designated 5G1.1 VL + 012  
CC (R77614), includes CDRs derived from mouse anti-C5 monoclonal  
CC antibody 5G1.1. DNA (T08486) coding for the light chain can be  
CC subcloned together with DNA (T08484) coding for a humanised Fc  
CC (R77611) into vector APEX-3P (T08476) for expression of humanised  
CC antibody in human 293 EBNA cells. Such recombinant antibodies retain  
CC the ability of Mab 5G1.1 to block human complement C5a generation and  
CC thus to reduce glomerular inflammation and kidney dysfunction  
CC associated with glomerulonephritis.  
SQ Sequence 236 AA;

Query Match 46.4%; Score 758; DB 15; Length 236;  
Best Local Similarity 47.1%; Pred. No. 5.74e-47;  
Matches 113; Conservative 53; Mismatches 63; Indels 11; Gaps 10;

[illegible]

RESULT	7	
ID	R20058 standard; Protein; 234 AA.	
AC	R20058;	
DT	25-MAR-1992 (first entry)	
DE	Light chain of 3D6 anti-HIV antibody.	
KW	Plasmid pUC3D6LC; human immunodeficiency virus; AIDS;	
KW	complementarity determining region.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Peptide	1..22
FT	/label= signal	
FT	Protein	23..234
FT	Region	23..45
FT	/label= Framework 1	
FT	Region	46..56
FT	/label= CDR_1	
FT	Region	57..71
FT	/label= Framework 2	
FT	Region	72..78
FT	/label= CDR 2	

[illegible]

PT formation between CD4<sup>+</sup> cells  
 PS Disclosure; Page 166-7; 205pp; English.  
 CC The sequence given is encoded by the insert of the vector pMDR1007.  
 CC pMDR1006 (see Q30919) and pSAB132 (see Q30906) were used in the  
 CC construction of this vector. Three fragments were ligated together  
 CC to generate pMDR1006; a 572 bp fragment of pMDR985 (see Q30913), a  
 CC 344bp AatII/EcoRV fragment of pMDR986 (see Q30918) and a 326 bp  
 CC EcoRV/BglII fragment of pMDR1003 (see Q30900). The ligation mixture  
 CC was used to transform E. coli JAZ21 (1q) to ampicillin resistance.  
 CC pMDR1006 was cleaved with NotI and the 1693 bp fragment isolated was  
 CC ligated into NotI linearised pSAB132 which had been dephosphorylated  
 CC by calf alkaline phosphatase. This generates the plasmid pMDR1007.  
 CC The dephosphorylated mixture was fractionated through low temperature  
 CC melting agarose and used to transform E. coli JAZ21 (1q) to ampicillin  
 CC resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3'  
 CC order, the immunoglobulin kappa chain signal peptide, amino acid (AA)  
 CC 1-AA112 of the humanised 5A8 light chain variable region (LV) followed  
 CC by genomic DNA encoding AA108-AA214 of the human kappa light chain,  
 CC ie. the light chain constant region (LC). This polypeptide is an  
 CC antibody homolog which was shown to bind to CD4 but did not block the  
 CC binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4<sup>+</sup>  
 CC lymphocytes (helper/inducer cells). The homolog blocked HIV-induced  
 CC syncytia formation. This homolog can be used in the detection,  
 CC prophylaxis and treatment of diseases caused by infective agents whose  
 CC primary targets are CD4<sup>+</sup> cells.  
 CC Sequence 241 AA;

Query Match 44.2%; Score 722; DB 5; Length 241;  
 Best Local Similarity 46.5%; Pred. No. 3.05e-44;  
 Matches 113; Conservative 52; Mismatches 66; Indels 12; Gaps 11;  
 Db 3 mrvpaqlglillwlpqargdvmgtspdsalvalgeratlncksgsallystngknyla 62  
 Qy 1 MRPVPAQLGLILLWLPQARGDVMGTSPDSALVALGERATLNCKSGSALLYSTNGK 55  
 Db 63 wyqgkqgppklliywastresgvdprfsgsgsgtdftltisaelqaedvayvycqy-ys 121  
 Qy 56 WYQQLPQTAPKLLIYDINKRPSGISDRFSCKSGTAAASIAITGLQTEADYVCOYDSS 115  
 Db 122 -y-rtfggtklei-krtvaapsvflfpssdeqlksgtasvcllnfypreakvqkvkd 178  
 Qy 116 LNAQVFGGTRLVLGQPKAAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAMKAD 175  
 Db 179 nalqsgsqevteqdkdstyslaetltlakadyekkhvacyavthqglsepvtkefnr 238  
 Qy 176 SSPKAGVETTPSKQSN-N-KYAASSYLSLTPQMKSHRSYSCQVTHEG-ST-VEKTVAP 232  
 Db 239 gec 241  
 Qy 233 TEC 235

RESULT 10  
 ID R52951 standard; Protein; 234 AA.  
 AC R52951;  
 DT 27-OCT-1994 (first entry)  
 DE Human anti-IgE MAb light chain.  
 KW Human IgE; CH4 region; trigetx mediator release;  
 KW Mast cells; Monoclonal antibody; allergy.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Region 21..128  
 FT /label= light chain variable region  
 PN EP-592230-A.

PD 13-APR-1994.  
 PF 07-OCT-1993; 308006.  
 PR 07-OCT-1992; JP-293800.  
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.  
 PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;  
 PI Yoshida T;  
 DR WPI; 94-120330/15.  
 DR N-PSDB; Q71872.  
 PT Human monoclonal anti-IgE peptide antibody - inhibits histamine  
 PT release from mast cells by allergen stimulation, useful for  
 PT preventing allergies  
 PS Claim 3; Page 12; 21pp; English.  
 CC R52951 shows the light chain of a human type anti-IgE peptide  
 CC monoclonal antibody which inhibits the signal transmemion for  
 CC the release of chemical mediator from mast cells and basophils  
 CC stimulated with allergen. The antibody can be used for the  
 CC prophylaxis and the therapy of allergy.  
 CC Sequence 234 AA;  
 Query Match 43.2%; Score 706; DB 10; Length 234;  
 Best Local Similarity 44.4%; Pred. No. 4.95e-43;  
 Matches 106; Conservative 56; Mismatches 68; Indels 9; Gaps 9;  
 Db 1 meapaqlfllillwlpdttgeivmtgepatlsvpgggraalacraasge-vsn-niawvqq 58  
 Qy 1 MRPVPAQLGLILLWLPQARGDVMGTSPDSALVALGERATLNCKSGSALLYSTNGK 59  
 Db 59 kpaqaprllygastratgiparfsgsgsgtdftltisaelqaedfaiyyccqy-ssw-pr 116  
 Qy 60 LPTAPKLLIYDINKRPSGISDRFSCKSGTAAASIAITGLQTEADYVCOYDSSINAQ 119  
 Db 117 tfggtkvdkg-tvaapsvflfpssdeqlksgtasvcllnfypreakvqkvkdhalq 175  
 Qy 120 VFGGTRLVLGQPKAAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAMKADSSPV 179  
 Db 176 sqnsqevteqdkdstyslaetltlakadyekkhvacyavthqglsepvtkefnrgec 234  
 Qy 180 KAGVETTPSKQSN-N-KYAASSYLSLTPQMKSHRSYSCQVTHEG-ST-VEKTVAPTEC 235

RESULT 11  
 ID R69093 standard; Protein; 106 AA.  
 AC R69093;  
 DT 30-AUG-1995 (first entry)  
 DE Anti-HIV Fab rev16/20 light chain.  
 KW HIV-1; human immunodeficiency virus type 1; AIDS; Rev protein;  
 KW Intracellular immunization; gene therapy; single chain antibody;  
 KW Fab; antibody engineering; resistance; cell immunity.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Misc difference 68  
 FT /note= "not known"  
 FT Misc difference 86  
 FT /note= "not known"  
 FT Misc difference 101  
 FT /note= "not known"  
 FT W09503832-A.  
 PN PD09503832-A.  
 PF 28-JUL-1994; U08448.  
 PR 30-JUL-1993; US-099870.  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 PI Duan L, Pomerantz R;  
 DR WPI; 95-082039/11.  
 PT Method for conducting gene therapy - comprises using recombinant







Dec 17 15:20

US-08-487-550-10.rag

17

Search completed: Tue Dec 17 15:35:10 1996  
Job time : 28 secs.

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2339	68.0	330	2	GHHU	Ig gamma-1 chain C r	0.00e+00
2	2335	67.8	329	5	S36861	Ig gamma-1 chain C r	0.00e+00
3	2208	64.1	470	5	S22080	Ig heavy chain precu	1.55e-286
4	2156	62.6	472	12	S31459	Ig gamma-1 chain - s	4.10e-279
5	2133	62.0	326	2	G2HU	Ig gamma-2 chain C r	7.84e-276
6	2133	62.0	327	2	G4HU	Ig gamma-4 chain C r	7.84e-276
7	1932	56.1	469	12	S37493	Ig gamma-2a chain -	3.45e-247
8	1863	54.1	475	12	S01321	Ig gamma-2b chain pr	2.27e-237
9	1846	53.6	446	12	S40295	Ig gamma-2a chain (m	5.93e-235
10	1815	52.7	474	14	S25057	Ig gamma-2b chain -	1.51e-230
11	1747	50.8	377	5	A23511	Ig gamma-3 chain C r	6.91e-221
12	1747	50.8	377	5	A60764	Ig gamma-3 chain C r	6.91e-221

#cross-referen

#cross-references MUID:71064024

```

#contents      myeloma protein Eu
#accession     B90563
#molecule_type protein
##residues     1-96,'R',98-135 ##label CUN
##note         this sequence has the G1m(3) marker, 97-Arg
REFERENCE
#authors       Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg,
                W.H.; Edelman, G.M.
#journal       Biochemistry (1970) 9:3171-3181
#title         The covalent structure of a human gammaG-immunoglobulin.
                VIII. Amino acid sequence of heavy-chain cyanogen bromide
                fragments H-S-H-7.
#cross-references MUID:71064025
#contents      Eu
#accession     A90564
#molecule_type protein
##residues     136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,
                'D',199-238,'E',240,'M',242-267,'DGEPE',273-329
                ##label RUT
##note         this sequence has the G1m(non-1) markers, 239-Glu and
                241-Met
REFERENCE
#authors       Ponstingl, H.; Hilschmann, N.
#journal       Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1571-1604
#title         Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins
                (Myelomprotein Nie), III. Die chymotryptischen Peptide der
                H-Kette, Anordnung der tryptischen Peptide und Diskussion
                der vollstaendigen Primaerstruktur.
#cross-references MUID:77070269
#contents      myeloma protein Nie
#accession     B91668
#molecule_type protein
##residues     1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',
                240,'L',242-268,'E',270-271,'D',273-330 ##label PON
##note         this sequence has the G1m(17) and G1m(1) markers
REFERENCE
#authors       Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
#journal       Hoppe-Seyler's Z. Physiol. Chem. (1983) 364:713-747
#title         Die Primaerstruktur des kristallisierten monoklonalen
                Immunglobulins IgG1 KOL, I.
#cross-references MUID:83289131
#contents      myeloma protein KOL; disulfide bonds
#accession     A91723
#molecule_type protein
##residues     1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',
                268-271,'D',273-330 ##label SCH
##note         this sequence has the G1m(3) and G1m(non-1) markers
REFERENCE
#authors       Gall, W.E.; Edelman, G.M.
#journal       Biochemistry (1970) 9:3188-3196
#title         The covalent structure of a human gammaG-immunoglobulin. X.
                Intrachain disulfide bonds.
#cross-references MUID:71064027
#contents      annotation; disulfide bonds
#accession     A91667
#authors       Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
#journal       Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1515-1540
#title         Rule of antibody structure. The primary structure of
                monoclonal IgG1 immunoglobulin (myeloma protein Nie), I:
                purification and characterization of the protein, the L-
                and H-chains and cyanogenbromide cleavage products, and the
                disulfide bridges.
#cross-references MUID:77070267
#contents      annotation; disulfide bonds

```

```

GENETICS
#gene          GDB:IGHG1
#map_position  14q32.33
#introns       99/1; 114/1; 224/1
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS       glycoprotein
FEATURE
20-85          #domain immunoglobulin homology #label IGG1\
137-206        #domain immunoglobulin homology #label IGG2\
243-310        #domain immunoglobulin homology #label IGG3\
27-83,144-204, #disulfide bonds #status experimental\
250-308        #disulfide_bonds interchain (to light chain) #status
103            experimental\
109,112        #disulfide_bonds interchain (to heavy chain) #status
                experimental\
180            #binding_site carbohydrate (Asn) (covalent) #status
                experimental
SUMMARY        #length 330 #molecular-weight 36106 #checksum 8773
Query Match    68.0%; Score 2339; DB 2; Length 330;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 aetkpsvflapskatsqtaalqclvkvdyfpepvtvsmesqaltsgvhtfpavlgss 60
|||||
Qy 147 ASTKGPVFLAPLAPSKSTSGCTAALGCLVKVDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
|||||
Db 61 gylslssvvtvpssalgtqtyicnvnhkpsntkvdkvpekscdkthccpccpapellgg 120
|||||
Qy 207 GLYSLSSVWTPVPSLSLTQTYICNVNHRPSNTKVDKKAEPKSCDKTHTCPCPAPELLGG 266
|||||
Db 121 psvflfppkpktlmsirtpevtcvvdvvhedpevkfnwydvdvghvuhnaktkpreeqn 180
|||||
Qy 267 PSVFLFPPKPKDLMISRTPEVTCVWDVSHEDPEVKFNWYVDGVGVHNAKTKPREEQYN 326
|||||
Db 181 styrvsvltvlhgdwlngkeykckvskkenkalpeplektiekakgqprepqvtyclppsrde 240
|||||
Qy 327 STYRVSVLTVLHQDWLNGKEYKCKVSKKALPAPTEKTSKAGQPREPQVYTLPPSRDE 386
|||||
Db 241 lcknqvslclvkgfypsdiavewesngqpennnykttppvldsdgsefflyskltvdkarw 300
|||||
Qy 387 LTRKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDKSRW 446
|||||
Db 301 qggnvfscsvmhcalhnhytqkslelspgk 330
|||||
Qy 447 QQGNVFCVSMHEALHNYTKQSLSLSPGK 476
|||||
RESULT 2
ENTRY        S36861 #type fragment
TITLE        Ig gamma-1 chain C region - human (fragment)
ORGANISM     #formal_name Homo sapiens #common_name man
DATE         31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change
                02-Aug-1994
ACCESSIONS   S36861; S33887
REFERENCE     S33904
#authors     Harris, L.J.
#submission  submitted to the EMBL Data Library, October 1992
#accession   S36861
#molecule_type DNA
##residues  1-329 ##label HAR
##cross-references EMBL:217370
REFERENCE     S33887

```

#authors	Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
#journal	Cell (1982) 29:671-679
#title	Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.
#accession	S33887
#molecule_type	DNA
#residues	87-112;234-329 ##label TAK
#cross-references	EMBL:Z17370
GENETICS	
#introns	98/1; 113/1; 223/1
CLASSIFICATION	#superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY	#length 329 #checksum 6336
Query Match	67.8%; Score 2335; DB 5; Length 329;
Best Local Similarity	99.7%; Pred. No. 0.00e+00;
Matches 328; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Db	1 atkpsvflpasesketeggtaaigclvkdyfpeptvsmnsqaltsgvhtfpavlgssq 60
Qy	148 STKGSEVFP LAPSSKTSGGTAAIGCLVKDYFPEPTVSMNSGALTSGVHTFPVAVLGSSG 207
Db	61 lyslesvvtvpssslgtctyicnvnhkpsntkvdkkvepkcdktktccpcapeallgpp 120
Qy	208 LYSLSVVVTPSSSLGTCTYICNVNHKPSNTKVDKKAEPKCDKTKTCCPAPPELLGPP 267
Db	121 svflfppkpkdtklmstpevtcvvvdshdedpvkfiwvydgvvevhnaktkpreeqyns 180
Qy	268 SVFLFPPKPKDTLMSTRPEVTCVVVDVSHEDDEVKENWYVDGVVEVHNAKTKPREQYNS 327
Db	181 tyrvsvslvtlhqdwlngdkeyckvsnkalpapielktiskakgprepqvvtlppsrdel 240
Qy	328 TYRVSVSLVTLHQDWLNGKEYCKVSNKALPAPIELKTSKAKGPQRPQVVTLPSPRDEL 387
Db	241 tknqvslctclkvfypsdiavewesngqennykttppvldsdgsfflyskltvdksrq 300
Qy	388 TRNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSGSEFFLYSKLTVDKSRMQ 447
Db	301 qgnvfscsvmhealnhhytqkalslapok 329
Qy	448 QGNVFSVNMHEALNHYHTQKLSLSLPCK 476

```

RESULT      3
ENTRY
TITLE       Ig heavy chain precursor (B/M.T.4A.17.H5.A5) - bovine
ALTERNATE_NAMES   Ig gamma-1 chain C region (clone 8.10)
ORGANISM     formal_name Bos primigenius taurus #common name cattle
DATE         06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
              26-May-1995
ACCESSIONS  S22080; S06610; A31303
REFERENCE    S22080
             Sanders, P.G.
             submitted to the EMBL Data Library, November 1991
             S22080
             preliminary
             ##status          preliminary
             ##molecule_type mRNA
             ##residues        1-470 ##label SAN
             ##cross-references EMBL:X62916
             S06610
             Symons, D.B.A.; Clarkson, C.A.; Beale, D.
             Mol. Immunol. (1989) 26:841-850
             Structure of bovine immunoglobulin constant region heavy
             chain gamma 1 and gamma 2 genes.

```

#cross-references MUID:90097956  
#accession S06610  
#molecule\_type DNA  
#residues 142-470 ##label\_SYM  
##cross-references EMBL:X16701  
#note the sequence was determined from the germline gene

GENETICS  
#gene Ig CH gamma-1  
#introns 98/1; 111/1; 221/1  
CLASSIFICATION  
#superfamily immunoglobulin C region; immunoglobulin homology  
antibody; complement; immunoglobulin; membrane protein  
KEYWORDS  
FEATURE  
318 #binding\_site carbohydrate (Asn) (covalent) #status  
predicted  
SUMMARY  
#length 470 #molecular-weight 50625 #checksum 2181

Query Match 64.1%; Score 2208; DB 5; Length 470;  
Best Local Similarity 63.6%; Pred. No. 1.55e-286;  
Matches 304; Conservative 87; Mismatches 77; Indels 10; Gaps 9;

Db 1 mnpwtllvlsapigvlsqvlresgpelvkpsqtlslctsvagfsals-yaltwvrdq 59  
Qy 1 MKHLHFFLLVAPRWLSQVQESGGLVKPSSETLSITCNVSGSGISGCGYGHGIRP 60  
Db 60 pqkalwvvggi--tsgtgyttnypalkerleltkenskqsvleavsvtbedtatycaret 118  
Qy 61 PGKLEWIGSFYSSGNTYINP SLKSVQTSITDTSTKNQFSLKLNMTAADTAVVYCVDR 120  
Db 119 -yevqdnai--dawggllvtveaaattapkvypslaccgdkssstvtlgclvsymp 175  
Qy 121 LFSWGYNNWFDMVNGEGLVTVSSASTKGPSVF LAPSSKSTSGGTAALGCLVKDYFP 180  
Db 176 epvtvtwnsgalkgshffpavlsqglvlsesmtvvgsteg-qtfctcnvahpasetkv 234  
Qy 181 EPVTVSNHGALTSVGHTFPAVLQSLGSLSSVWTVPSSSLTGTQYICNVNHPKPSNTKV 240  
Db 235 dkavdp--tc-kpsedccppelpggsavfifppkpkdtlciagtpvtcvvdvghddp 292  
Qy 241 DKRAEPKCDKTHCPCPAPELLGCPVFLFPKPKDTLMISRTPEVTCVVDVSHEDP 300  
Db 293 evkfwfvdvntattkpreeqfnstyrvsalrighqdwgtgkfkfkhvnehlpap 352  
Qy 301 EVKFNWYVDGVEVHNATKPREQYNSTYRVSVSLTVLHQDWLNGKEYCKVKSNKALPAP 360  
Db 353 ivrtlartkpareqpyvlappqealektavslctmvtstfpydylavewarngqesed 412  
Qy 361 IERTSKAGQPREQYVTLPPSRDELTKNQVSLTCLVKGYPSDIAVEESNGQPEN-N 419  
Db 413 kyttppqldadysflvsklrivdrnsvsqedqctycvmheahlnhytqketskagk 470  
Qy 420 -YKTTTPVLDSDGSEFLYSKLTVDKSRMQGNQVFCFSVMHEALHHNYTKSLSLSPGK 476

RESULT 4  
ENTRY  
TITLE Ig gamma-1 chain - sheep (fragment)  
ORGANISM #formal\_name Ovis orientalis aries, Ovis ammon aries  
#common name domestic sheep  
DATE 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
ACCESSIONS S31459  
REFERENCE S31459  
#authors Patri, S.; Nau, F.  
#submission submitted to the EMBL Data Library, December 1992

```

#accession S31459
#status preliminary
#molecule_type mRNA
##residues_ 1-472 ##label PAT
##cross-references EMBL:X69797
SUMMARY
#length 472 #checksum 9485

Query Match 62.68; Score 2156; DB 12; Length 472;
Best Local Similarity 62.24; Pred. No. 4,10e-279;
Matches 296; Conservative 90; Mismatches 82; Indels 8; Gaps 8;

Db 2 lwtllfvaaprgvlsqrlqesgslatllqtlsvtcttsgfslmnygvdwvqapqk 60
Qy 4 lmfelllvaaprnwlsvoqlqesgclwpeetlsllcavsgsgisgcygwqirpck 63
Db 61 alewlqgs-gydedl.dynpvlkerlsitkdeksqvaltlstvttdetavvyccarvdyds 119
Qy 64 GLEWIGSFYSSGWTYYNFSLSKQVITSTDSKNQFSLKLNKNTAADTAVYICVDRLEFS 123
Db 120 shafayas-ydfwpglllsvlsastppkvypltsccgdtessivtlgclvssympv 178
Qy 124 VGMVYNNFDMVCGPGLVTVSSASTKGSVFPLAPSKSTSGCTAALGCLVKDFYFPEPV 183
Db 179 tvtnsgallsgvhtfpallqsglylsesvvtvpaatsgaqtficnvahpaestkvdkr 238
Qy 184 TVSNWNSCALTSQVHTFPVAVLQSSGLYSLSSVTVPSSSLSGTQTYICNVNKKPSNTKYDKK 243
Db 239 vep-gcpdpckhcr-cppelpgpgsvffipppkdkltltsgtptvctcvvdvvgddp 296
Qy 244 AEPKSC-DKTHTCPCPAPELLGCPVFLEPPKPKDTLMISRTPEVTCVVDVSHDEPEV 302
Db 297 qfswfdvnevtrartkpreedfnstfirvsealplqdwtdgkfkckvhealpapiv 356
Qy 303 KFNWYVDGVEVHNKAKTPREEDYNSTTRVSVLTVLHQDMLNGREYKCRVSNKALPAPIE 362
Db 357 tlietkqatepgvviapqeeleketlsvtclvtgfydpdiavewkngqpsedky 416
Qy 363 KTISSKAGQPREQVYTLPPSRDELTKNQVSLTCLVRGFYPSDIAVENESNQPEN-N-Y 420
Db 417 gtttsqladsgsyflysrirvdksawegdtyacvvhhealhhvhtqskisppk 472
Qy 421 KTTTPPVLDSDGSFFLYSKLTVDRKRWQGNVFCVSMHEALHNHYTKQSLSLSPGK 476

RESULT 5
ENTRY G2HU #type complete
TITLE Ig gamma-2 chain C region - human
ORGANISM #formal name Homo sapiens #common name man
DATE 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change
08-Dec-1994
ACCESSIONS A93906; A92809; A90752; A93132; A02148
REFERENCE A93906
#authors Ellison, J.; Hood, L.
#journal Proc. Natl. Acad. Sci. U.S.A. (1982) 79:1984-1988
#title Linkage and sequence homology of two human immunoglobulin
gamma heavy chain constant region genes.
#cross-references M01D:82197621
#accession A93906
#molecule_type DNA
##residues_ 1-326 ##label ELL
#note Lys-326 is probably removed posttranslationally
REFERENCE A92809
#authors Wang, A.C.; Tung, E.; Fudenberg, H.H.
#journal J. Immunol. (1980) 125:1048-1054
```

```

#title The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.
#cross-references M01D:81007873
#contents myeloma protein Til
#accession A92809
#molecule_type protein
##residues_ 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 ##label WAN
#note Trp-156 is at or near the complement-binding site
REFERENCE A90752
#authors Connell, G.E.; Parr, D.M.; Hofmann, T.
#journal Can. J. Biochem. (1979) 57:758-767
#title The amino acid sequences of the three heavy chain constant
region domains of a human IgG2 myeloma protein.
#cross-references M01D:80001357
#contents myeloma protein Zie
#accession A90752
#molecule_type protein
##residues_ 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,
'D',195-196,'Q',198-234,'Z',236-263,'BGEZ',269-325
##label CON
#note this sequence has since been revised
REFERENCE A93132
#authors Hofmann, T.; Parr, D.M.
#journal Mol. Immunol. (1979) 16:923-925
#title A note on the amino acid sequence of residues 381-391 of
human immunoglobulin gamma chains.
#cross-references M01D:80114419
#contents Zie
#accession A93132
#molecule_type protein
##residues_ 238-275 ##label HOF
REFERENCE A94591
#authors Hofmann, T.; Parr, D.M.
#journal submitted to the Atlas, March 1980
#contents annotation; Zie, revisions to residues 25, 59, 60, and
264-268
#note the revised sequence differs from that shown in having 60-Ala
and in the amidation states of residues 58, 194, and 197;
the amidation states of residues 172-174, 176, and 235 were
not determined
REFERENCE A90253
#authors Milstein, C.; Frangione, B.
#journal Biochem. J. (1971) 121:217-225
#title Disulphide bridges of the heavy chain of human immunoglobulin
G2.
#cross-references M01D:72033500
#contents annotation; myeloma protein Sa, disulfide bonds
REFERENCE A93157
#authors Frangione, B.; Milstein, C.; Pink, J.R.L.
#journal Nature (1969) 221:145-148
#title Structural studies of immunoglobulin G.
#cross-references M01D:69064124
#contents annotation; Sa, disulfide bonds
GENETICS
#gene GDB:IGHG2
#map_position 14q32.33
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-85 #domain immunoglobulin homology #label ICG1\
133-202 #domain immunoglobulin homology #label ICG2\
239-306 #domain immunoglobulin homology #label ICG3\
14 #disulfide bonds interchain (to light chain) #status
experimental\
27-83,140-200,
```

```
c 246-304 #disulfide_bonds #status experimental\
102,103,106,109 #disulfide_bonds interchain (to heavy chain) #status
experimental
SUMMARY #length 326 #molecular-weight 35884 #checksum 7982

Query Match 62.0%; Score 2133; DB 2; Length 326;
Best Local Similarity 90.9%; Pred. No. 7.84e-276;
Matches 300; Conservative 15; Mismatches 11; Indels 4; Gaps 3;

Db 1 aatkgsavfplapcstrstestaalgclvdkdyfpepvtvwnsgaltsgvhtfpavlgss 60
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 147 ASTKGPVPLAPSSKSTSGTAAAGCLVKDYFPEPVTVSNWSGALTSGVHTFPAVLQSS 206

Db 61 glylsavvtvpssnfgtqtcvndhkpentkvdkverkkc--ve-cpccpappv-ag 116
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 207 GLYLSAVVTVPSSSLGTQTYICNVNHRPSNTKVDKKAEPKCDKTHTCPPELIGG 266

Db 117 psvflfpkpkdtlmiertpertcvvvdvhehdpevqfnvydvgevhnaktkpreeqfn 176
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 267 PSVFLFPKPKDTLMSRTPEVTCVVDVSHEDPEVKFNWYVDGEVHNAKTKPREEQYN 326

Db 177 stfrwsvltvldhqdwlngkeyckvenkgplapietkietkkgpqpvytlppsree 236
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 327 STYRWSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 386

Db 237 mtknqvslclvkgfypsdiavewesngqpennnykttppmlsdsgsflyslkltvdkerw 296
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 387 LTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSRW 446

Db 297 qqgnvfscsvmhhealhhnytkqslslspgk 326
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 447 QQGNVFSCSVMHHEALHHNYTKQSLSLSPGK 476
```

```
RESULT 6
ENTRY G4HU #type complete
TITLE Ig gamma-4 chain C region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
23-Mar-1995
ACCESSIONS A90933; A90249; A02150
REFERENCE A90933
#authors Ellison, J.; Buxbaum, J.; Hood, L.
#journal DNA (1981).1:11-18
#title Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
#cross-references MUID:83157104
#accession A90933
#molecule_type DNA
#residues 1-327 ##label ELL
##note the sequence was determined from the germline gene
REFERENCE A90249
#authors Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
#journal Blochem. J. (1970) 117:33-47
#title Human immunoglobulin subclases. Partial amino acid sequence
of the constant region of A gamma4 chain.
#cross-references MUID:70207560
#accession A90249
#molecule_type protein
#residues 1-30;81-326 ##label PIN
GENETICS
#gene GDB:IGHG4
#map_position 14q32.33
#introns 99/1; 111/1; 221/1
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
```

```
FEATURE
20-85 #domain immunoglobulin homology #label IGG1\
99-110 #region hinge\
134-203 #domain immunoglobulin homology #label IGG2\
240-307 #domain immunoglobulin homology #label IGG3\
14 #disulfide_bonds interchain (to light chain) #status
experimental\
27-83,141-201, #disulfide_bonds #status predicted\
247-305 #disulfide_bonds interchain (to heavy chain) #status
106,109 experimental
SUMMARY #length 327 #molecular-weight 35940 #checksum 907

Query Match 62.0%; Score 2133; DB 2; Length 327;
Best Local Similarity 90.6%; Pred. No. 7.84e-276;
Matches 299; Conservative 17; Mismatches 11; Indels 3; Gaps 3;

Db 1 aatkgsavfplapcstrstestaalgclvdkdyfpepvtvwnsgaltsgvhtfpavlgss 60
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 147 ASTKGPVPLAPSSKSTSGTAAAGCLVKDYFPEPVTVSNWSGALTSGVHTFPAVLQSS 206

Db 61 glylsavvtvpssnfgtqtcvndhkpentkvdkveresk-yg-p-cpccpapeflgg 117
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 207 GLYLSAVVTVPSSSLGTQTYICNVNHRPSNTKVDKKAEPKCDKTHTCPPELIGG 266

Db 118 psvflfpkpkdtlmiertpertcvvvdvhehdpevqfnvydvgevhnaktkpreeqfn 177
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 267 PSVFLFPKPKDTLMSRTPEVTCVVDVSHEDPEVKFNWYVDGEVHNAKTKPREEQYN 326

Db 178 styrwsvltvldhqdwlngkeyckvenkgplapietkietkkgpqpvytlppsree 237
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 327 STYRWSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 386

Db 238 mtknqvslclvkgfypsdiavewesngqpennnykttppvldsdsgsflyslkltvdkerw 297
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 387 LTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSRW 446

Db 298 qqgnvfscsvmhhealhhnytkqslslspgk 327
||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 447 QQGNVFSCSVMHHEALHHNYTKQSLSLSPGK 476

RESULT 7
ENTRY S37483 #type complete
TITLE Ig gamma-2a chain - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
06-Jan-1995
ACCESSIONS S37483
REFERENCE S37483
#authors Duncanson, F.F.D.
#submission submitted to the EMBL Data Library, February 1993
#accession S37483
#status preliminary
##molecule_type mRNA
##residues 1-469 ##label DUC
##cross-references EMBL:X70423
SUMMARY #length 469 #molecular-weight 51549 #checksum 7833

Query Match 56.1%; Score 1932; DB 12; Length 469;
Best Local Similarity 56.8%; Pred. No. 3.45e-247;
Matches 269; Conservative 90; Mismatches 104; Indels 11; Gaps 8;

Db 5 wiflllsgtagvhcqlqgsgpelvkggaevklsckasgyftdyi-i-nwvkkpqqg 63
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\* CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology  
SUMMARY #length 377 #molecular-weight 41287 #checksum 8588

Query Match 50.8%; Score 1747; DB 5; Length 377;  
Best Local Similarity 82.8%; Pred. No. 6.91e-221;  
Matches 312; Conservative 15; Mismatches 3; Indels 47; Gaps 9;

Db 1 aetkgpsvflapscrsrtsgtaalgclvdyfpepvtvwnsgaltgvtfpavlgss 60  
|||||

Qy 147 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPVTVWNsgALTGSHVTFPAVLQSS 206  
|||||

Db 61 glyelssvvtvpsslgtqytcnvnhkpkntkvdrrvelkplgdthtctpcrpepksc 120  
|||||

Qy 207 GLYSLSSVVTPSSSLGTQYTCNVNHRKPSNTKVDK-----KA-----EPKSC 249  
|||||

Db 121 dtpppcrpepkscdtpppcrcrpepkscdtpppcrcrpepkscdtpppcrcrpepksc 180  
|||||

Qy 250 D-----K---T-----H-----TC-----P-P-CPAPELLGGPSVFLFPKPKDT 279  
|||||

Db 181 lmsrtpevtcvvvdshedpevfkwvdygvevhnaktkpreeqynatfrvsvltvlh 240  
|||||

Qy 280 LMSRTPEVTCVVVDVSHEDPEVFKNYVGVVHNACTKPREEQYNSTRYRVSVLTVLH 339  
|||||

Db 241 qdwlngkeyckvknkalpapietkiaktkgprpqvtylpsreemtknqvslclvk 300  
|||||

Qy 340 QDWLNGKEYCKVKNKALPAPIETKISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVK 399  
|||||

Db 301 gfypsdiavewessgqpennnyntppmlsdsgsfflyskltvdkerwqgnvfscvmhe 360  
|||||

Qy 400 GFYPSDIAVWESNGQPNENYKTPPVLDSDGSFFLYSKLTVDKSRMQQGNVFCSCVMHE 459  
|||||

Db 361 alhnrtqkelslspgk 377  
|||||

Qy 460 ALHNHYTQKSLSLSPGK 476  
|||||

RESULT 12

ENTRY A60764 #type complete  
TITLE Ig gamma-3 chain C region, form IAT - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 12-Apr-1995

ACCESSIONS A60764  
REFERENCE A60764

#authors Huck, S.; Lefranc, G.; Lefranc, M.P.  
#journal Immunogenetics (1989) 30:250-257  
#title A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IGHG4 converted region and three hinge exons.

#accession A60764  
#status preliminary

#molecule\_type DNA  
#residues 1-377 #label HUC

CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology  
SUMMARY #length 377 #molecular-weight 41270 #checksum 9390

Query Match 50.8%; Score 1747; DB 5; Length 377;  
Best Local Similarity 82.8%; Pred. No. 6.91e-221;  
Matches 312; Conservative 15; Mismatches 3; Indels 47; Gaps 9;

Db 1 aetkgpsvflapscrsrtsgtaalgclvdyfpepvtvwnsgaltgvtfpavlgss 60  
|||||

Qy 147 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPVTVWNsgALTGSHVTFPAVLQSS 206  
|||||

Db 61 glyelssvvtvpsslgtqytcnvnhkpkntkvdrrvelkplgdthtctpcrpepksc 120  
|||||

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Qy 207 GLYSLSSVVTPSSSLGTQYTCNVNHRKPSNTKVDK-----KA-----EPKSC 249  
|||||

Db 121 dtpppcrpepkscdtpppcrcrpepkscdtpppcrcrpepkscdtpppcrcrpepksc 180  
|||||

Qy 250 D-----K---T-----H-----TC-----P-P-CPAPELLGGPSVFLFPKPKDT 279  
|||||

Db 181 lmsrtpevtcvvvdshedpevfkwvdygvevhnaktkpreeqynatfrvsvltvlh 240  
|||||

Qy 280 LMSRTPEVTCVVVDVSHEDPEVFKNYVGVVHNACTKPREEQYNSTRYRVSVLTVLH 339  
|||||

Db 241 qdwlngkeyckvknkalpapietkiaktkgprpqvtylpsreemtknqvslclvk 300  
|||||

Qy 340 QDWLNGKEYCKVKNKALPAPIETKISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVK 399  
|||||

Db 301 gfypsdiavewessgqpennnyntppvldsdgsfflyarltvdkerwqgnvfscvmhe 360  
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Qy 400 GFYPSDIAVWESNGQPNENYKTPPVLDSDGSFFLYSKLTVDKSRMQQGNVFCSCVMHE 459  
|||||

Db 361 alhnrtqkelslspgk 377  
|||||

Qy 460 ALHNHYTQKSLSLSPGK 476  
|||||

RESULT 13

ENTRY S31866 #type complete  
TITLE Ig gamma-C4 chain C region - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

ACCESSIONS S31866  
REFERENCE S31866

#authors Filpula, D.  
#submission submitted to the EMBL Data Library, February 1993  
#description Screening method for protein-protein interactions of cloned gene products.

#accession S31866  
#status preliminary  
#molecule\_type mRNA  
#residues 1-255 #label FIL  
#cross-references EMBL:X70421

SUMMARY #length 255 #molecular-weight 28325 #checksum 2783

Query Match 49.0%; Score 1686; DB 11; Length 255;  
Best Local Similarity 99.6%; Pred. No. 3.14e-212;  
Matches 231; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 eekscdtkthtccpcpapellggpsvflfppkpkdtlmsrtpevtcvvvdshedpevkf 83  
|||||

Qy 245 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 304  
|||||

Db 84 nwyvdgvevhnaktkpreeqynstrvsvltvlhqdwlngkeyckvknkalpapietk 143  
|||||

Qy 305 NNYVDGVEVHNACTKPREEQYNSTRYRVSVLTVLHQQDWLNGKEYCKVKNKALPAPIETK 364  
|||||

Db 144 iekagprpqvtylpsrdeltknqvslclvkgyfypadiavewesngqpennnyktp 203  
|||||

Qy 365 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSDIAVWESNGQPNENYKTP 424  
|||||

Db 204 pvltdsdgsfflyskltvdkerwqgnvfscvmhealhnhytqkelslspgk 255  
|||||

Qy 425 PVLTDSDGSFFLYSKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476  
|||||

\* RESULT 14

```

ENTRY .
TITLE      Ig gamma chain C region - chimpanzee
ORGANISM   #formal name Pan troglodytes #common name chimpanzee
DATE       23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change
          12-Apr-1995
ACCESSIONS PT0207
REFERENCE   #type complete
#authors    Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
#journal    Mol. Immunol. (1991) 28:319-322
#title      Nucleotide sequence of chimpanzee Fc and hinge regions.
#cross-references MUID:91287716
#accession  PT0207
#molecule_type mRNA
##residues 1-234 ##label EHR
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY       #length 234 #molecular-weight 26330 #checksum 6128

Query Match 48.7%; Score 1677; DB 5; Length 234;
Best Local Similarity 98.3%; Pred. No. 5.93e-211;
Matches 230; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1  entkvdkvkpscdtthtcpcapellqgsvflfpkpkdtlmisrtpevtcvrvdv 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 236  SNTKVDKKAPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV 295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61  shedpevkfnyvdgvevhnaktpreeqnatsyrvsvltvlhqdwlngkeyckkvank 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 296  SHEDPEVKFNWYVDGVEVHNKTRPEEQNTSYRVSVLTVLHQLDWLNGKEYCKKVSNK 355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121  alpapiektiskakgprepyvtlpsrdeitknqvelclvkgfyfysdiavewessgq 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 356  ALPAPIEKTISKAKGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181  pennykttppvldsdgfflyskltvdksrwqqnfvscsvmhealnhnhtqks 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 416  PENNYKTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVMHEALNHNHTQKS 469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
ENTRY .
TITLE      Ig gamma chain C region - rabbit
ORGANISM   #formal name Oryctolagus cuniculus #common_name domestic
          rabbit
DATE       #sequence_revision 15-Nov-1984 #text_change 04-Nov-1994
ACCESSIONS A91749; A90290; A93928; A90245; A94416; A02161
REFERENCE   A91749
#authors    Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
#journal    Immunogenetics (1983) 18:387-397
#title      Nucleotide sequence of a rabbit IgG heavy chain from the
          recombinant F-1 haplotype.
#cross-references MUID:84030930
#accession  A91749
#molecule_type mRNA
##residues 1-323 ##label BER
##note      this sequence has the d12 allotypic marker, 104-Thr, and
          the e14 marker, 185-Thr
REFERENCE   A90290
#authors    Pratt, D.M.; Mole, L.E.
#journal    Biochem. J. (1975) 151:337-349
#title      Sequence studies on the constant region of the Fd sections of
          rabbit immunoglobulin G of different allotype.
#cross-references MUID:76135469
#accession  A90290

```

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#molecule_type protein
#residues 1-47,'E',49-71,'PV',72-128 ##label PRA
REFERENCE   A93928
#authors    Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight,
          K.L.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1982) 79:6018-6022
#title      Heavy chain genes of rabbit IgG; isolation of a cDNA encoding
          gamma heavy chain and identification of two genomic C-gamma
          genes.
#cross-references MUID:83299917
#accession  A93928
#molecule_type mRNA
##residues 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266
          ##label MAR
##note      this sequence has the d11 allotypic marker, 104-Met, and
          the e15 allotypic marker, 185-Ala
REFERENCE   A90245
#authors    Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
#journal    Biochem. J. (1970) 116:249-259
#title      Sequence studies of the Fd section of the heavy chain of
          rabbit immunoglobulin G.
#cross-references MUID:70110015
#accession  A90245
#molecule_type protein
##residues 132-143,'E',145-161 ##label FRU
REFERENCE   A94416
#authors    Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
          in Gamma Globulins, Nobel Symp. 3, Killander, J., ed.,
          pp.109-127, Almqvist and Wiksell, Stockholm, 1967
#accession  A94416
#molecule_type protein
##residues 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',
          202-217,'E',219-232,'Q',234-245,'D',247-255,'G',
          257-259,'D',261-265,'D',267-279,'W',281-283,'S',
          285-322 ##label HIL
##note      this has the e15 allotypic marker, 185-Ala
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-82.      #domain immunoglobulin homology #label IGG1\
130-199     #domain immunoglobulin homology #label IGG2\
236-303     #domain immunoglobulin homology #label IGG3
SUMMARY     #length 323 #molecular-weight 35404 #checksum 1467

Query Match 48.5%; Score 1669; DB 2; Length 323;
Best Local Similarity 70.0%; Pred. No. 8.09e-210;
Matches 229; Conservative 46; Mismatches 45; Indels 7; Gaps 3;

Db 4  kapsvfglapccgdtpstvtlqclvkglpepvtvtwnsgltngvtftpsvrgesgly 63
    :||||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 150  KPSVFFLAPSKSTSGTAALGCLVKDIFPEPTVTVSWNSGALTSCVHTFPVAVLASSGLY 209
    :||||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 64  alsavsvetlss--qpvtcnvahpatntkvdktvapstcskp-tcgp--pellggpsv 116
    ||||| : ||| | ||| : ||||| | : | ||| ||||| |||||
Qy 210  SLSSVTVFVPSLGLQTYTCNVNHRKSNTKVDKAEKPKSCDKTHTCPCPAPELLGGPSV 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117  flfppkpkdtlmisrtpevtcvrvdvaqddpevqftwyinneqvartarpplreqqfnati 176
    :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 270  FLFPPKPKDTLMISRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNKTRPEEQYNSTY 329
    :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177  rvvtlplthqdlrgkfkckvhnkalpapietkargqpkpkyvmgppreeles 236
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 330  RWSVSLVTLHQDLNGKEYCKVSNKALPAPTEKTSKAKGQPREPQVYTLPPSRDELTK 399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237  rveltcmingfypsdiavewekingkaednykttpavldsdgsyflynklevptsewqrg 296

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Qy 390 NQVSLTCLVKGFPDIAVEESNGQPNYKTPPVLDSDGSGFFLYSKLTVOKSRWQQG 449

Db 297 dvftcsymhealhnhytqksisrpgk 323

Qy 450 NVFSCSYMHEALHNHYTKSLSPCK 476

Search completed: Tue Dec 17 15:41:48 1996  
Job time : 55 secs.



RN [4]  
 R2 SEQUENCE (MYELOMA PROTEIN NIE).  
 RX MEDLINE; 77070269.  
 RA PONTING L.H., HILSCHMANN N.;  
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1571-1604 (1976).  
 RN [5]  
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
 RX MEDLINE; 83289131.  
 RA SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N.;  
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 364:713-747 (1983).  
 RN [6]  
 RP DISULFIDE BONDS.  
 RX MEDLINE; 71064027.  
 RA GALL W.E., EDELMAN G.M.;  
 RL BIOCHEMISTRY 9:3188-3196 (1970).  
 RN [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE; 77070267.  
 RA DREXER L., SCHWARZ J., REICHEL W., HILSCHMANN N.;  
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1515-1540 (1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE; 81208100.  
 RA DEISENHOFER J.;  
 RL BIOCHEMISTRY 20:2361-2370 (1981).  
 CC -/- NIE HAS THE GIM(17) ALLOTYPE MARKER, 97-K, & THE GIM(1) MARKERS,  
 CC 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM  
 CC (NON-1) MARKERS.  
 CC -/- NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35, 116, 198, 269 & 272.  
 CC -/- EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177,  
 CC 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.  
 CC -/- KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198, 267 & 272.  
 DR EMBL; J00228; J00228.  
 DR PIR; A02146; GHU.  
 DR PDB; 1FC1; 15-JUL-92.  
 DR PDB; 1FC2; 15-JUL-92.  
 DR MIM; 147100; 11TH EDITION.  
 DR PROSITE; PS00290; IG MHC.  
 KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; 3D-STRUCTURE.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 223 CH2.  
 FT DOMAIN 224 330 CH3.  
 FT DISULFID 27 83  
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 144 204  
 FT DISULFID 250 308  
 FT CARBOHYD 180 180  
 FT VARIANT 97 97 K -> R (IN GIM(3) MARKER).  
 FT VARIANT 239 239 D -> E (IN GIM(NON-1) MARKER).  
 FT VARIANT 241 241 L -> M (IN GIM(NON-1) MARKER).  
 FT MOD\_RES 330 330 REMOVED POST-TRANSLATIONALLY.  
 FT STRAND 123 126  
 FT HELIX 130 134  
 FT TURN 136 137  
 FT STRAND 141 148  
 FT STRAND 158 162  
 FT TURN 163 164  
 FT STRAND 165 166  
 FT STRAND 175 178  
 FT STRAND 183 190

FT HELIX 193 197  
 FT TURN 198 199  
 FT STRAND 202 206  
 FT STRAND 215 219  
 FT STRAND 227 227  
 FT STRAND 230 234  
 FT HELIX 238 240  
 FT TURN 241 242  
 FT STRAND 245 256  
 FT STRAND 260 266  
 FT TURN 267 268  
 FT STRAND 269 270  
 FT STRAND 274 276  
 FT STRAND 280 281  
 FT TURN 283 284  
 FT STRAND 287 296  
 FT HELIX 297 301  
 FT TURN 302 303  
 FT STRAND 306 312  
 FT TURN 313 314  
 FT TURN 316 317  
 FT STRAND 320 324  
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 Best Local Similarity 99.7%; Pred. No. 0.00e+00;  
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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 QY 147 ASTKPSVFLAPSSKSTSGTAALGCLVKDVFPEPVTVSMNSAGALTSGVHTFPVAVLQSS 206  
 Db 61 glyelsvvtvpssslgtqiyicnvnhkpkentkvdkvpekscdtkhtccppcpapellgg 120  
 QY 207 GLYELSSVVTVPSSSLGTQIYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPPELLGG 266  
 Db 121 psvflfppkpkdtlmiartpevtcvvvdvshedpevkfnwydvgevhnaktkpreegn 180  
 QY 267 PSVFLFPPPKPDTLMIARTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKAKTKPREEQYN 326  
 Db 181 styrvsvltvlhqdwlngkeykckvsnkalpapietkakiakgqgprepqvylppsrde 240  
 QY 327 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 386  
 Db 241 ltknqvslclvkgyfspdlaivesngqpennykttppvldadgsfflyakltvdkerw 300  
 QY 387 LTKNQVSLTCLVKGYFSPDIAIVESNGQPENNYKTTTPPVLDSDGSFELYSLTKVDRGRW 446  
 Db 301 qggnvfscvmhealhnhytqkslsispkg 330  
 QY 447 QGQNVFSCVMHEALHNHYTQKSLSLSPGK 476  
  
 RESULT 2  
 ID GC2 HUMAN STANDARD; PRT; 326 AA.  
 AC P01859;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE IG GAMMA-2 CHAIN C REGION.  
 GN IGHG2.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.

RN SEQUENCE FROM N.A.  
RX MEDLINE; 82197621.  
RA ELLISON J.W., HOOD L.E.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 79:1984-1988 (1982).  
RN [2]  
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
RX MEDLINE; 81007873.  
RA WANG A.-C., TUNG E., FUDENBERG H.H.;  
RL J. IMMUNOL. 125:1048-1054 (1980).  
RN [3]  
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN 21E).  
RX MEDLINE; 80001357.  
RA CONNELL G.E., PARR D.M., HOFMANN T.;  
RL CAN. J. BIOCHEM. 57:758-767 (1979).  
RN [4]  
RP SEQUENCE OF 238-275 (21E).  
RX MEDLINE; 80114419.  
RA HOFMANN T., PARR D.M.;  
RL MOL. IMMUNOL. 16:923-925 (1979).  
RN [5]  
RP ZIE, REVISIONS TO 25; 59; 60 AND 264-268.  
RA HOFMANN T., PARR D.M.;  
RL SUBMITTED (MAR-1980) TO THE PIR DATA BANK.  
RN [6]  
RP SEQUENCE OF 1-121 (DOT).  
RA STOPPINI M., BELLOTTI V., NEGRI A., MERLINI G., GARVER F., FERRI G.;  
RL EUR. J. BIOCHEM. 0:0-0 (1995).  
RN [7]  
RP MYELOMA PROTEIN SA, DISULFIDE BONDS.  
RX MEDLINE; 72033500.  
RA MILSTEIN C., FRANGIONE B.;  
RL BIOCHEM. J. 121:217-225 (1971).  
RN [8]  
RP SA, DISULFIDE BONDS.  
RX MEDLINE; 69064124.  
RA FRANGIONE B., MILSTEIN C., PINK J.R.L.;  
RL NATURE 221:145-148 (1969).  
DR ENBL; V00554; V00554.  
DR PIR; A02148; G2H0.  
DR HSP; P01857; 1BBJ.  
DR MIM; 147110; 11TH EDITION.  
DR PROSITE; PS00290; IG\_MHC.  
RW IMMUNOGLOBULIN C REGION.  
FT NON\_TER 1 1  
FT DOMAIN 1 98  
FT DOMAIN 99 110  
FT DOMAIN 111 219  
FT DOMAIN 220 326  
FT DISULFID 14 14  
FT DISULFID 27 83  
FT DISULFID 102 102  
FT DISULFID 103 103  
FT DISULFID 106 106  
FT DISULFID 109 109  
FT DISULFID 140 200  
FT DISULFID 246 304  
FT VARIANT 60 60  
FT SITE 156 156  
FT MOD\_RES 326 326  
SQ SEQUENCE 326 AA; 35384 MW; 629390 CN;  
Query Match 62.0%; Score 2133; DB 3; Length 326;  
Best Local Similarity 90.9%; Pred. No. 0.00e+00;

Matches 300; Conservative 15; Mismatches 11; Indels 4; Gaps 3;  
Db 1 astkqpsvfplapcrstsestaalqclvkdypcpvtvswmsgaltaqvhftfavlges 60  
QY 147 ASTKGFVFFPLAPSSKSTSGTAALGCLVKDYFPEFTVSWNSGALTSGVHTFPAVLQSS 206  
Db 61 glyelaaevvtvpsenfqtqtcytcnvdhkpanktvdkcc--ve-cpcpappv-ag 116  
QY 207 GLYSLSSVWTVFSSSLGTQTYICNVNHRKPSNTKVDKAEKPSCDKTHTCPPCPAPELLGG 266  
Db 117 psvflfppkpkdtlmisrtpevtcvvvdshedpevfqfnwvdygvevhnaktkpreeqfn 176  
QY 267 PSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWVDGVEVHNAKTKPREEQYN 326  
Db 177 stfrvsvltvvhqdwlngkeykckvsnkglpapietkiaktkggprepyvtlppsee 236  
QY 327 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 386  
Db 237 mtkngvaltclvkgfypsdiavewesngqpennnykttppmlsdgsefflyskltvdksrw 296  
QY 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKGRW 446  
Db 297 qggnvfscvmhealhhnhytqskelslpgk 326  
QY 447 QGQNVFSCVMHEALHHNHYTQSKLSLSPGK 476  
RESULT 3  
ID GC4 HUMAN STANDARD; PRT; 327 AA.  
AC P01861;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)  
DE IG GAMMA-4 CHAIN C REGION.  
GN IGHG4.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 83157104.  
RA ELLISON J.W., BUxbaum J.N., HOOD L.E.;  
RL DNA 1:11-18 (1981).  
RN [2]  
RP SEQUENCE OF 1-30 AND 81-326.  
RX MEDLINE; 70207560.  
RA PINK J.R.L., BUTTERY S.H., DE VRIES G.M., MILSTEIN C.;  
RL BIOCHEM. J. 117:33-47 (1970).  
DR PIR; A02150; G4H0.  
DR HSP; P01857; 1BBJ.  
DR MIM; 147130; 11TH EDITION.  
DR PROSITE; PS00290; IG\_MHC.  
RW IMMUNOGLOBULIN C REGION.  
FT NON\_TER 1 1  
FT DOMAIN 1 98  
FT DOMAIN 99 110  
FT DOMAIN 111 220  
FT DOMAIN 221 327  
FT DISULFID 14 14  
FT DISULFID 27 83  
FT DISULFID 106 106  
FT DISULFID 109 109  
FT DISULFID 141 201  
FT DISULFID 247 305  
INTERCHAIN (WITH A LIGHT CHAIN).  
INTERCHAIN (WITH A HEAVY CHAIN).  
INTERCHAIN (WITH A HEAVY CHAIN).







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DR HSP; P01857; 1FC1.  
DR MM; 147120; 11TH EDITION.  
DR PROSITE; PS00290; IG MHC.  
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.  
FT DOMAIN 12 73 HINGE.  
FT DOMAIN 74 183 CH2.  
FT DOMAIN 184 289 CH3.  
FT REPEAT 29 43  
FT REPEAT 44 58  
FT REPEAT 59 73  
FT MOD\_RES 1 1  
FT CARBOHYD 6 6  
FT DISULFID 7 7  
FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
FT CARBOHYD 140 140  
FT MOD\_RES 290 290  
FT VARIANT 126 127 REMOVED POST-TRANSLATIONALLY.  
FT VARIANT 134 134 QV -> EB (IN ZUC).  
FT VARIANT 139 139 P -> L (IN OMM).  
FT VARIANT 182 182 F -> Y (IN OMM).  
FT VARIANT 227 227 T -> A (IN OMM).  
FT VARIANT 227 227 S -> N (IN OMM).  
FT VARIANT 227 227 MISSING (IN ZUC).  
FT VARIANT 279 279 F -> Y (IN OMM).  
SQ SEQUENCE 290 AA; 32331 MW; 485009 CN;

Query Match 46.2%; Score 1590; DB 3; Length 290;  
Best Local Similarity 90.1%; Pred. No. 0.00e+00;  
Matches 210; Conservative 17; Mismatches 6; Indels 0; Gaps 0;  
Db 58 pepkscdtpcpccpacellggsavflfpkpkdtlmisrtpevtcvvvdvshedpevq 117  
Qy 244 AEPKSCDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 303  
Db 118 flwydygvqhnaktkpreqdfnstfrvsvltvlnqwidgkeykckvsnkalpapie 177  
Qy 304 FNWYDGVGVHNAKTKPREQDYNSTYRWVSLVTLVLDQWLNKKEYKCKVSNKALPAPIEK 363  
Db 178 tsktkgqprepytllpreamtknqvaltolvkgfypsdiavewesegqennnytt 237  
Qy 364 TISKAKQPREPYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGENNYKTT 423  
Db 238 pmlidsgafflysklvtksrqgnifacsvmhealhnrfckslslspgk 290  
Qy 424 PPVLDSGSEFFLYSKLVDSRWQQGVFSCVMHEALHNHYTKQSLSLSPGK 476

RESULT 7  
ID GC1 RAT STANDARD; PRT; 326 AA.  
AC P20759;  
DT 01-FEB-1991 (REL. 17, CREATED)  
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
DE IG GAMMA-1 CHAIN C REGION.  
OS RATTUS NORVEGICUS (RAT).

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
RN EUTHERIA; RODENTIA.  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89232738.  
RA BRUEGGEMANN M.;  
RL GENE 74:473-482(1988).  
DR PIR; PS0017; PS0017.  
DR HSP; P01857; 1FC1.  
DR PROSITE; PS00290; IG MHC.  
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.  
FT NON\_TER 1 1  
FT DOMAIN 1 97 CH1.  
FT DOMAIN 98 112 HINGE.  
FT DOMAIN 113 219 CH2.  
FT DOMAIN 220 326 CH3.  
FT DISULFID 27 82  
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 140 200  
FT DISULFID 246 304  
FT CARBOHYD 176 176 POTENTIAL.  
SQ SEQUENCE 326 AA; 35946 MW; 630958 CN;

Query Match 46.0%; Score 1582; DB 3; Length 326;  
Best Local Similarity 63.3%; Pred. No. 0.00e+00;  
Matches 209; Conservative 60; Mismatches 57; Indels 4; Gaps 4;  
Db 1 aettapvypplagtalksnmvtlgclvkgyfpeptvtvnsagalseghvhtfpavlg- 59  
Qy 147 ASTRGPSVFPLAPSSKSTSGGTAALGCLVKVDYFPEPTVSMNSGALTSGVHTFPAVLQSS 206  
Db 60 glyltlesvtvpswtpsqvtcnvahpaestkvdskivprncg-gd-ckpcictgs-ev 116  
Qy 207 GLYSLSVVTVESSLGTQTYICNVNHNKPSNTKVDKAEKPKCDKTHTCPPAPELLGG 266  
Db 117 ssvfifppkpkdvltitltpkvtcvvvdvshedpevfewfvdvdevhtaqtrpbeegin 176  
Qy 267 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYN 326  
Db 177 stfsvselplhqdwngrtfrckvtasaafspeiktiskpegtrtqvphvymaptkee 236  
Qy 327 STYRWVSLVTLVLDQWLNKKEYKCKVSNKALPAPIEKTSKAKQPREPQVYTLPPSRDE 386  
Db 237 mctneveitcmkvgyppdiyveqmgqgqenykntpctmdtdsgelysklnvkkew 296  
Qy 387 LTKQVSLTCLVKGFYPSDIAVEMESNQGENNYKTPPVLDSDGSEFFLYSKLVDSKRW 446  
Db 297 qggnftfcsvlhghhhtekslshspgk 326  
Qy 447 QQGVFSCVMHEALHNHYTKQSLSLSPGK 476

RESULT 8  
ID GC3\_MOUSE STANDARD; PRT; 329 AA.  
AC P22436;  
DT 01-AUG-1991 (REL. 19, CREATED)  
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)  
DT 01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)  
DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;





Db 180 qftrvstlhqgwmegkfckvnmkdlpelektiskpqrkqtpqvtyppreq 239  
QY 327 STYRVSVLTVLHQDWLNGKCYKCKVSKALPAPTEKTISKAGQRPFPQVYTLPPSRDE 386  
Db 240 meknkvalcmvtsfypasisevewerleqdykntlpvldeseyflyeklsvtdsw 299  
QY 387 LTKNQVSLTCLVKGYFSDIAVENESNGQPENNYKTTPVLDSDGSFELYSLKTVDKSRW 446  
Db 300 mrgdiytcsvwhealhhhtqnlrsgpk 329  
QY 447 QCGNFCSCVMHEALHHYTKQSLSPGK 476

## RESULT 12

ID GC1M MOUSE STANDARD; PRT; 393 AA.  
AC P01869;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RX SEQUENCE FROM N.A.  
RX MEDLINE; 80045036.  
RA HONJO T., ORATA M., YAMAWAKI-KATAOKA Y., KATAOKA T., KAWAKAMI T.,  
RA TAKAHASHI N., MANO Y.;  
RL CELL 18:559-568 (1979).  
RN [2]  
RP SEQUENCE OF 323-393 FROM N.A.  
RX MEDLINE; 82197626.  
RA TYLER B.M., COWAN A.F., GERONDAKIS S.D., ADAMS J.M., BERNARD O.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 79:2008-2012 (1982).  
RN [3]  
RP SEQUENCE OF 323-366 FROM N.A.  
RX MEDLINE; 82115295.  
RA ROGERS J., CHOI E., SOUZA L., CARTER C., WORD C.J., KUEHL M.,  
RA EISENBERG D., WALL R.;  
RL CELL 26:19-27 (1981).  
RN [4]  
RP SEQUENCE OF 1-44 FROM N.A.  
RX MEDLINE; 8222190.  
RA YAMAWAKI-KATAOKA Y., NAKAI S., MIYATA T., HONJO T.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 79:2623-2627 (1982).  
CC -/- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA  
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED  
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-  
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED  
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND  
CC SEGMENT OF MU CHAINS.  
DR EMBL; V00793; V00793.  
DR PIR; B02159; G1MSM.  
DR HSSP; P01857; IBAF.  
DR PROSITE; PS00290; IG MHC.  
KW IMMUNOGLOBULIN C REGION; ALTERNATIVE SPLICING; TRANSMEMBRANE;  
KW GLYCOPROTEIN.  
FT NON TER 1 1  
FT DOMAIN 1 97 CH1.  
FT DOMAIN 98 110 HINGE.  
FT DOMAIN 111 217 CH2.  
FT DOMAIN 218 324 CH3.  
FT DISULFID 27 82  
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 138 198  
FT CARBOHYD 174 174  
FT DISULFID 244 302  
FT TRANSMEM 340 357  
FT DOMAIN 358 393 POTENTIAL.  
SQ SEQUENCE 393 AA; 43386 MW; 885119 CN; CYTOPLASMIC (POTENTIAL).

Query Match 45.3%; Score 1559; DB 3; Length 393;  
Best Local Similarity 62.0%; Pred. No. 0.00e+00;  
Matches 204; Conservative 63; Mismatches 56; Indels 6; Gaps 4;  
Db 1 aktppsvyplapgsaaqtnsmvlgclvkgyfpepvtvtnsgalsgvtftfavlgsd 60  
QY 147 ASTKGPSVFPPLAPSSKSTSGCTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPVQLSS 206  
Db 61 -lytssvtpvpsrpsrtvtcnvahpaastkvdklvprdg-cpkci-ctvpev--- 114  
QY 207 GLYSLSVTVTFSSSLGTQTYICNVNKHPSNTRVKKAEKPKCDKTHTCPPCPAPELLGG 266  
Db 115 savfipkpkdvltitlpkvtcvvvdiskddpevfawfddvvhvtaqtqpreeqfn 174  
QY 267 PSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNHYDGVENNAKTREEQYN 326  
Db 175 stfrsveelpmhqdwlngkefkcrvnsaafapiaktiaktgkpkapqvtyppkqeq 234  
QY 327 STYRVSVLTVLHQDWLNGKCYKCKVSKALPAPTEKTISKAGQRPFPQVYTLPPSRDE 386  
Db 235 makdkvltcmittffeditvewqmgpaenykntqpmntngsyfysklnvqknw 294  
QY 387 LTKNQVSLTCLVKGYFSDIAVENESNGQPENNYKTTPVLDSDGSFELYSLKTVDKSRW 446  
Db 295 eagntftcsvlheglhnhhtekslshpg 323  
QY 447 QCGNFCSCVMHEALHHYTKQSLSPG 475

## RESULT 13

ID GCAA MOUSE STANDARD; PRT; 330 AA.  
AC P01863;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)  
DE IG GAMMA-2A CHAIN C REGION, A ALLELE.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 81076554.  
RA SKORAV J.-L., AUFRAY C., ROUGEON F.;  
RL NUCLEIC ACIDS RES. 8:3143-3155 (1980).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 81198976.  
RA YAMAWAKI-KATAOKA Y., MIYATA T., HONJO T.;  
RL NUCLEIC ACIDS RES. 9:1365-1381 (1981).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 81223894.  
RA OLLO R., AUFRAY C., MORCHAMPS C., ROUGEON F.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 78:2442-2446 (1981).

RN \* [4]  
 RP MYELOMA PROTEIN MOPC 173.  
 RX MEDLINE; 74175517.  
 RA BOURGOIS A., FOUGEREAU M., ROCCA-SERRA J.;  
 RL EUR. J. BIOCHEM. 43:423-435 (1974).  
 RN [5]  
 RP MOPC 173, DISULFIDE BONDS.  
 RX MEDLINE; 73056887.  
 RA DE PREVAL C., FOUGEREAU M.;  
 RL EUR. J. BIOCHEM. 30:452-462 (1972).  
 DR EMBL; V00798; V00798.  
 DR PIR; A02152; G2MSA.  
 DR HSSP; P01857; IFC1.  
 DR PROSITE; PS00290; IG MHC.  
 KW IMMUNOGLOBULIN C REGION.  
 FT NON\_TER 1 1  
 FT DISULFID 15 15  
 FT DISULFID 27 82  
 FT DISULFID 107 107  
 FT DISULFID 110 110  
 FT DISULFID 112 112  
 FT DISULFID 144 204  
 FT DISULFID 250 308  
 FT MOD\_RES 330 330  
 SQ SEQUENCE 330 AA; 36389 MW; 643174 CN;  
 Query Match 45.0%; Score 1549; DB 3; Length 330;  
 Best Local Similarity 63.6%; Pred. No. 0.00e+00;  
 Matches 211; Conservative 52; Mismatches 65; Indels 4; Gaps 3;  
 Db 1 akttapsvypapvcgdtgssvtlgclvkgyfpepvtltwmsgalsgwhftfavlgsd 60  
 QY 147 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 206  
 Db 61 -lytssvvtstpsgeitcnvhaasstkvdkieprg-ptikpcppckcpapall 118  
 QY 207 GLYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKAEKSCDKTHCTPC--PAPELL 264  
 Db 119 ggsavflfpkikdvlmisepivtcvvvdseddpdvqlswfvmnvvehtagtqthred 178  
 QY 265 GGSVFELFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWTVDGVEVNNAKTPREEQ 324  
 Db 179 ynstlrvaalpiqhqdmsgkefkckvnnkdlpapiertiskpgsvrapqyvvlpppe 238  
 QY 325 YNSTYRVSVLTVLHQDLNGKEYCKVSKALPAPIETISKAKGQPREPQVYTLPPSR 384  
 Db 239 eemtkkvltcmvtdfmpediyevwtngktelnkntepwldsdgsyfmysklrvckk 298  
 QY 385 DELTKNQVSLTCLVKGFYPSDIAVEWESNQENNYKTPPVLDSDGSFFLYSKLTVDKS 444  
 Db 299 nwvernsyevsvhheglhnhhtkefertpgk 330  
 QY 445 RMOQGNVFCSCVMHEALHNHYTKQKLSLSPGK 476

RESULT 14  
 ID GCB\_RAT STANDARD; PRT; 333 AA.  
 AC P20761;  
 DT 01-FEB-1991 (REL. 17, CREATED)  
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
 DE IG GAMMA-2B CHAIN C REGION.  
 OS EUTARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89232738.  
 RA BRUEGGEMANN M.;  
 RL GENE 74:473-482 (1988).  
 DR PIR; P50018; P50018.  
 DR HSSP; P01857; IFC1.  
 DR PROSITE; PS00290; IG MHC.  
 KW IMMUNOGLOBULIN C REGION.  
 FT NON\_TER 1 1  
 FT DISULFID 15 15  
 FT DISULFID 27 80  
 FT DISULFID 106 106  
 FT DISULFID 109 109  
 FT DISULFID 112 112  
 FT DISULFID 115 115  
 FT DISULFID 147 207  
 FT DISULFID 253 311  
 SQ SEQUENCE 333 AA; 36497 MW; 642683 CN;  
 Query Match 44.9%; Score 1546; DB 3; Length 333;  
 Best Local Similarity 64.0%; Pred. No. 0.00e+00;  
 Matches 215; Conservative 52; Mismatches 60; Indels 9; Gaps 4;  
 Db 1 aqttapsvypapvcgdtgssvtlgclvkgyfpepvtltwmsgalsdvhtfpavlgs- 59  
 QY 147 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 206  
 Db 60 glyltssvt--stwpstvtcnvhaasstkvdkieprgghkpcptchkcpcv 117  
 QY 207 GLYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKAEKSCDKTHCTC--P---CPA 260  
 Db 118 pelggpsvfiipkpkdilllsgnakvtcvcvvdseepdvqfswfvmnvvehtagtqcp 177  
 QY 261 PELLGGSVFELFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWTVDGVEVNNAKTKP 320  
 Db 178 reegynstfrvrsalpiqhqdmsgkefkckvnnkalpsiektiskpgkvlrpkqvym 237  
 QY 321 REEQYNSTRVRSVLTVLHQDLNGKEYCKVSKALPAPIETISKAKGQPREPQVYTL 380  
 Db 238 gppteqltqetvslctltsgfipndigvewtngkieknkntepvmdsdgsfmyekln 297  
 QY 381 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNQENNYKTPPVLDSDGSFFLYSKLT 440  
 Db 298 verserwsrapfsvsvhheglhnhhveksisrppgk 333  
 QY 441 VDKSRWQGNVFCSCVMHEALHNHYTKQKLSLSPGK 476

RESULT 15  
 ID GCAM\_MOUSE STANDARD; PRT; 399 AA.  
 AC P01865;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)  
 DE IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 8222190.  
 RA YAMAWAKI-KATAOKA Y., NAKAI S., MIYATA T., HONJO T.;



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Description: (1-476) from US08487550 pep

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Scoring table: PAM 150

Cap 11

Searched: 81589 seqs, 9523651 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16

Statistics: Mean 35.321; Variance 182.065; scale 0.194

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3095	89.9	475	16	R93553 Monoclonal antibody D	4.71e-243
2	2850	82.8	467	4	R22759 Reshaped CD4 antibody	1.28e-222
3	2848	82.7	467	4	R22758 Reshaped CD4 antibody	1.88e-222
4	2819	81.9	470	4	R22757 Reshaped CAMPATH-1 an	4.90e-220
5	2791	81.1	481	5	R24442 Sequence of antibody	1.06e-217
6	2781	80.8	453	6	R33311 Humanised MaE11 Verel	7.20e-217
7	2771	80.5	475	3	R20057 Heavy chain of 3D6 an	4.91e-216
8	2755	80.0	476	6	R31023 Antibody D heavy chai	1.06e-211
9	2719	79.0	459	8	R42066 Human anti-HBs heavy	1.06e-211
10	2716	78.9	461	8	R42162 Anti-HIV-1 recombinan	1.88e-211
11	2698	78.4	449	7	R43339 Completely humanised	5.94e-210
12	2678	77.8	477	8	R47453 chIT84.12 H3 heavy ch	2.75e-208

13	2672	77.6	454	6	R30774 H52H4-160 murine anti	8.71e-208
14	2661	77.3	466	5	R24812 Sequence encoded by t	7.18e-207
15	2632	76.5	466	7	R40750 Sequence encoded by t	1.87e-204
16	2620	76.1	470	3	P60351 Chimeric human-mouse	1.87e-203
17	2620	76.1	470	2	P70547 Sequence of novel mou	1.87e-203
18	2590	75.2	467	15	R80617 Anti-human IL-4 human	5.88e-201
19	2499	72.6	468	5	R28808 pre-5A8 humanised hea	2.22e-193
20	2461	71.5	371	1	P91918 Sequences of the linke	3.23e-190
21	2455	71.3	371	1	P93558 Linkered human IgG1 (	1.02e-189
22	2347	68.2	534	5	R26531 Sequence of CD4-IgG1	9.85e-181
23	2347	68.2	729	4	P93008 Sequence encoded by a	9.85e-181
24	2341	68.0	351	8	R43685 Human kappa immunoglo	3.11e-180
25	2318	67.3	528	10	R52952 Human anti-IgE MAB he	2.54e-178
26	2276	66.1	330	1	P81026 C region of H chain (	7.90e-175
27	2260	65.7	327	8	R41045 Peptide for linking C	1.69e-173
28	2251	65.4	337	3	R20129 SEQ ID No. 4 of the c	9.46e-173
29	2226	64.7	330	3	R20130 SEQ ID No. 5 of the c	1.13e-170
30	2141	62.2	530	5	R26783 CD4-IgG2 chimeric hea	1.31e-163
31	2132	61.9	530	9	R46679 CD4-IgG2 chimeric hea	7.32e-163
32	2051	59.6	552	6	R30775 pH52-8.0 humanised mu	3.90e-156
33	1969	57.2	464	13	R76088 MAB 55.1 heavy chain.	2.49e-149
34	1944	56.5	448	8	R43673 Mouse anti-bovine gro	2.95e-147
35	1941	56.4	465	12	R66758 Anti-tobacco mosaic v	5.23e-147
36	1934	56.2	445	13	R76085 MAB 55.1 heavy chain.	1.99e-146
37	1932	56.1	469	8	R40384 Monoclonal antibody M	2.92e-146
38	1922	55.8	448	2	R06476 Heavy chain of anti-b	1.97e-145
39	1907	55.4	468	3	RI3061 Monoclonal antibody O	3.46e-144
40	1886	54.8	477	8	R47450 T84.12 Heavy chain.	1.90e-142
41	1886	54.8	599	16	R90837 3B1 single chain anti	1.90e-142
42	1879	54.6	466	4	P40032 Gamma anti-carcinomb	7.25e-142
43	1877	54.5	461	8	R44494 Sequence of the immun	1.06e-141
44	1810	52.6	464	3	RI3049 CD4-specific CDR-graf	3.79e-136
45	1775	51.6	447	1	P93037 Chimeric antibody hea	3.01e-133

## ALIGNMENTS

RESULT 1  
ID R93553 standard; Protein; 475 AA.  
AC R93553;  
DT 20-AUG-1996 (first entry)  
DE Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.  
KW Polymerase chain reaction; primer; amplify; PCR; light chain; MAB;  
KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /note= "Signal peptide"  
FT Protein 20..475  
FT /note= "Mature heavy chain"  
PN J08038178-A.  
PD 13-FEB-1996.  
PF 20-FEB-1995; 030742.  
PR 18-FEB-1994; JP-021628.  
PA (NIN ) NISSHINO IND INC.  
PA (TANA/) TANAKA H.  
DR WPI; 96-154852/16.  
DR N-PSDB; T18059.  
PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -  
PT produced by primer amplification, used in the diagnosis of hCMV  
PT infection  
PS Claim 4; Page 16-18; 22pp; Japanese.  
CC The sequences given in R93553-54 represent the heavy and light chains  
CC respectively of a monoclonal antibody against a 65 kD antigen of human

CC cyomegalovirus (hCMV). The DNA's encoding these sequences were  
 CC amplified using the sequences given in T18040-58. The monoclonal  
 CC antibody may be used in the diagnosis of hCMV.  
 SQ Sequence 475 AA;

Query Match 89.9%; Score 3095; DB 16; Length 475;  
 Best Local Similarity 91.6%; Pred. No. 4.71e-243;  
 Matches 437; Conservative 16; Mismatches 21; Indels 3; Gaps 3;  
 Db 1 mklhfflllvaaprwlslqldgqglvksqtsltctvsgdsisrasygciqr 60  
 Qy 1 MKLHFFLLVAAAPRWLSQVQESGPGLVKPSFETLSLTCVSGSIS-GGQGWIRQ 59  
 Db 61 ppkglewigtlyys-gstynpkelkervtisvdaannqfalklsvtaadtavycart 119  
 Qy 60 PPKGLEWIGSFYSSSCNTYTNPSIKSQVTISTDTSKNQFSIKLNSMTAADTAVYVCVRD 119  
 Db 120 sp-qyydlitgsfpywgqglvtvsaetkgsfvflapasesketagtaalgclvkdyf 178  
 Qy 120 RLFSVVGVMYNNFDMWGPGLVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYF 179  
 Db 179 pepvtvsnegaltsgvhtfpavlqsglylsesvvtvpsasltgttyicvnhkpankt 238  
 Qy 180 PEPVTVSNAGLTSGVHTFPVAVLQSGGLYLSVSVTVPSSSLGTQTYICVNNHKPSNKT 239  
 Db 239 vdkkpeksdktctcpapellggpsvflfpkpkdtlmiertpvrcvrvdshad 298  
 Qy 240 VDKKAEPSCKDHTCFPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHED 299  
 Db 299 pevkfnwydgvevhnaktkpreeqnystyrsvvltvlhqdwlngkeyckvsnkalpa 358  
 Qy 300 PEVKFNWYDGVVHNKTKPREEQNSTYRWSVLTVLHQDLWLNKGYCKVSNKALPA 359  
 Db 359 piektiskakgprepyvltlpsrdeltknqvslclvkgyfypsdiavemesngqpenn 418  
 Qy 360 PIEKTISKAKGPREPYVLTLPSSRDELTKNQVSLCLVKGYFYPSDIAVEMESNGQPENN 419  
 Db 419 ykttpevlidsdgfflyskltvdkrswqgnvfscvmhealhnhytqkslslepgk 475  
 Qy 420 YKTTPEVLDSGFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPCK 476

RESULT 2  
 ID R22759 standard; Protein; 467 AA.  
 AC R22759;  
 DT 20-OCT-1992 (first entry)  
 DE Reshaped CD4 antibody heavy chain CD4VHNEW-Ser30.  
 KW Antigen; CD4; complementarity determining region; graft rejection;  
 KW autoimmune diseases; rheumatoid arthritis; allergy.  
 OS Rattus rattus.  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "signal peptide"  
 FT Peptide 20..467  
 FT /note= "mature peptide"  
 FT Region 50..54  
 FT /note= "Complementarity determining region 1"  
 FT Region 69..85  
 FT /note= "Complementarity determining region 2"  
 FT Region 118..126  
 FT /note= "Complementarity determining region 3"  
 PN W0205274-A.  
 PD 02-APR-1992.  
 PF 16-SEP-1991; G01578.

PR 17-SEP-1990; GB-020282.  
 PA (GORMA) GORMAN S D.  
 PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.  
 DR WPI; 92-132139/16.  
 DR N-PSDB; Q23581.  
 PT Humanisation of antibodies binding to human CD4 antigen - by  
 PT mutation of framework-encoding regions of DNA encoding variable  
 PT domain of rat or mouse antibody chain  
 PS Disclosure; Fig 7; 74pp; English.  
 CC The sequence is that of the reshaped CD4 antibody heavy chain  
 CC CD4VHNEW-Ser30. Reshaped CD4 antibody can be used to induce tolerance  
 CC against an antigen. It can also be used to alleviate autoimmune diseases  
 CC such as rheumatoid arthritis, and to prevent graft rejection. Tolerance  
 CC to a graft, e.g. an organ graft or a bone marrow transplantation can  
 CC also be useful to alleviate allergies. Tolerance to allergens could  
 CC also be achieved. See also R22753-R22763.  
 SQ Sequence 467 AA;

Query Match 82.8%; Score 2850; DB 4; Length 467;  
 Best Local Similarity 87.3%; Pred. No. 1.28e-222;  
 Matches 411; Conservative 31; Mismatches 20; Indels 9; Gaps 6;  
 Db 6 iilflvatatvhsqvlqesgpglvpsqtlstctvsgftfen-ygmawvrgppgrgl 64  
 Qy 6 FFLLVAAAPRWLSQVQESGPGLVKPSFETLSLTCVSGSISGGYGMGWIROPKGL 65  
 Db 65 ewigtishdgdyfrdevkgrvmtlvdtsknqfslasvtaadtavycarg--tia 122  
 Qy 66 EWIGTSFSSGNTYTNPSIKSQVTISTDTSKNQFSIKLNSMTAADTAVYVCVRDLFSV 125  
 Db 123 g-i---r-h-wggslvtvsaetkgsfvflapasesketagtaalgclvkdyfpepvtv 176  
 Qy 126 GMVYNNFDMWGPGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV 185  
 Db 177 swnsagaltsgvhtfpavlqsglylsesvvtvpsasltgttyicvnhkpanktvdkkve 236  
 Qy 186 SWNSGALTSGVHTFPVAVLQSGGLYLSVSVTVPSSSLGTQTYICVNNHKPSNKTVDKAE 245  
 Db 237 pkscdtkhtcpapellggpsvflfpkpkdtlmiertpvrcvrvdshadpevkfn 296  
 Qy 246 PKSCDKTHTCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKEN 305  
 Db 297 wyvdgvevhnaktkpreeqnystyrsvvltvlhqdwlngkeyckvsnkalpapiecti 356  
 Qy 306 WYVDGVEVHNKTKPREEQNSTYRWSVLTVLHQDLWLNKGYCKVSNKALPAPIEKT 365  
 Db 357 skakgqprepyvltlpsrdeltknqvslclvkgyfypsdiavemesngqpennktpp 416  
 Qy 366 SKAKGQPREPYVLTLPSSRDELTKNQVSLCLVKGYFYPSDIAVEMESNGQPENNKTPP 425  
 Db 417 vldsgsflyskltvdkrswqgnvfscvmhealhnhytqkslslepgk 467  
 Qy 426 VLDSGFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPCK 476

RESULT 3  
 ID R22758 standard; Protein; 467 AA.  
 AC R22758;  
 DT 20-OCT-1992 (first entry)  
 DE Reshaped CD4 antibody heavy chain CD4VHNEW-Thr30.  
 KW Antigen; CD4; complementarity determining region; graft rejection;  
 KW autoimmune diseases; rheumatoid arthritis; allergy.  
 OS Rattus rattus.  
 FH Key Location/Qualifiers

FT	Peptide	1..19	
FT	/note= "signal peptide"		
FT	Peptide	20..467	
FT	/note= "mature peptide"		
FT	Region	50..54	
FT	/note= "Complementarity determining region 1"		
FT	Region	69..85	
FT	/note= "Complementarity determining region 2"		
FT	Region	118..126	
FT	/note= "Complementarity determining region 3"		
PN	W09205274-A.		
PD	02-APR-1992.		
PF	16-SEP-1991; G01578.		
PR	17-SEP-1990; GB-020282.		
PA	(GORM/) GORMAN S D.		
PI	Clark M R, Cobbold S P, Gorman S D, Waldmann H.		
DR	WPI; 92-132139/16.		
DR	N-PSDB; Q23571.		
PT	Humanisation of antibodies binding to human CD4 antigen - by		
PT	mutation of framework-encoding regions of DNA encoding variable		
PT	domain of rat or mouse antibody chain		
PS	Disclosure; Fig 6; 74pp; English.		
CC	The sequence is that of the reshaped CD4 antibody heavy chain		
CC	CD4VHNEW-Thr30. Reshaped CD4 antibody can be used to induce tolerance		
CC	against an antigen. It can also be used to alleviate autoimmune diseases		
CC	such as rheumatoid arthritis, and to prevent graft rejection. Tolerance		
CC	to a graft, e.g. an organ graft or a bone marrow transplantation can		
CC	also be useful to alleviate allergies. Tolerance to allergens could		
CC	also be achieved. See also R22753-R22763.		
SQ	Sequence	467 AA;	

Query Match	82.7%	Score 2848;	DB 4;	Length 467;	
Beat Local Similarity	87.0%;	Pred. No. 1.89e-222;			
Matches	410;	Conservative 32;	Mismatches 20;	Indels 9;	Gaps 6;
Db	6	ilflivatqvhsgvqlqesgqlvrpqtlltctvsgfftn-ygmawvrqpqgql	64		
Qy	6	FFLLVAAPRWLSQVQLQESGPGCLVKPSETLSLTCAVSGGSGCGYGWGHIQDPGKGL	65		
Db	65	ewlgtishdgsctyfrdsvkgrvtmldvsknqfslrlasvtaadtavvyrcarqg--tia	122		
Qy	66	EWIGSFYSSGNTYYPNLSKQSTVITDTSKQFSLKLSMTAADTAVYVCYRDLRFVW	125		
Db	123	g-i---r-h-wggslvtvssaastkqpsvflapaseketegtgtaalgcldkdyfpeptv	176		
Qy	126	GWYNNMFDMGPGVLVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTV	185		
Db	177	snwsgaltesghcfpavlqesgylsleavvtvpssslgtqtycnvnhkpsentckvdkkve	236		
Qy	186	SNWSGALTSGVHFFPAVLQSGCLYSLSVTVTPSSSLGTQTYCNVNHKPSNTKVDKAAE	245		
Db	237	pkscdkthtccppcappelggpsvflfpkpkdtlmrlertpevtcvvdvshedspevkn	296		
Qy	246	PKSCDKTHTCPPCAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKEN	305		
Db	297	wyvdgvevhnaktkpreegnystrvvvltvlhqdwlngkeyckvsnkalpapiecti	356		
Qy	306	WYVDGVEVHNAKTKPREEQYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETTI	365		
Db	357	skakgcprepqvtylpsrdeitknqvsitclvkgfyfypsdiavewesngqennmyktcpp	416		
Qy	366	SKAKGCPREPQVYTLPPSRDEITKNQVSLTCLVKGFPYPSDIAVESNGQEPENNYKTTTP	425		
Db	417	vldsdsqfflyskltdvkrwggqgnvfscsvmhealhnhvtdqklslepgak	467		

QY	426	VLDSDGSFFLYSKLVDSKSWQQNVFSCSVMEALHNHYTKSLSPCK	476
RESULT	4		
ID	R22757	standard; Protein; 470 AA.	
AC	R22757;		
DT	20-OCT-1992	(first entry)	
DE	Reshaped CAMPATH-1 antibody heavy chain.		
KW	Antigen; CDR; complementarity determining region; graft rejection;		
KW	autoimmune diseases; rheumatoid arthritis; allergy.		
OS	Rattus rattus.		
FH	Key	Location/Qualifiers	
FT	Region	50..54	
FT	/note=	"Complementarity determining region 1"	
FT	Region	69..87	
FT	/note=	"Complementarity determining region 2"	
FT	Region	101..110	
FT	/note=	"Complementarity determining region 3"	
FT	Peptide	1..19	
FT	/note=	"signal peptide"	
FT	Peptide	20..470	
FT	/note=	"mature peptide"	
PN	W09205274-A.		
PD	02-APR-1992.		
PF	16-SEP-1991; G01578.		
PR	17-SEP-1990; GB-020282.		
PA	(GORM/) GORMAN S D.		
PI	Clark M R, Cobbold S P, Gorman S D, Waldmann H.		
DR	WPI: 92-132139/16.		
DR	N-PSDB; Q23570.		
PT	Humanisation of antibodies binding to human CD4 antigen - by		
PT	mutation of framework-encoding regions of DNA encoding variable		
PT	domain of rat or mouse antibody chain		
PS	Disclosure; Fig 5; 74pp; English.		
CC	The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.		
CC	Reshaped CD4 antibody can be used to induce tolerance against an		
CC	antigen. It can also be used to alleviate autoimmune diseases such		
CC	as rheumatoid arthritis, and to prevent graft rejection. Tolerance		
CC	to a graft, e.g. an organ graft or a bone marrow transplantation can		
CC	also be useful to alleviate allergies. Tolerance to allergens could		
CC	also be achieved. See also R22754-R22763.		
SC	Sequence	470 AA;	

[illegible]

Db 238 vepkscdtkhtcpapellgpgsvflfppkpkdtlmistpvtcvvvdshedpvrk 297  
 QY 244 AEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 303  
 Db 298 fnwydvgevhnahtkpreeqynstyrsvvltvlhqdwlngkeyckvsnkalpapiak 357  
 QY 304 ENWYDVGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAP IEK 363  
 Db 358 tsiskagqprepqvyltppsdeltknqvsitclvkgfydpadiaveangpennykt 417  
 QY 364 TISKAGQPREPQVYTLPPSDELTKNQVSLTCLVKGFPDSDIAVENESNGQPENNYKT 423  
 Db 418 ppyldsdgfflyskltdvkarwqgnvfscsvmhcalnhnhtkqslslepak 470  
 QY 424 PPVLSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHALNHHTYTKSLSLSPGK 476

## RESULT 5

ID R24442 standard; Protein; 481 AA.  
 AC R24442;  
 DT 02-JAN-1992 (first entry)  
 DE Sequence of antibody molecule IgG1.  
 KW Antibody; immunoglobulin G1.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Misc difference 308  
 FT /label= N  
 FT /note= "Substn. to create glycan addition site"  
 FT Misc difference 310  
 FT /label= S  
 FT /note= "see above"  
 FT Misc difference 321  
 FT /label= N  
 FT /note= "see above"  
 FT Misc difference 329  
 FT /label= N  
 FT /note= "see above"  
 FT Misc difference 331  
 FT /label= S  
 FT /note= "see above"  
 FT Misc difference 356  
 FT /label= N  
 FT /note= "see above"  
 FT Misc difference 369  
 FT /label= N  
 FT /note= "see above"  
 PN W09209293-A.  
 PD 11-JUN-1992.  
 PF 18-NOV-1991; U08605.  
 PR 23-NOV-1990; US-618314.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PI Seed B, Walz G;  
 DR WPI; 92-215789/26.  
 DR N-PSDB; Q25443.  
 PT Inhibition of cell adhesion mediated through ELAM-1 mol. binding  
 PT - used in treating chronic inflammation, rheumatoid arthritis,  
 PT psoriasis, etc.  
 PS Disclosure; Fig 1; 46pp; English.  
 CC The IgG1, in its nascent form, bears no sialyl-Lex side chains. The  
 CC inventors designed a molecule including several such sites for  
 CC attachment of sialyl-Lex side chains (see R24442, FT). The  
 CC additional N-linked glycosylation sites are introduced at locations  
 CC which impair complement fixing and Fc receptor binding ability. They  
 CC are preferably located in the CH2 region of the Ig molecule.

CC Antibodies bearing multiple sialyl-Lex determinants are useful for  
 CC disrupting undesirable interactions between cells or proteins.  
 CC Disrupting this interaction has therapeutic applications, for  
 CC example, in minimising inflammation following tissue injury.  
 SQ Sequence 481 AA;

Query Match 81.1%; Score 2791; DB 5; Length 481;  
 Best Local Similarity 82.4%; Pred. No. 1.06e-217;  
 Matches 394; Conservative 35; Mismatches 46; Indels 3; Gaps 3;

Db 5 mndwtzrflffvvaatavqsvqlvqgaevktpgsvkvckasgttfss-yaiswvrq 63  
 QY 1 MKHLMFLLIV-AAPRWLVLSQVLQESGPGVLPKSETLSLTCVAVSGSISGGYGMQIRQ 59  
 Db 64 apqgglemwggilpifgtanyaqkfgrvrtitadeetaymelsalreadtavvyocard 123  
 QY 60 PPGKGLEWIGSFYSSSGNTYYPNLSKSQVTISTDTSKNQFSLKINSMTAADTAVYCYVRD 119  
 Db 124 ngaycggsgyqgfdpwggqgtlvtvsaastkgsfvfplapeekatsgtaalgclvkdy 183  
 QY 120 R-LFSVWGMVYNNWFDWPGVILVTVSSASTKCPSEVFLAPLSPKSTSGTALGCLVKDY 178  
 Db 184 fpeptvsvmsgalteqvhftfpavlgseglyslsvvtvpsselgtqtiyicnvnhkpsnt 243  
 QY 179 FPEPTVSWNSGALTSGVHTPEPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHRPSNT 238  
 Db 244 kvdkkvepkcdtkhtcpapellgpgsvflfppkpkdtlmistpvtcvvvdsheshe 303  
 QY 239 KVDKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHE 298  
 Db 304 dpevkfnwydvgevhnahtkpreeqynstyrsvvltvlhqdwlngkeyckvsnkalp 363  
 QY 299 DPEVKFNWYDVGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALP 358  
 Db 364 apiektiskagqprepqvyltppsdeltknqvsitclvkgfydpadiaveangqpen 423  
 QY 359 APIEKTISKAGQPREPQVYTLPPSDELTKNQVSLTCLVKGFPDSDIAVENESNGQPEN 418  
 Db 424 nykttppvldsdgfflyskltdvkarwqgnvfscsvmhcalnhnhtkqslslepak 481  
 QY 419 NYKTTPPVLSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHALNHHTYTKSLSLSPGK 476

## RESULT 6

ID R33311 standard; Protein; 453 AA.  
 AC R33311;  
 DT 05-JUL-1993 (first entry)  
 DE Humanised MaE11 Version 1 (intact IgG) heavy chain.  
 KW Antibody; high affinity; FCEH; low affinity; FCEL;  
 KW IgE receptor; histamine; mast cell; basophil; Kabat;  
 KW CDR; murine; MAE11; Fab; humaelivl.  
 OS Synthetic.  
 PN W09304173-A.  
 PD 04-MAR-1993.  
 PF 14-AUG-1992; U06860.  
 PR 14-AUG-1991; US-744768.  
 PR 07-MAY-1992; US-879495.  
 PA (GETH ) GENENTECH INC.  
 PI Jardieu PM, Presta LG;  
 DR WPI; 93-094004/11.  
 PT Polypeptide (s) binding to specific Fc epsilon receptors - act as  
 PT IgE antagonists; useful for treating and preventing IgE-mediated  
 PT disorders e.g. allergies  
 PS Example 4; Fig 3; 113pp; English.

CC Residues were selected from MaE11 and inserted or substituted into  
CC a human Fab antibody background (Vh region Kabat subgroup III and VI  
CC region kappa subgroup I). A first version, humael1v1 or version 1 is  
CC given below. The affinity of version 1 was assayed and found to be  
CC ca. 100 times lower than that of the donor antibody MaE11.  
CC Therefore, further modifications in the sequence of version 1  
CC were made.  
SQ Sequence 453 AA;

```
Query Match      80.8%; Score 2781; DB 6; Length 453;
Best Local Similarity 86.5%; Pred. No. 7.20e-217;
Matches 398; Conservative 23; Mismatches 29; Indels 10; Gaps 4;

Db 1 evqlveggglvpggsrlscavsgvsltsqyewnwiragpgkglawvasi-tydgstn 59
   :||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| : |||
Qy 20 QVQLQESGPGLVKPSETLSLTCVAVSGSISGGYGMGWIRQPPKGLIEWIGSFYSSGNTY 79
   :||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| : |||
Db 60 yadsvkgftrtsrddeknfylvlqmnaltaedtavvyrcargshy-----fghwhfawwq 113
   | :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : ||| |||
Qy 80 YNPSLKQVTLTDTSTKQFSLKNSMTAADTAVYTCVDRDLFSVVGWYANNW-FDWGCP 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 114 gtlvtvsaatkqgkpsvfplapsksetaggtaalglvkdypfpvvtvsmnsgaltsgv 173
   | ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 139 GVLVTVSSASTKG--PSVPEPLAPSSKTSGGTAAALGCLVKDYRPEPVPVWNSGALTSGV 196
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 htfpavlqseglyslsvvtvpssalgtqtyicnvnhkpsntkvdkkvepkcdtkhtcp 233
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 197 HTPFVAVLQSSGLYSLSVWVTPSSSLGTQTYICNVNHRKPSNTKVDKAEFKSCDKTHTCP 256
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 pcpapellgpgsvflfpkpkdtlmisrtpetvctvvvdshedpevkfnwvvdgvevha 293
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 257 PCPAPELLGPGSVFLFPKPKDTLMISRTPEVTCVVDVDSHEDPEVRFNWVVDGVEVHNA 316
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 294 ktprceqynetyrvvsvltvlhqdlnghgkeyckvknkalpapietktsakgprepq 353
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 317 KTKPREEQYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQ 376
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 354 vyltppsreentknqslclvkgfypsdiavewesngqpennykttppvldsdgffly 413
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 377 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLY 436
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 414 skltvdkerwqgnvfscsvmhhealnhhytqkelslspgk 453
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 437 SKLTVDKSRWQQGNVFSCSVMHHEALNHHTYTKSLSPGK 476
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT
ID R20057 standard; Protein; 475 AA.
AC R20057;
DT 25-MAR-1992 (first entry)
DE Heavy chain of 3D6 anti-HIV antibody.
KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;
KM complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= signal
FT Region 20..49
FT /label= Framework_1
FT Region 50..54
FT /label= CDR-1
FT Region 55..68
FT /label= Framework_2
FT Region 69..85
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FT /label= CDR_2      86..117
FT Region            Framework_3
FT /label= Framework_3
FT Region            118..134
FT /label= CDR_3      135..145
FT Region            Framework_4
FT /label= Framework_4
FT Region            146..475
FT /label= Constant_region
PN W09118983-A.
PD 12-DEC-1991.
PF 28-MAY-1991; 100067.
PR 29-MAY-1990; AT-001178.
PA (JUNG/) JUNGAUER A.
PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;
DR WPI; 92-007468/01.
DR N-PSDB; Q20066.
PT Recombinant protein which binds to complex viral antigen and
PT HIV-1 - contains variable region of antibody derived from 3D6
PT cell line, used for detecting HIV-1 antigen
PS Claim 2; Page 24; 52pp; German.
CC The variable region of the heavy chain is used in a recombinant
CC protein with the variable region from the kappa light chain of 3D6,
CC the two V regions being joined by a linker. The recombinant protein
CC binds to HIV gp160.
CC See also Q20067 and Q20068.
SQ Sequence 475 AA;

Query Match      80.5%; Score 2771; DB 3; Length 475;
Best Local Similarity 83.3%; Pred. No. 4.91e-216;
Matches 393; Conservative 31; Mismatches 45; Indels 3; Gaps 2;

Db 7 wiflailkg--vqcevqlvesggilvqgrrslrlscasgftfnd-yamhwvraqpgkq 63
   ||| ||| : | :||| ||| ||| ||| : ||| ||| ||| ||| : ||| ||| |||
Qy 5 WFFLLVLAAPRWLVLSQVLQESGPGLVKPSSETLSLTCVAVSGSISGGYGMGWIRQPPGK 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 lewvsgiswdesi:gyadvskgrftisrdnaknelylqmnslraedmalnyvcvkgdyd 123
   ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 65 LEWIGSFYSSTGNTYNPISKQVTSITDTSTKQFSLKNSMTAADTAVYTCVDRDLFSV 124
   ||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 eggyftvafdlwgggtmvtvasastkpsvfplapsksetaggtaalglvkdypfpv 183
   | : ||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 125 VGVYNNWFDMWGPVILVTVSSASTKGPSVEPLAPSSKTSGGTAAALGCLVKDYRPEPT 184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 vsmnsgaltsgvhtfpavlqseglyslsvvtvpssalgtqtyicnvnhkpsntkvdkv 243
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 185 VSNNSGALTSGVHTFPVAVLQSSGLYSLSVWVTPSSSLGTQTYICNVNHRKPSNTKVDKKA 244
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 epkscdtkhtcpccapellgpgsvflfpkpkdtlmisrtpetvctvvvdshedpevkf 303
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 245 EPKSCDKTHTCPPCPAPELLGPGSVFLFPKPKDTLMISRTPEVTCVVDVDSHEDPEVKF 304
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 nwyvdgvevhnaktkpreeqynstrvsvltvlhqdlnghgkeyckvknkalpapietk 363
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 305 NWYVDGVEVHNKTPREEQYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETK 364
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 isakgqprepqvyltppsreentknqslclvkgfypsdiavewesngqpennyktt 423
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 365 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 424
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 pvlsdgsefflyskltvdkerwqgnvfscsvmhhealnhhytqkelslspgk 475
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 425 PVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHHEALNHHTYTKSLSPGK 476
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Query Match 80.0%; Score 2755; DB 6; Length 476;  
Best Local Similarity 81.8%; Pred. No. 1.06e-214;  
Matches 390; Conservative 36; Mismatches 49; Indels 2; Gaps 2;

Query Match 19.

Query Match 79.0%; Score 2719; DB 8; Length 459;



Best Local Similarity 84.6%; Pred. No. 1.06e-211;  
Matches 389; Conservative 31; Mismatches 33; Indels 7; Gaps 4;

Db 7 vqcqvlesggvvgvqrsrlscasagftfsn-smhwraqpgkglewvavilydgn 65  
Qy 17 VLSQVLQESGGLVKVKTSETLSLTCVSGSISGCGYGMQIRQPPKGLWIGSFYSSG 76  
Db 66 hkfvyadvkgftisrdnknkntlylevkalqtdetgyvycirdqy---g-v--hrfdaw 119  
Qy 77 NTTYNESLKASQWTTTDTSTKQNFSLKLNMTAADTAVYTCVRDLFSVWGMVNNWEDW 136  
Db 120 qggclvtvssastkgsfvplapssketaggtaalglclvkdypfpvptvsmnsgalasv 179  
Qy 137 GPGVLTVSSASTKGSFVPLAPSSKTSGGTAALGLCLVKDYFEPVTVSMNSGALTSGV 196  
Db 180 htfpavlqsglyelsvvtvpssslgtqtyicnvnkhpkentkdkkvepkscdkthtctp 239  
Qy 197 HTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNKHGNTKVDKKAEPKSCDKTHTCP 256  
Db 240 pcpapellqgsvflfppkpkdtlmisrtpevtcvvvdshbedvknwydvgevhna 299  
Qy 257 PCPAPELLGGSFVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVFNWYDGEVHNA 316  
Db 300 tkpreeqynstyrsvvltvhlqdwlngkeyckvknkalpapiektiekakgprep 359  
Qy 317 KTKPREEQYNSTYRWVSVLTVLHQDWLNGKEYCKVKNKALPAPTEKTSKAKGQPREPQ 376  
Db 360 vyltpperdeltknqvelclvkgfypsdiavewesngpennnyktpvldsdgsffly 419  
Qy 377 VYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLY 436  
Db 420 skltvdksrwqgnvfscvmhealnhhytqkslslepgk 459  
Qy 437 SKLTVDKSRWQGNVFCSCVMHEALNHHTYQKSLSLSPGK 476

## RESULT 10

ID R42162 standard; Protein; 461 AA.  
AC R42162;  
DT 27-APR-1994 (first entry)  
DE Anti-HIV-1 recombinant antibody 447-52D heavy chain.  
KW Human immunodeficiency Virus; antigen; ELISA; recombinant antibody;  
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;  
KW acquired immune deficiency syndrome; chimeric antibody;  
KW surface glycoprotein gp120; V3 loop.  
OS Homo sapiens.  
PN W09319785-A.  
PF 14-OCT-1993.  
PD 23-MAR-1993; U02629.  
PR 01-APR-1992; US-861701.  
PA (MERI) MERCK & CO INC.  
PA (JOHN) JOHNSON L.S.  
PA (PFAR) PFARR D.S.  
PI Conley AJ, Emini EA, Johnson LS, Mark GE, Pfarr DS;  
DR WPI; 93-336600/42.  
DR N-PSDB; Q49834.  
PT New recombinant human antibody - with HIV neutralising activity  
PT against at least two isolates, useful for preventing or treating  
PT infection in diagnosis, etc.  
PS Example 9; Fig 2A; 154pp; English.  
CC EBV-transformed cell lines and mouse-human heterohybridomas  
CC producing human MAb specific for the gp120 V3 loop of HIV-1 MN  
CC isolate were obtained. MAb 447-52D was found to recognise the  
CC tetrapeptide motif GPGK, i.e. the Principal Neutralising

CC Determinant common to the V3 loop of different HIV isolates.  
CC A recombinant Ab was produced in which the H chain V region was  
CC derived from 447-52D and to which a signal sequence and a H chain  
CC intronic sequence are appended, fused to a fragment contg. a short  
CC intronic segment of the human gamma 1 C region and the human gamma  
CC 1 encoding domain in its genomic form.  
SQ Sequence 461 AA;

Query Match 78.9%; Score 2716; DB 8; Length 461;  
Best Local Similarity 85.1%; Pred. No. 1.88e-211;  
Matches 394; Conservative 23; Mismatches 38; Indels 8; Gaps 6;

Db 1 evqlvesggglvkgpgelrltcaagftfsdv--wlnwraqpgkglewvrikartdgg 58  
Qy 20 QVQLQESGGLVKVKTSETLSLTCVSGSISGCGYGM-QHTRQPPKGLWIGSFYS-SSGN 77  
Db 59 ttdyaasvkgftisrdskntlylgmslktedavyscttdgfmirgvaedyyvym 118  
Qy 78 TY-YNPSLKASQWTTTDTSTKQNFSLKLNMTAADTAVYTCVRDLFSVWGMV--YNNWF- 133  
Db 119 dwkggtvtvssastkgsfvplapssketaggtaalglclvkdypfpvptvsmnsgalt 178  
Qy 134 DWMGPGVLTVSSASTKGSFVPLAPSSKTSGGTAALGLCLVKDYFEPVTVSMNSGALT 193  
Db 179 egvhtfpavlqsglyelsvvtvpssslgtqtyicnvnkhpkentkdkkvepkcdkth 238  
Qy 194 SGVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNKHGNTKVDKKAEPKSCDKTH 253  
Db 239 tcpcpapellqgsvflfppkpkdtlmisrtpevtcvvvdshbedvknwydvgevev 298  
Qy 254 TCFPCPAPELLGGSFVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVFNWYDGEV 313  
Db 299 hnaktkpreeqynstyrsvvltvhlqdwlngkeyckvknkalpapiektiekakgpr 358  
Qy 314 HNAKTKPREEQYNSTYRWVSVLTVLHQDWLNGKEYCKVKNKALPAPTEKTSKAKGQPR 373  
Db 359 eqvytlpperdeltknqvelclvkgfypsdiavewesngpennnyktpvldsdgsf 418  
Qy 374 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 433  
Db 419 flyskltvdksrwqgnvfscvmhealnhhytqkslslepgk 461  
Qy 434 FLYSKLTVDKSRWQGNVFCSCVMHEALNHHTYQKSLSLSPGK 476

## RESULT 11

ID R43339 standard; Protein; 449 AA.  
AC R43339;  
DT 29-NOV-1993 (first entry)  
DE Completely humanised C4G1 Ig heavy chain.  
KW Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIb;  
KW monoclonal antibody; platelet agglutination; humanised antibody.  
OS Synthetic.  
PN W09313133-A.  
PD 08-JUL-1993.  
PE 15-DEC-1992; J01630.  
PR 20-DEC-1991; US-812111.  
PR 09-JUN-1992; US-895952.  
PR 11-SEP-1992; US-944159.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
PA (YAMA) YAMANOUCHI PHARM CO LTD.  
PI Co MS, Tao JY;  
DR WPI; 93-227275/28.  
PT Compens. contg. immunoglobulin specific for the GP-IIB and -IIIA



[illegible][illegible]

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US-08-487-550-12.rag

19

Qy 307 YVDGVEVHNKTRREEQYNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAIEXTIS 366  
Db 355 kagqgprepyvtlppstreentknqslctclvkgyfspdlaivesngqppennykttppv 414  
Qy 367 KMGQPREQYVTLPPSRDELTKQVSLCLVKGFPSDIAVESNGQPPENNYKTTTPV 426  
Db 415 ldsdgsfflyskltvdksrwqggnvfscvmhealhnhytqkslslspgk 464  
Qy 427 LDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKSLSLSPGK 476

RESULT 15

ID R40750 standard; Protein; 466 AA.  
AC R40750;  
DT 01-OCT-1993 (first entry)  
DE Sequence encoded by the heavy chain expression  
DE vector pAG4235.  
KW Chimeric monoclonal antibody; expression plasmid.  
OS Synthetic.  
PN W09311252-A.  
PD 10-JUN-1993.  
PF 24-NOV-1992; U10207.  
PR 26-NOV-1991; US-798696.  
PA (REGC ) UNIV CALIFORNIA.  
PI Haatings A, Morrison SL, Wims L;  
DR WPI; 93-197069/24.  
DR N-PSDB; Q43497.  
PT Expression plasmids and derivs. - used to produce protein  
PT molecules esp. chimaeric monoclonal antibodies  
PS Disclosure; Fig 3; 54pp; English.  
CC The expression plasmid pAG4235 (ATCC No. 75038) is claimed. It is  
CC used to express chimeric monoclonal antibodies. It contains genes  
CC with leader sequences and is functional. The variable region and  
CC constant regions exons were sequenced, however the other sequences  
CC are from published references and have not been verified for this  
CC particular plasmid. Regions for which there is no sequence  
CC information are indicated by N's with the length determined by sizes  
CC of fragments observed on agarose gels.  
SQ Sequence 466 AA;

Query Match 76.5%; Score 2632; DB 7; Length 466;  
Best Local Similarity 80.1%; Pred. No. 1.87e-204;  
Matches 382; Conservative 37; Mismatches 46; Indels 12; Gaps 6;  
Db 1 mdwlnllfpmasaglsqdiqlvsgpqlkpggetvkiackasgyftn-ygmmwvkqa 59  
Qy 1 MKHLWFFLLVAPRWVLSQVQLQESGPGLVKPSSETLSUTCAVSGGSISGGYGWGIKRP 60  
Db 60 gqgklwmqwtntgeptyteefkgrfaisletsantayllimlnknedatyfcarg- 118  
Qy 61 PKGLEWICGSFYSSGNTYINPILKQVITSTDTSKNQFSILKNSMTAADTAVYVCVRDR 120  
Db 119 ---g---hawgfaywgggtlvtvsaatkgpavfplapsekstsggtaalgcivkdyf 171  
Qy 121 LFSVWGMVYNNW-FDVWGPGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179  
Db 172 pepvtvwnsgaltsgvhtfpavllqsglyslsavvtvpesslgtqtyicnvnkhkpentk 231  
Qy 180 PEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHPNNTK 239  
Db 232 ydkkvepkcdkthtccpcapellggpsvflfppkpkdtlmisrtpevtcvvvdvshed 291  
Qy 240 VDKKAEPKSCDKHTCCPCAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVDSHED 299

Dec 17 15:26

US-08-487-550-12.rag

20

Db 292 pevknfwydvgevhnahtkpreeqynstyrsvavltvlhqdwlngkyckvsnkalpa 351  
Qy 300 PEVKFNWYVDGVEVHNKTRREEQYNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPA 359  
Db 352 piektisk--gqprepqvvtlppsrdeltnqvalctclvkgyfypediaivesngqppenn 409  
Qy 360 PIEKTIKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVESNGQPPENN 419  
Db 410 ykttppvldsdsqsflyskltvdkrwqggnvfscvmhealhnhytqkslslspgk 466  
Qy 420 YKTTTPVLDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKSLSLSPGK 476

Search completed: Tue Dec 17 15:40:34 1996  
Job time : 51 secs.

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SET AUHELP OFF

FILE 'WPIDS' ENTERED AT 07:40:35 ON 18 DEC 96

E ANDERSON D/AU  
L1 87 S E3,E22  
E BRAMS P/AU  
L2 13 S E3  
E HANNA N/AU  
L3 20 S E3-E7  
E SHESTOWSK W/AU  
L4 1 S E4  
L5 0 S L1 AND L2 AND L3 AND L4  
L6 120 S L1-L4  
L7 0 S B7 AND L6  
L8 0 S (B71 OR B72) AND L6  
L9 0 S B() 7 AND L6  
E 16C10  
E 7C10  
L10 1 S E3  
E 20C9  
L11 1 S E3  
E 7B6  
L12 1 S E3  
L13 1 S L10-L12 AND MONOCLONAL?

FILE 'HCAPLUS' ENTERED AT 07:49:36 ON 18 DEC 96

E ANDERSON D/AU  
L14 272 S E3,E33,E34,E85,E86,E88,E89  
E BRAMS P/AU  
L15 7 S E3,E4  
E HANNA N/AU  
L16 100 S E3-E12  
E SHESTOWSK /AU  
L17 4 S E4,E5  
L18 0 S L14 AND L15 AND L16 AND L17  
L19 380 S L14-L17  
L20 0 S L19 AND B7  
L21 0 S L19 AND B7#  
L22 429 S B7() (1 OR 2)

L23 28 S 16C10 OR 7C10 OR 20C9 OR 7B6  
L24 0 S L22 AND L23  
L25 0 S L19 AND L23  
L26 2 S B7 AND L23  
L27 45 S (?16C10? OR ?7C10? OR ?20C9?)/IA  
L28 1 S P7B6  
L29 46 S L27,L28  
L30 0 S L29 AND L19  
L31 2 S L27 AND B7  
L32 3 S L26,L28,L31

FILE 'BIOSIS' ENTERED AT 07:59:57 ON 18 DEC 96

E ANDERSON D/AU  
L33 1087 S E3,E30  
E BRAMS P/AU  
L34 20 S E3  
E HANNA N/AU  
L35 215 S E3-E11  
E SHESTOWSK /AU  
L36 4 S E4,E5  
L37 0 S L33 AND L34 AND L35 AND L36  
L38 1321 S L33-L36  
L39 0 S L38 AND B7  
L40 19 S 16C10 OR 7C10 OR 20C9 OR 7B6  
L41 0 S L38 AND L40  
L42 2 S L40 AND B7

FILE 'USPATFULL' ENTERED AT 08:01:24 ON 18 DEC 96

E ANDERSON D/AU  
L43 7 S E4,E26,E28,E31  
E BRAMS P/AU  
L44 3 S E4  
E HANNA N/AU  
L45 11 S E4,E5  
E SHESTOWSK /AU  
L46 1 S E4  
L47 0 S L43 AND L44 AND L45 AND L46  
L48 22 S L43-L46  
L49 0 S L48 AND B7/BI,AB  
L50 19 S (16C10 OR 7C10 OR 20C9 OR 7B6)/BI,AB  
L51 0 S L50 AND L48  
L52 3 S L50 AND B7/BI,AB  
L53 0 S L52 AND (MONOCLONAL OR ANTIBOD? OR MAB#)/BI,AB

FILE 'MEDLINE' ENTERED AT 08:04:11 ON 18 DEC 96

E ANDERSON D/AU  
L54 686 S E3,E24  
E BRAMS P/AU  
L55 8 S E3  
E HANNA N/AU  
L56 136 S E3-E10  
E SHESTOWSK /AU  
L57 9 S E2,E4-E7  
L58 0 S L54 AND L55 AND L56 AND L57  
L59 837 S L54-L57  
L60 0 S L59 AND B7  
L61 16 S 16C10 OR 7C10 OR 20C9 OR 7B6  
L62 0 S L59 AND L61  
L63 2 S L61 AND B7

FILE 'EMBASE' ENTERED AT 08:06:01 ON 18 DEC 96

E ANDERSON D/AU  
L64 605 S E3,E27  
E BRAMS P/AU  
L65 9 S E3  
E HANNA N/AU  
L66 124 S E3-E8  
E SHESTOWSK /AU  
L67 3 S E4,E5  
L68 0 S L64 AND L65 AND L66 AND L67  
L69 739 S L64-L67  
L70 0 S L69 AND B7  
L71 11 S 16C10 OR 7C10 OR 20C9 OR 7B6  
L72 2 S L71 AND B7  
L73 0 S L69 AND L71  
L74 2 S L71 AND B7

FILE 'WPIDS, HCAPLUS, BIOSIS, MEDLINE, EMBASE' ENTERED AT 08:08:28  
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L75 4 DUP REM L13 L32 L42 L63 L72 (6 DUPLICATES REMOVED)

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=> d bib ab 1-4

L75 ANSWER 1 OF 4 HCAPLUS COPYRIGHT 1996 ACS DUPLICATE 1  
AN 1994:75033 HCAPLUS  
DN 120:75033  
TI Induction of B cell costimulatory function by recombinant murine  
CD40 ligand  
AU Kennedy, Mary K.; Mohler, Kendall M.; Shanebeck, Kurt D.; Baum,  
Peter R.; Picha, Kathleen S.; Otten-Evans, Carol A.; Janeway,  
Charles A., Jr.; Grabstein, Kenneth H.  
CS Immunex Res. and Dev. Corp., Seattle, WA, USA  
SO Eur. J. Immunol. (1994), 24(1), 116-23  
CODEN: EJIMAF; ISSN: 0014-2980  
DT Journal  
LA English  
AB T cell-dependent regulation of B cell growth and differentiation  
involves an interaction between CD40, a B cell surface mol., and the  
CD40 ligand (CD40L) which is expressed on activated CD4+ T cells.  
Recombinant membrane-bound murine CD40L induces B cells to express  
costimulatory function for the proliferation of CD4+ T cells.  
CD40L- or lipopolysaccharide (LPS)-activated, but not  
control-cultured B cells were strong costimulators and anti-CD3 or  
alloantigen-dependent T cell responses. The mol. interactions  
responsible for the increased costimulatory functions were examd. by  
analyzing the activated B cells for changes in the expression of two  
costimulatory mols., B7 and heat-stable antigen (HSA), as  
well as by the use of antagonists of B7 and HSA (CTLA4.Fc  
and 20C9, resp.). The expression of both B7 and  
HSA was enhanced on B cells activated with LPS. The costimulatory  
activity of the LPS-activated B cells was dependent on both  
B7 and HSA and was completely inhibited in the presence of a  
combination of CTLA4.Fc and 20C9. In contrast, activation  
of B cells and CD40L induced the expression of B7 but did  
not enhance the expression of HSA. In addn. the costimulatory



activity of the CD40L-activated B cells was partially, but not completely, inhibited by the combination of CTLA4.Fc and **20C9**. Thus, CD40L regulates costimulatory function of B cells in part by inducing the expression of **B7**, and CD40L-activated B cells may express an addnl. costimulatory activity that is not assocd. with LPS-activated B cells.

L75 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 1996 ACS  
 AN 1993:511509 HCAPLUS  
 DN 119:111509  
 TI 7B6, a ubiquitous mRNA: with significant homology to L41 human ribosomal protein RNA  
 AU Francis, S. E.; Duff, G. W.  
 CS Sect. Mol. Med., Univ. Sheffield, Sheffield, S10 2JF, UK  
 SO Nucleic Acids Res. (1993), 21(12), 2944  
 CODEN: NARHAD; ISSN: 0305-1048  
 DT Journal  
 LA English  
 AB The nucleotide sequence of a 350 base pair cDNA clone previously designated **p7B6** is reported here. This clone has been used as an invariant control in Northern blot anal. but no DNA sequence was available. The cDNA hybridizes to a constantly expressed mRNA that appears to be abundant in human tissue and mammalian cell lines cultured in different physiol. conditions, thus providing a good control transcript that may be very useful for RNA quantification. The cDNA sequence was obtained from the original clone (**p7B6**/pBR322) using a conventional double-stranded sequencing method. FASTA searching of the EMBL database revealed that **p7B6** shared homol. (95.4% identity in a 283bp overlap) to the mRNA for the human ribosomal protein L41 which participates in amino acyl-tRNA binding ensuring fidelity in translation of mRNA. Now that the cDNA sequence for **p7B6** is available, it may also prove useful as an invariant control in quant. RT-PCR expts. with eukaryotic cells and tissues.

L75 ANSWER 3 OF 4 WPIDS COPYRIGHT 1996 DERWENT INFORMATION LTD  
 AN 92-270165 [33] WPIDS  
 DNN N92-206513 DNC C92-120444  
 TI New **monoclonal** antibody specific for Derf 11 - useful for immunologically identifying and determining Derf 11.  
 DC B04 D16 S03  
 IN AKAGAWA, M; ANDOH, T; HAYASHI, Y; MORI, T; SUGIYAMA, S  
 PA (ASAK) ASAHI BREWERIES LTD; (TORI) TORII & CO LTD; (ASAH) ASAHI KASEI KOGYO KK; (TORI) TORII YAKUHHN KK  
 CYC 4  
 PI EP 498124 A1 920812 (9233)\* EN 20 pp  
 AU 9187026 A 920827 (9242)  
 CA 2054551 A 920807 (9243)  
 JP 05207892 A 930820 (9338) 12 pp  
 US 5286628 A 940215 (9407) 15 pp  
 AU 654506 B 941110 (9445) ,  
 CA 2054551 C 960604 (9634)  
 JP 02516842 B2 960724 (9634) 10 pp  
 ADT EP 498124 A1 EP 91-312058 911227; AU 9187026 A AU 91-87026 911106;  
 CA 2054551 A CA 91-2054551 911030; JP 05207892 A JP 91-35018 910206;  
 US 5286628 A US 91-798483 911126; AU 654506 B AU 91-87026 911106; CA 2054551 C CA 91-2054551 911030; JP 02516842 B2 JP 91-35018 910206  
 FDT AU 654506 B Previous Publ. AU 9187026; JP 02516842 B2 Previous Publ. JP 05207892

PRAI JP 91-35018 910206

AB EP 498124 A UPAB: 931025

A new **monoclonal** antibody (Ab) selectively recognises Derf II (the major allergen of the house dust mite *Dermatophagoides farinae*); is of IgG or IgM class and is produced by immunising a mammal with Derf II. Also new are hybridoma cell lines which produce Ab.

Pref. Ab are designated 1B2(FERM BP-3247); **7C10** (BP-3248); 15E11 (BP-3249); 18G8(BP-3250); 13A4(BP-3251) and 24B7(BP-3252), and may be labelled with an enzyme, fluorophore or chemiluminescent cpd.

USE/ADVANTAGE - Ab are useful (1) in affinity chromatography for purification of Derf II (for use in desensitisation therapy) and (2) as immunoassay reagent for detecting and quantifying Derf II, e.g. in house dust. Derf II is a major allergen in cases of bronchial asthma, rhinitis, etc. This assay is simpler, more sensitive (down to 10ng/ml Derf II) and more specific than known methods which use antibodies raised against extracts of the mites.

1/8

Dwg.1/8

L75 ANSWER 4 OF 4 HCAPLUS COPYRIGHT 1996 ACS

DUPLICATE 2

AN 1993:57667 HCAPLUS

DN 118:57667

TI Co-stimulation of murine CD4 T cell growth: cooperation between **B7** and heat-stable antigen

AU Liu, Yang; Jones, Bryan; Brady, William; Janeway, Charles A., Jr.; Linley, Peter S.

CS Sch. Med., Yale Univ., New Haven, CT, USA

SO Eur. J. Immunol. (1992), 22(11), 2855-9

CODEN: EJIMAF; ISSN: 0014-2980

DT Journal

LA English

AB The contributions of B cell activation antigen **B7**/BB1 and heat-stable antigen (HSA) to the co-stimulatory activity of antigen-presenting cells (APC) were evaluated. Mouse **B7** provides co-stimulatory activity for murine CD4 T cells in anti-CD3-induced proliferation. Human CTLA4Ig, a chimeric mol. comprising the extracellular region of CTLA-4 fused to an Ig C.gamma. fragment, binds to murine **B7**. Therefore, human CTLA4IG and the hamster anti-HSA monoclonal antibody **20C9** were used to analyze the relative contributions of **B7** and HSA to the co-stimulatory activity of murine spleen APC. The data reveal that both murine **B7** and HSA are expressed by dendritic cells and by low-d. spleen B cells. Either CTLA4Ig alone or anti-HSA alone inhibited CD4 T proliferation to anti-CD3 by >90%, while CTLA4Ig and anti-HSA together were far more efficient in inhibiting clonal expansion of CD4 T cells. Thus, functionally defined co-stimulation involves at least **B7** and HSA; perhaps signals delivered by **B7** and HSA synergize in promoting T cell growth.